

The AnyBody™ Modeling System

Tutorials

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Tutorials

The AnyBody tutorials are step by step introductions to the use of the AnyBody system and in particular to construction of models in AnyScript. The tutorials are tightly linked to a collection of demo AnyScript files. These samples are usually developed as a response to popular requests by our users. The demo comes first, and a tutorial is subsequently developed around it.

This pdf-document is a collection of the tutorials exported directly from the AnyBody web page. Each of the following chapter is indeed one tutorial. We apologize for broken links and other parts of the text that is not well-designed as a text document in this format. This document is primarily aimed at printing the text, in case you prefer to read a paper version. When working with the tutorials, we recommend that you use an electronic version, either the online version or a version installed on your computer together with AnyBody.

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Getting Started



This tutorial is the starting point for new users. Its purpose is to allow users to get the first model up and running fairly quickly.

The AnyBody Modeling System can be approached on a number of levels depending on the amount of detail the modeling task requires. Listing the approaches in top-down order may produce the following:

- Loading a model defined by somebody else and changing simple parameters like the applied load or the posture. For instance, the so-called StandingModel from the model repository allows for addition of loads to certain predefined points on the model, and the system will compute the muscular reactions.
- Modifying a model made by somebody else but similar to what you want to obtain. For instance, one of the bicycle models from the repository could be changed into a recumbent bike.
- Building a new model by taking a predefined collection of body parts from the repository and equipping it with boundary conditions and an environment to interact with. For instance, it is rather

easy to create a model of a gymnastic exercise on the floor this way.

- Constructing a model from single predefined body parts in the repository. This allows for detailed control of which body parts are included in the model and may be useful for, for instance, detailed investigations of the internal forces in a single limb.
- Constructing a body model and its environment bottom-up. This is recommended for users interested in development models that are not covered by the current model repository. This could either be detailed models of missing body parts or perhaps single joints, or it could be models of various animals. The basic steps of such bottom-up model construction are described in the tutorial [Getting Started with AnyScript](#), which is a good place to start for new users, even if you do not plan to build models bottom-up.

These various levels of model building complexity are covered in [The Building Block Tutorial](#).

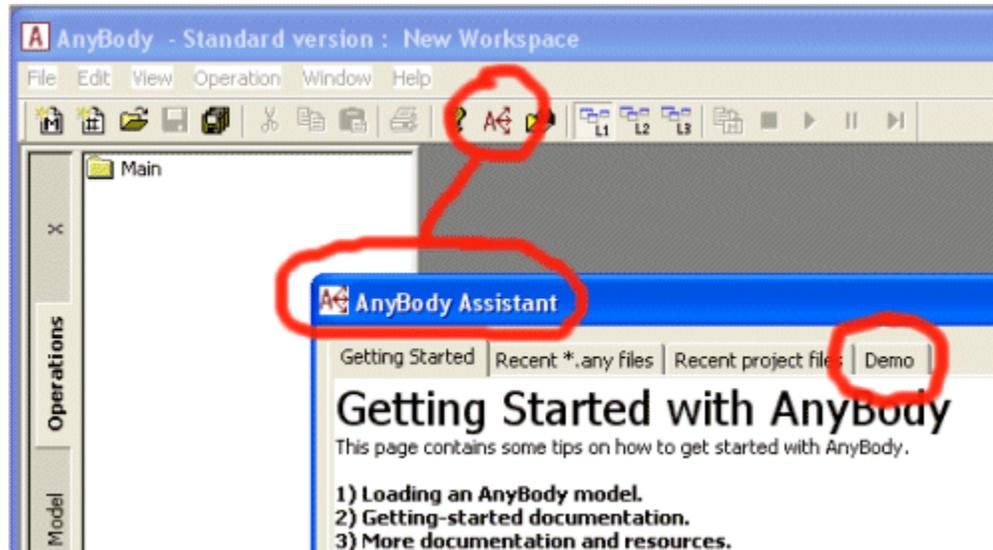
As you can see above, the more detailed approaches are covered by other tutorials. To get you up and running quickly, we shall take the top-down approach in this tutorial and use the model library to accomplish the following:

1. Load the predefined standing model, place it in a given posture, and apply an external force to it.
2. Modify the predefined standing model to carry a hand bag.
3. Create a new model and import a predefined collection of body parts from the library to obtain a model of a simple gymnastics exercise.

This entire tutorial relies heavily on the body model repository. It is a library of predefined models and body parts developed by scientists as a research undertaking. The models are placed in the public domain and are therefore totally open to scrutiny and are consequently improved and changed constantly. The effort is coordinated by the AnyBody Research Project at Aalborg University in Denmark. If you are a new user and unfamiliar with the structure of the repository, then it is strongly recommended that you pop over to the scientific homepage for a short interlude to familiarize yourself with the structure and idea behind it. When you feel familiar with the ideas, come back here and continue the tutorial. The link to the repository on the scientific homepage is here: www.anybody.aau.dk/Repository/.

Before you continue you must download the entire repository and save it on your hard disk. A selection of models from the repository are included in the demo collection which is installed with AnyBody. These demo models should be sufficient for your work with this and other tutorials, but because the repository keeps getting updated it may be a good idea to download and unpack the newest version from www.anybody.aau.dk/Repository/ before you start any serious modeling work.

The demo models, including the Standing Model to be used in this tutorial, are available from the Demo tab of the AnyBody Assistant dialog box.



When you open AnyBody for the first time, the Demo tab does not contain any models, but only a short guide on how to extract the demo models. After having done this, brief descriptions and links to the models are available in the tab. In addition, it is easy to reinstall the demo models later, which may be useful when you have been playing around with them for a while; this way you can reset all the changes you have made. You can also reinstall them to a new location, if you wish to keep your own changes to the first installation.

Now you are all set to go, and you can proceed with the [lesson 1: Using the standing model](#).

Lesson 1: Using the standing model

The model repository contains a number of applications that are generic in nature and can serve dual purposes: Either they can be used with minor modifications or they can with minor modifications become a model of something else. The Standing Model is one of these general applications, and we shall use it here by virtue of its first ability, i.e. pretty much as it is.

The standing model can be found in the repository under ARep/Aalborg. This position indicates that it is an application as opposed to merely a body part, and that it was developed by the AnyBody Research Group at Aalborg University. The model comprises most of the available body parts in the library. The main file is called StandingModel.Main.any, and this is the one you must load.

You can open the file with the file manager in AnyBody or by Windows Explorer, but it can be recommend that you use the demo files installed together with AnyBody. In this case, you can take the shortcut via the the Demo tab of the AnyBody Assistant dialog box. The Demo tab will contain links to many interesting models including the Standing Model.

Before you hit the load button, please have a look at the structure of the main file. The first part of it should look like this:

```
Main = {
    #include "DrawSettings.any"

    AnyFolder Model={
        AnyFolder HumanModel={
```

```

//This model is only for kinematic analysis and should be used when playing
//around with the kinematics of the model since leaving the muscles out, makes
//the model run much faster
#include
"..\..\..\BRep\Aalborg\BodyModels\FullBodyModel\BodyModel_NoMuscles.any"

//This model uses the simple constant force muscles
//#include "..\..\..\BRep\Aalborg\BodyModels\FullBodyModel\BodyModel.any"

//This model uses the simple constant force muscles for shoulder-arm and spine
//but the 3 element Hill-type model for the legs
//Remember to calibrate the legs before running the inverse analysis
//This is done by pressing Main.Bike3D.Model.humanModel.CalibrationSequence in
the
//operationtree(lower left corner of screen)
//#include "..\..\..\BRep\Aalborg\BodyModels\FullBodyModel\BodyModel_Mus3E.any"

AnyFolder StrengthParameters={
  AnyVar SpecificMuscleTensionSpine= 90; //N/cm^2
  AnyVar StrengthIndexLeg= 1;
  AnyVar SpecificMuscleTensionShoulderArm= 90; //N/cm^2
};

//Pick one of the scaling laws
//Do not scale
#include "..\..\..\BRep\Aalborg\Scaling\ScalingStandard.any"
//Scaling uniformly in all directions to match segments lengths
//#include "..\..\..\BRep\Aalborg\Scaling\ScalingUniform.any"
//Scaling taking length and mass of the segments into account
//#include "..\..\..\BRep\Aalborg\Scaling\ScalingLengthMass.any"
//Scaling taking length, mass and fat of the segments into account
//#include "..\..\..\BRep\Aalborg\Scaling\ScalingLengthMassFat.any"

//      Scaling={
//          #include "..\..\..\BRep\Aalborg\Scaling\AnyFamilyAnyJack.any"
//      };
};

```

Please notice that depending on who touched the file last, the choice of body model and scaling option as defined by the lines commented in or out may be different for you than shown above. Please make sure that you have chosen the BodyModel_NoMuscles and the ScalingStandard options, and that the Scaling folder is commented out.

The standing model has a few things, which are predefined, and some that you can modify. Here is a short list:

- The model is supported by having both its feet rigidly connected to ground. This condition applied no matter what posture the model is put into.
- The posture of the model is controlled via angles for all major joints except the ankles. So the model has a place where joint angles can be specified directly, and the model will assume the posture defined by the joint angles. We shall return to this topic shortly.
- The model automatically balances its posture by means of the ankle angles such that its collective center of mass remains vertically above the ankle joints. For instance, if the model extends the arms in front of it, then the ankles will adjust and move the entire model slightly backwards to maintain the balance.
- The model has a set of predefined points to which can be applied three-dimensional external forces simply defined as spatial vectors. When doing so, the muscles of the model will be recruited to

balance the external forces. Please notice that it is possible to apply an external force large enough to require tension between the feet and the floor. Because of the rounding condition of the feet such a tension will be provided by the model but the situation may not be realistic because real feet rarely stick to the ground.

It is time to load the model. You do this by pressing one of the Load Model buttons that look like this  and are located in left hand side of the toolbar of the AnyScript Editor windows and on the main frame toolbar. F7 is a convenient shortcut when reloading the same model many times. Since the model currently has no muscles, it should load very quickly. Pressing the menu Window -> Model View (new) should produce the following result:



The icons in the toolbar at the top of the Model View window allows you to modify the image, zoom, pan, rotate, etc. They should be mostly self explanatory. Now is a good time to play a bit around with them and

familiarize yourself with the options.

Having loaded the model it is time to proceed to [lesson 2: Controlling the posture](#).

Lesson 2: Controlling the posture

The Standing Model has been developed to a fairly complex level, automating many of the operations that are necessary to specify the posture of a full body model. The short story about the kinematics of the model is that it is based on a specification of angles in all the joints. These specifications can be found in one of the model files, mannequin.any. You can see where this file is included if you scroll down a bit in the StandingModel.any file until you come to this point:

```
//This file contains joint angles which are used at load time for
//setting the initial positions
#include "Mannequin.any"
```

If you double-click the Mannequin.any file name in the editor window, then the file opens up a new window. You will see a file with the following structure:

```
AnyFolder Mannequin = {
    AnyFolder Posture = {
        AnyFolder Right = {
        };
        AnyFolder Left = {
        };
    };
    AnyFolder PostureVel={
        AnyFolder Right = {
        };
        AnyFolder Left = {
        };
    };
    AnyFolder Load = {
        AnyFolder Right = {
        };
        AnyFolder Left = {
        };
    }; // Loads
};
```

(We have removed all the stuff in between the braces.) This file is typical for the AnyScript language in the sense that it is organized into so-called folders, which is a hierarchy formed by the braces. Each pair of braces delimits an independent part of the model with its own variables and other definitions.

Everything in this file is contained in the Mannequin folder. It contains specifications of joint angles, movements, and externally applied loads on the body. Each of these specifications is again subdivided into parts for the right and left hand sides of the body respectively.

The first folder, Posture, contains joint angle specifications. You can set any of the joint angles to a reasonable value (in degrees), and when you reload the model it will change its posture accordingly. Please make sure that the values are as follows:

```

AnyFolder Right = {
  //Arm
  AnyVar SternoClavicularProtraction=-23; //This value is not used for initial
position
  AnyVar SternoClavicularElevation=11.5; //This value is not used for initial
position
  AnyVar SternoClavicularAxialRotation=-20; //This value is not used for initial
position

  AnyVar GlenohumeralFlexion = 0;
  AnyVar GlenohumeralAbduction = 10;
  AnyVar GlenohumeralExternalRotation = 0;

  AnyVar ElbowFlexion = 0.01;
  AnyVar ElbowPronation = 10.0;

  AnyVar WristFlexion =0;
  AnyVar WristAbduction =0;

  AnyVar HipFlexion = 0.0;
  AnyVar HipAbduction = 5.0;
  AnyVar HipExternalRotation = 0.0;

  AnyVar KneeFlexion = 0.0;

  AnyVar AnklePlantarFlexion =0.0;
  AnyVar AnkleEversion =0.0;
};

```

When these parameters are set for the right hand side, the left hand side automatically follows along and creates a symmetric posture. This happens because each of the corresponding settings in the Left folder just refers back to the setting in the right folder. The ability to do this is an important part of the AnyScript language: Anywhere a number is expected, you can substitute a variable.

If at any time you want a non-symmetric posture, simply replace some of the variable references in the Left folder by numbers of your choice.

Further down in the Mannequin.any file you find the folder PostureVel. This is organized exactly like Posture, but the numbers you specify here are joint angle velocities in degrees per second. For now, please leave all the values in this folder to zero.

Finally, the last section of the file is named Load. At this place you can apply three-dimensional load vectors to any of the listed points. These load vectors are in global coordinates, which means that x is forward, y is vertical, and z is lateral to the right. Let us apply a vertical load to the right hand as if the model was carrying a bag:

```

AnyFolder Load = {
  AnyVec3 TopVertebra = {0.000, 0.000, 0.000};

  AnyFolder Right = {
    AnyVec3 Shoulder = {0.000, 0.000, 0.000};
    AnyVec3 Elbow = {0.000, 0.000, 0.000};
    AnyVec3 Hand = {0.000, -50.000, 0.000};
    AnyVec3 Hip = {0.000, 0.000, 0.000};
    AnyVec3 Knee = {0.000, 0.000, 0.000};
    AnyVec3 Ankle = {0.000, 0.000, 0.000};
  };
  AnyFolder Left = {
    AnyVec3 Shoulder = {0.000, 0.000, 0.000};
    AnyVec3 Elbow = {0.000, 0.000, 0.000};
  };
};

```

```

AnyVec3 Hand      = {0.000, 0.000, 0.000};
AnyVec3 Hip       = {0.000, 0.000, 0.000};
AnyVec3 Knee      = {0.000, 0.000, 0.000};
AnyVec3 Ankle     = {0.000, 0.000, 0.000};
};
}; // Loads

```

The downward load of -50 N in the right hand roughly corresponds to a weight of 5 kg. To enable the model to actually carry the load we must equip it with muscles. This is done by selecting a body model with muscles:

```

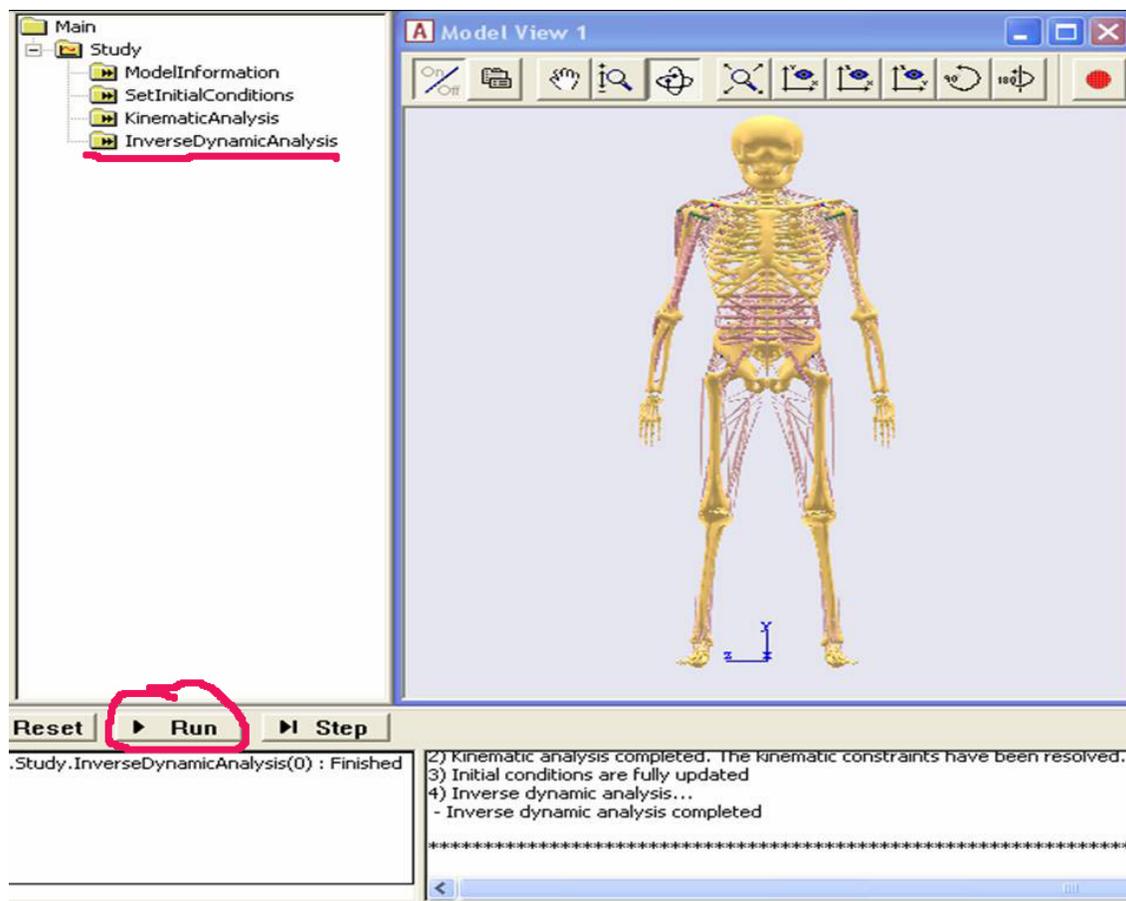
//This model should be used when playing around with the model in the
//initial modelling phase since leaving the normal muscles out, makes the
//model run much faster. The model uses artificial muscles on each dof. in
//the joints which makes it possible also to run the inverse analysis.
//#include "..\..\..\BRep\Aalborg\BodyModels\FullBodyModel\BodyModel_NoMuscles.any"

//This model uses the simple constant force muscles
#include "..\..\..\BRep\Aalborg\BodyModels\FullBodyModel\BodyModel.any"

```

When you reload the model (by pressing F7) it will take more time than before because it is now equipped with more than 500 muscles. If you have done everything right, you should see the comforting message 'Loaded Successfully' in the message window at the lower left hand side of the AnyBody main frame window. Now it is time to analyze muscle and joint forces.

Also at the upper left hand side of the screen you will see a tree containing 'Main' and 'Study'. If you unfold 'Study' you will get the following:



If you click once on `InverseDynamicAnalysis` and then on the `Run` button in the bottom of the window then the system will start analyzing the muscle and joint forces in the model under the influence of gravity and the load we applied to the hand. This takes a few seconds during which you will see the muscles standing out from the body and subsequently falling into place. When the analysis is finished you will notice a slight color change in the muscles and also some bulging, primarily in the right arm. The bulging is proportional to the force in each muscle, and the degree of red color is proportional to the muscles tone.

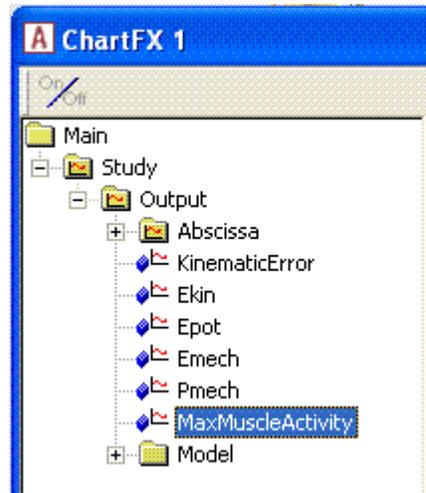
You have just completed your first analysis of an AnyBody model. In the next lesson we shall briefly examine the results. [Lesson 3: Reviewing analysis results.](#)

Lesson 3: Reviewing analysis results

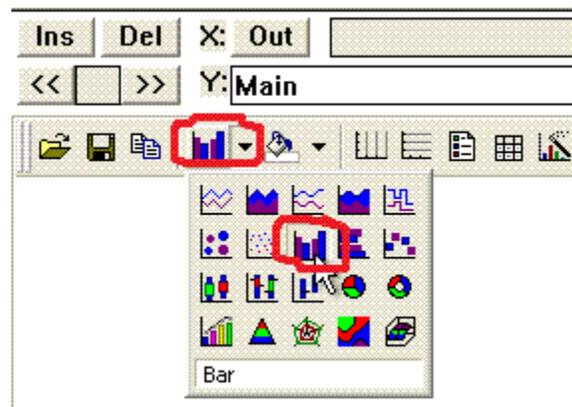
The muscle bulging in the Model View window provides an immediate feedback on the overall stress state of the body, but it does not give much detailed information. For detailed investigation of results, the system provides several charting facilities. Here we shall just review the basic functionality: The ChartFX View. It provides the basic ability to make two-dimensional diagrams depicting the results. You can also export the graphs to the clipboard on several different formats or as text for pasting into a spreadsheet.

The first step is to click `Window -> ChartFX 2D (new)`. A new window containing a blank field in the middle and a tree view in the left hand pane appears.

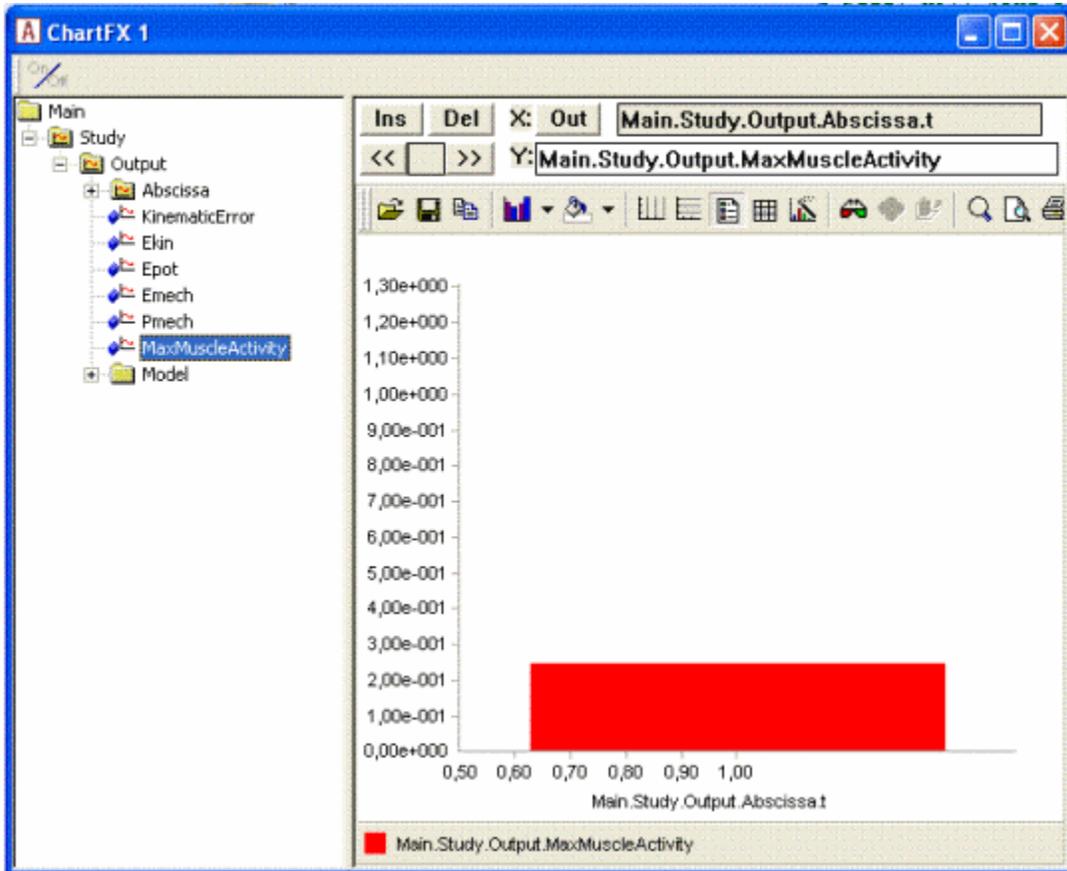
The tree expands to reveal the entire structure of output data generated by AnyBody. Every element in the model generates some form of output from the analysis, so the tree is very large. One of the first nodes you encounter is the `MaxMucleActivity` variable:



Clicking the node produces an empty coordinate system in the large field. The reason why it is empty is that the standard setting of the ChartFX View is to display time-varying data for moving models. In this simple case our model is static, so it does not make much sense to draw curves. Instead we shall switch the setting to Bar diagrams in by the Gallery button in the toolbar:

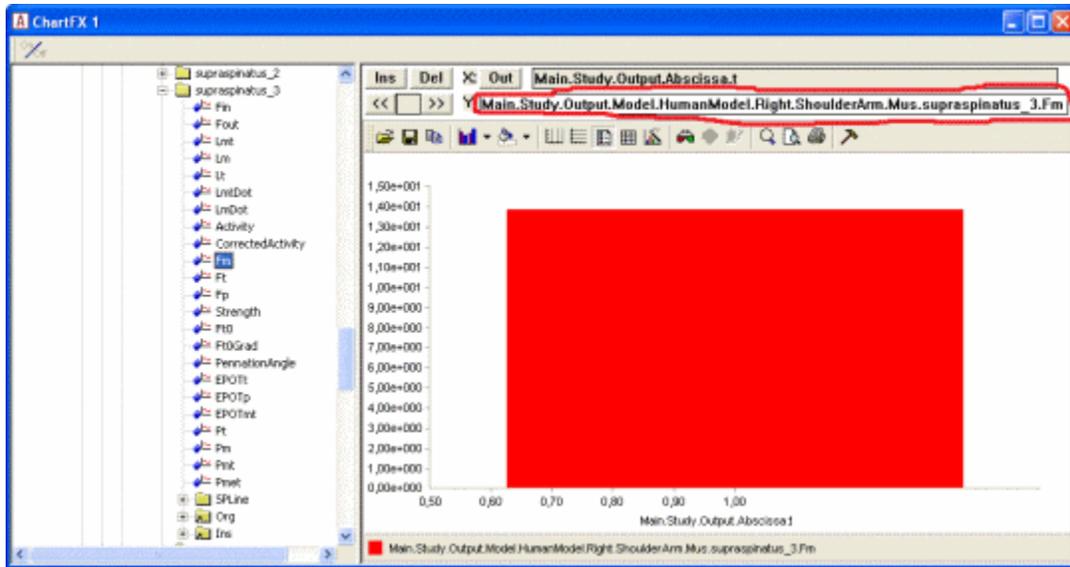


You will obtain the following Image:



This tells you that to stand upright and carry the 50 N load in the right hand, the model is using $4.00e-001 = 40\%$ of its maximum voluntary contraction. This means that the relative load of the muscle with the highest activity in the system is 40% of the muscle's strength. Even though one number is a very simplified way of regarding a system with hundreds of muscles, there are good mathematical reasons why this particular number is a good measure of the human effort of a particular task.

You can obtain more detailed information if you expand the Model branch in the tree view on the left hand side of the bar diagram. Going down through Model -> HumanModel -> Right -> ShoulderArm -> Mus gives you a long list of all the muscles in the right shoulder and arm. A bit down this list you can find the rotator cuff muscle supraspinatus, which tends to be one of the sources of rotator cuff pain. Like many of the muscles in the model, the anatomical muscle supraspinatus is divided into several mechanical branches to account for fibers going in different directions and attaching to different bones. If you open up Supraspinatus_3 you can find the property Fm inside. Click it once, and you should see a new bar illustrating the force in this muscle element similar to the picture below.



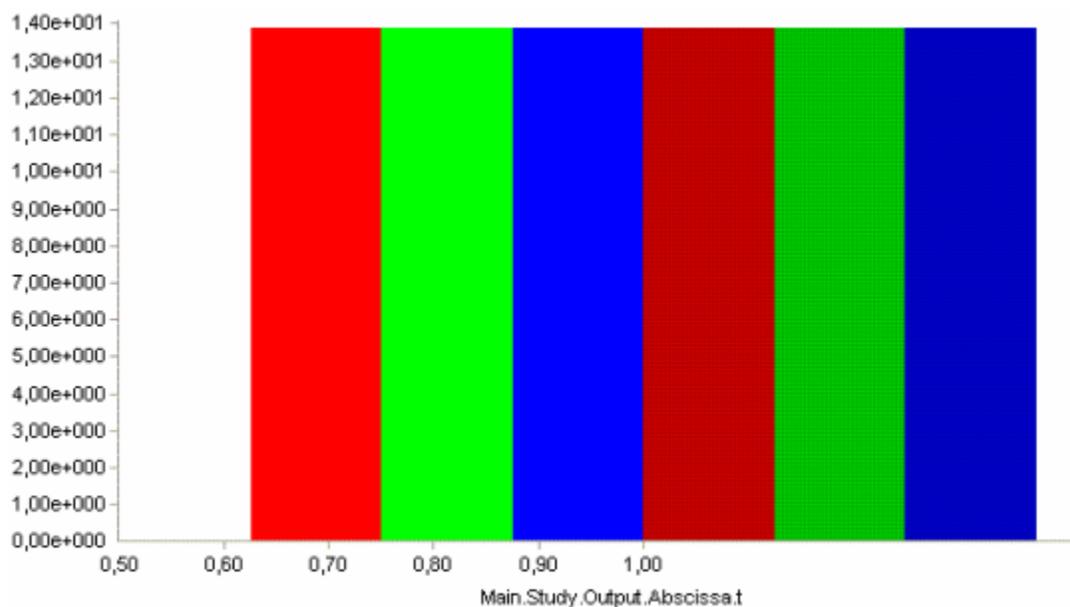
This shows that the force in this muscle branch is roughly 18 N. Notice the specification line above the graphics pane marked with the red circle above. This is where the specification of the current picture is listed. You can use this to plot several muscles at the same time. If you change

Main.Study.Output.Model.HumanModel.Right.ShoulderArm.Mus.supraspinatus_3.Fm

to

Main.Study.Output.Model.HumanModel.Right.ShoulderArm.Mus.supraspinatus_*.Fm

i.e. replace the figure 3 with an asterix, '*', then you should see a bar diagram of all the supraspinatus muscles in the right hand side of the body.



complex modeling tasks.

The syntax of AnyScript is much like a Java, JavaScript, or C++ computer program. If you already know one of these programming languages, you will quickly feel at home with AnyScript. But don't be alarmed if you have no programming experience. AnyScript is very logically constructed, and this tutorial is designed to help new users getting started as gently as possible.

So let us take the bull by the horns and get you introduced to the world of body modeling with AnyScript. This tutorial comprises six lessons during which you will complete your first AnyScript model, a simplified model of an arm.

Each lesson (after lesson 1) begins with a link to a file with the AnyScript code. If you have a problem making your own code work, simply download the file and start from there.

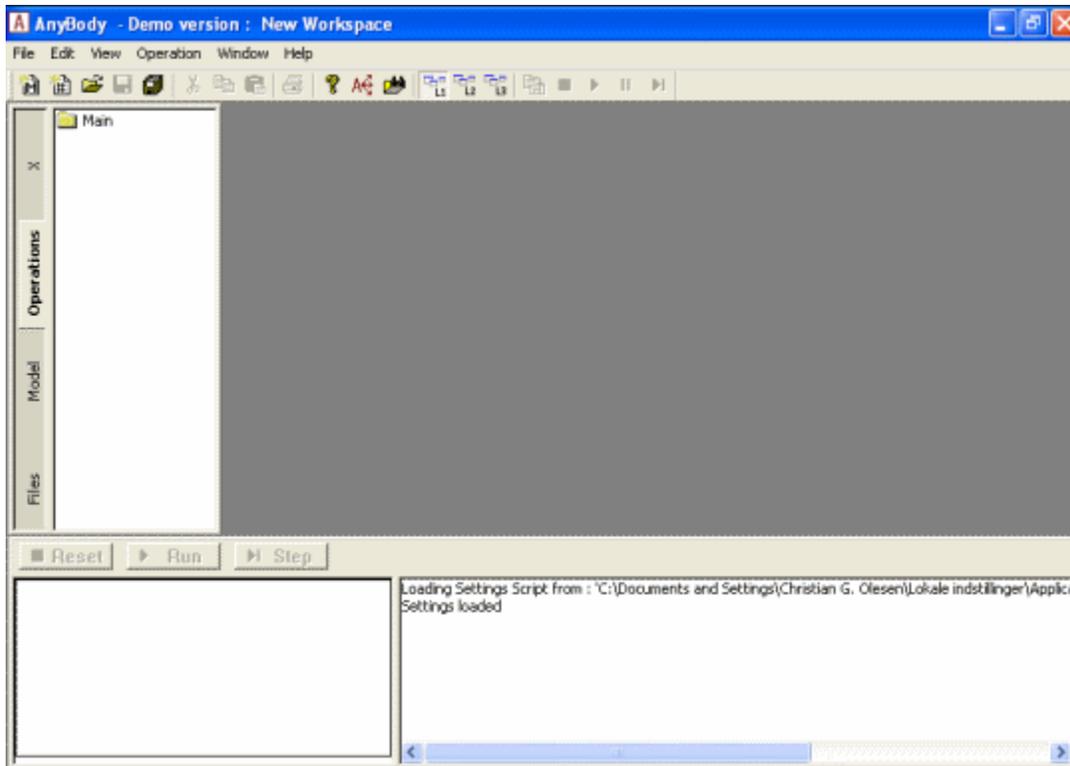
This tutorial consists of the following lessons:

- [Lesson 1: Basic concepts](#)
- [Lesson 2: Defining segments and displaying the model](#)
- [Lesson 3: Connecting segments by joints](#)
- [Lesson 4: Definition of movement](#)
- [Lesson 5: Definition of muscles and external forces](#)
- [Lesson 6: Adding real bone geometries](#)

Let's get started with [Lesson 1: Basic concepts](#)

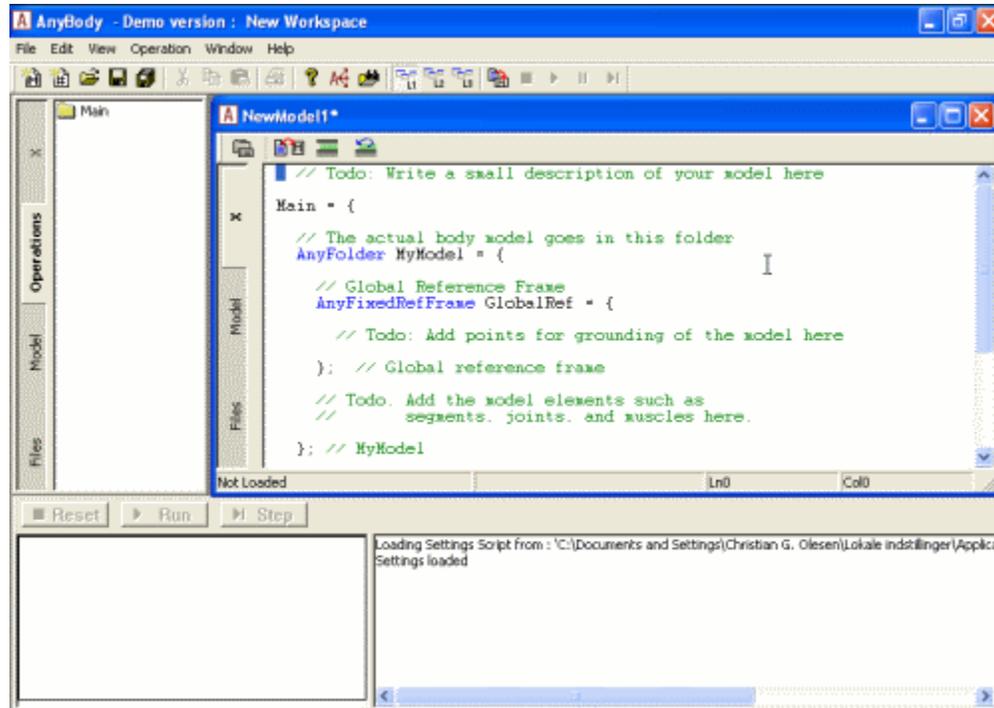
Lesson 1: Basic concepts

The AnyBody system contains an editor designed for authoring AnyScript files. So the first thing to do is to get AnyBody up and running. Double-click the AnyBody icon, and you should be greeted by the AnyBody Assistant and behind that an empty workspace.



As you can see, the Main Frame window contains a smaller frame at the bottom. This frame provides much of your interaction with the system once you have a model running. Notice now in particular the empty rectangular lower portion of the frame. It is the Output Window. The system talks to you through this window. Notice that this window as well as many other text views in AnyBody can contain active links like in a HTML browser. These links can help you navigate faster around in the system.

As computer software goes, AnyBody is much like any other Computer-Aided Engineering tool. You can create data from scratch, you can read in previously defined data, and you can exchange data between models. Once you have your data in place, you can perform various actions on it. Let us begin by creating a new AnyScript model. The menu clicks File -> New Main will bring up a new window in which you can construct your model using the AnyScript language.



The new windows is basically a text editor. This main pane of the Editor window will contain the actual AnyScript text. The system has already created the skeleton of a model for you from a built-in template.

The narrow pane attached to the left side of the Main Frame is a tree view pane, where you find hierarchical representations of the model defined in the text window. If you are familiar with modern feature-based CAD systems, this idea will be very familiar to you. Almost the same tree views are available on the Editor windows containing the AnyScript code, but they are closed by default. These additional tree views give you the possibility to browse large models in several views at a time. The following tree views are available to you:

- The Model Tree View shows all objects in the model. It is current
- The Operation Tree (only on the Main Frame) shows a subset of the model objects but in the same structural ordering. The objects in this subset are so-called operations that are the things you can do to the model. An operation can be selected in the Operation Tree and thereafter controlled by the Run, Step, Reset, etc. buttons below (or on the Main Frame toolbar or the Operations menu). More about operations will follow later.
- The File Tree shows all the files in a model. So far we will only be working with one file, the so-called Main file.

On the Editor windows, you will additionally find some tree views that do not show the objects of the model, but things available to you while modeling.

- The Class Tree shows all the classes in the AnyScript language and it can assist you in inserting the code to create objects.
- The Global and Function Trees show the globally available elements, hereunder functions, in the language.

So far the Model, the Operation and the File Trees are empty, because the model is not yet loaded into the system. In the upper left corner of the editor you see the little icon . This means "Script to Model". When you click this icon, the system processes whatever text you have in the editor window and tries to form a valid AnyBody model. The tree view gets generated and updated this way. A similar button is found

in the Main Frame toolbar and the key F7 is a convenient shortcut for this function.

The script to model operation also saves your model files. The first time you save a new file, AnyBody requires you to give your model a name, so clicking the  icon the first time produces a "Save As" dialog.

Let's have a look at what the system has generated for you. If we forget about most of the text and comments, the overall structure of the model looks like this:

```
Main = {
  AnyFolder MyModel = {
  }; // MyModel
  AnyBodyStudy MyStudy = {
  };
}; // Main
```

What you see is a hierarchy of braces - just like in a C, C++, or Java computer program. The outermost pair of braces is named "Main". Everything else in the model goes between these braces.

Right now, there are two other sections inside the Main braces: The "AnyFolder MyModel" and the "AnyBodyStudy MyStudy". These are the two basic elements of most AnyBody models. The term "AnyFolder" is very general. In fact, any pair of braces in AnyScript is a folder. You can think of a folder as a directory on your hard disk. A directory can contain other directories and files. It's exactly the same with folders. They can contain other folders and elements of the model. The "AnyFolder MyModel" is the folder containing the entire model you are going to build. The name "MyModel" can be changed by you to anything you like. In fact, let's change it to ArmModel (in the forthcoming AnyScript text we'll highlight each change by red. Just type the new name into the file, and *don't forget to also change other occurrences of MyModel to ArmModel* in the file.

Notice the prefix "Any". All reserved words in AnyScript begin with "Any". This way you can distinguish the elements that belong to the system from what the user defines. Another way of recognizing reserved words is by virtue of their color in the editor. Class names are recognized by the editor as soon as you type them and colored blue.

It must be emphasized that AnyScript is case sensitive.

There is more to an AnyScript file than the model. Once you have a model, you can perform various operations on it. These operations are often collected in "studies", and the "AnyBodyStudy MyStudy" is indeed such a study. You can think of a study as the definition of a task or set of tasks to perform. The study also contains methods to perform the tasks. The [Study of Studies](#) tutorial contains much more information about these subjects. For now, let's just rename "MyStudy" to "ArmModelStudy".

Let's look a little closer at the contents of what is now the ArmModel folder:

```
// The actual body model goes in this folder
AnyFolder ArmModel = {
  // Global Reference Frame
  AnyFixedRefFrame GlobalRef = {
    // Todo: Add points for grounding
    // of the model here
  }; // Global reference frame
  // Todo. Add the model elements such as
  // segments, joints, and muscles here.
}; // ArmModel
```

Most of what you see above is just comments. It is always useful to add lots of comments to your models.

may know it from C++ or the Java language. Notice also that lines are terminated by semicolon ';'. Even the lines with closing braces must be terminated by a semicolon. If you do not terminate with a semicolon, then the statement continues on the next line. You can comment and uncomment a block of lines in one click by means of the buttons at the top of the Editor window.

The only actual model element in the ArmModel is the declaration of the "AnyFixedRefFrame GlobalRef". All models need a reference frame - a coordinate system - to work in, so the system has created one for you.

An AnyFixedRefFrame is a predefined data type you can use when you need it. What you have here is the definition of an object of that type. The object gets the name "GlobalRef", and we can subsequently refer to it anywhere in the ArmModel by that name.

You will notice that there is a "to do" comment inside the braces of this reference frame suggesting that you add points for grounding the model. Don't do it just yet. We will return to this task later.

But here's an important notice: Everything you define in this tutorial from now on is part of the ArmModel folder and should go between the its pair of braces. If you define something outside these braces that should have been inside, then the necessary references between the elements of the model will not work.

What you have here is actually a valid AnyScript model, although it is empty and cannot do much. If you have typed everything correctly, then you should be able to press the  icon and get the messages

```

Loading Main : "C:\...\NewModel1.any"
Scanning...
Parsing...
Constructing model tree...
Linking identifiers...
Evaluating constants...
Configuring model...
Evaluating model...
Loaded successfully.
Elapsed Time : 0.063000

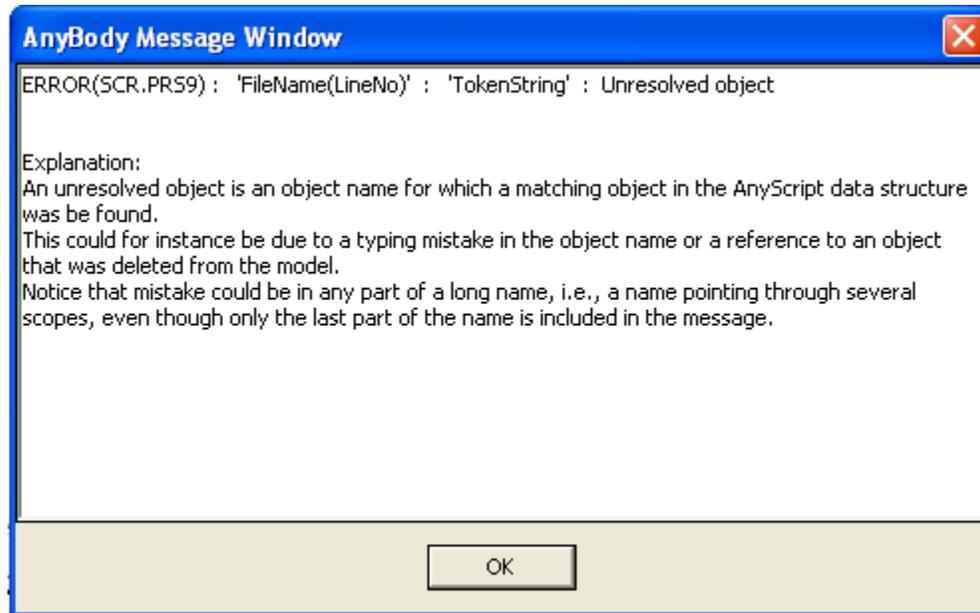
```

in the Output Window. But what happens if you mistype something? If your typo leads to a syntactical error, then it will be found by the AnyBody system when it parses the file, and instead of the "AnyScript loaded successfully", you will get an impolite message that something is wrong. A common mistake is to forget a semicolon somewhere. Try removing the last semicolon in the AnyScript file, and load again. You get a message saying something like:

```

ERROR(SCR.PRS11) : C:\...\NewModel1.any(27) : 'EOF' unexpected
Model loading skipped

```



We now assume that you have removed eventual errors and have loaded the model successfully.

If you are up to it, let's continue onward to [Lesson 2: Segments](#).

This is a typical error message. First there is a message ID, then a file location and finally the body of the message. The former two are written in blue ink and underlined to show the underlying active links. The file location is the line where the bug was found by the system. If you double-click this link, the cursor in the Editor Window jumps to the location of the error. Notice that this is where the system found the error, but the error can sometimes be caused by something you mistyped earlier in the file so that you actually have to change something elsewhere in your model. If you are in doubt of what the error message means, try clicking the error number `ERROR(SCR.PRS11)`. This will give you a little pop-up window with a more complete explanation:

Lesson 2: Defining segments and displaying objects

Here's an AnyScript file to start on if you have not completed the previous lesson:
[demo.lesson2.any](#)

There are some elements that must be present in a body model for it to make any sense at all. The first one is segments. They are the rigid elements of the body that move around when the model does its stuff. When modeling a human or other higher life form, they usually correspond to the bones of the body. However, they can also be used to model machines, tools, and other things that might be a part of the model but do not belong to the human body. Hence the more general term "segment".

A segment is really nothing but a frame of reference that can move around in space and change its orientation. It has an origin where its center of mass is assumed to be located, and it has axes coinciding with its principal inertia axes.

We shall start by defining a folder for the segments. Please add the following text to your model (new text marked by red):

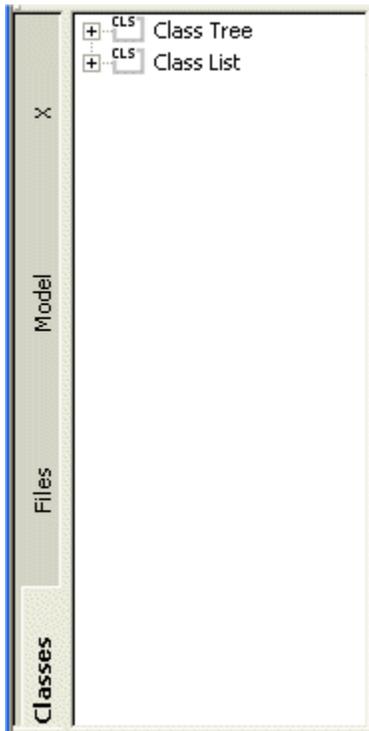
```
// The actual body model goes in this folder
AnyFolder ArmModel = {
  // Global Reference Frame
  AnyFixedRefFrame GlobalRef = {
```

```

    // Todo: Add points for grounding
    // of the model here
}; // Global reference frame
// Segments
AnyFolder Segs = {
}; // Segs folder
}; // ArmModel

```

Did you notice that the word `AnyFolder` turned blue as soon as you typed its last letter? If it did not, you have mistyped something. Try loading the model by clicking the  icon (or pressing F7). If you expand the `ArmModel` branch in the tree view, you should see a new, empty branch named `Segs`. It is the new folder you just defined. We are now ready to add a segment to the model, and this would probably be a good time to introduce you to the object inserter.



If you look at the left hand side of the tree view in the editor window, you will notice tabs running down the vertical edge. The tabs give you access to different tree views or let you close the tree view completely if you would rather use the space for something else. One of the tabs is called "Classes" and it produces a tree that has two branches at its root. Both of these branches contain all the predefined classes in AnyScript. In the first branch, "ClassTree", the classes are ordered hierarchically. This reflects the object-oriented idea that classes inherit properties from each other. This might be a way of locating a class with particular properties if you are not sure of the class name.

The other branch, "Class List", simply contains an alphabetical list of all the classes. This is useful if you know the name of the class you are looking for. Try opening each of the two trees and look for the class `AnySeg`. Then make sure the cursor in the editor window is located inside the newly defined `AnyFolder Segs`. Finally, right-click the `AnySeg` class name in the tree and choose "Insert object". You should get this:

```

// Segments
AnyFolder Segs = {
  AnySeg <ObjectName>
  {
    //r0 = {0, 0, 0};
  }
};

```

```

    //rDot0 = {0, 0, 0};
    //Axes0 = {{1, 0, 0}, {0, 1, 0}, {0, 0, 1}};
    //omega0 = {0, 0, 0};
    Mass = 0;
    Jii = {0, 0, 0};
    //Jij = {0, 0, 0};
    //sCoM = {0, 0, 0};
};
}; // Segs folder

```

The object inserter has created a template of a segment for you. It contains all the properties you can set for an AnySeg object. Some of them are active while other are commented out by two leading slashes. The ones that are commented out are optional properties. You can set them if you like, but if you leave them out they will retain the values already indicated in the inserted lines. If you do not plan on using them, you can erase them. The object properties without leading slashes are those that must be set. This is the case for Mass and Jii, for instance, which are respectively the mass of the segment and the diagonal elements of the inertia tensor. In a system that simulates dynamics, all segments must have mass and inertia. The system allows you to set them to zero, but it does not make sense not to set them at all.

More formally, object properties are divided into three different groups:

- Obligatory. Like Mass and Jii, these must be set by the user when the object is defined
- Access denied. These are computed automatically by the system and cannot be specified by the user.
- Optional. These can be set by the user or left to their default values.
You can find a complete description of all possible properties of all objects in the [reference manual](#).

Let us give the new segment the name UpperArm and set its Mass = 2 and also assign reasonable values for Jii:

```

AnySeg UpperArm = {
    //r0 = {0, 0, 0};
    //Axes0 = {{1, 0, 0}, {0, 1, 0}, {0, 0, 1}};
    Mass = 2;
    Jii = {0.001, 0.01, 0.01};
}; //UpperArm

```

Click  again (or press F7). Among the messages you get are:

Model Warning: Study 'Main.ArmStudy' contains too few kinematic constraints to be kinematically determinate.

Don't worry about it just now. It only means that you are not finished with the necessary elements to do an actual analysis yet.

Now that we have a physical object in the model, let's see what it looks like. To make something visible in AnyBody, you have to add a line that defines visibility:

```

AnySeg UpperArm = {
    //r0 = {0, 0, 0};
    //Axes0 = {{1, 0, 0}, {0, 1, 0}, {0, 0, 1}};
    Mass = 2;
    Jii = {0.001, 0.01, 0.01};
    AnyDrawSeg drw = {};
}; // UpperArm

```

Reload the model, and then choose the menu Window -> Model View (new). This opens a graphics window and displays what looks like a long yellow ellipse. On the toolbar at the top of the graphics window, click the



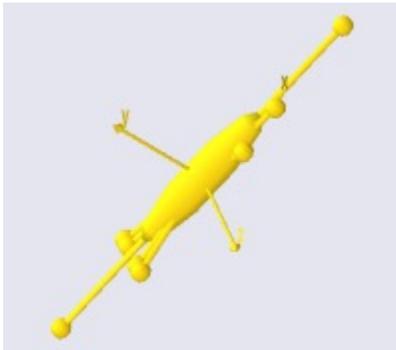
. Then click inside the graphics field and drag the mouse in some direction. This causes the yellow ellipse to rotate, and you will see that it is actually an ellipsoid with a coordinate system through it. If you entered the inertia properties in the Jii specification as written above, then your ellipsoid should be ten times as long as it is wide. Try changing the "0.001" to "0.01" and reload. The ellipsoid becomes spherical. The dimensions of the ellipsoid are scaled this way to fit the mass properties of the segment you are defining. It is best to change Jii back to {0.001,0.01,0.01} again.

As you can see, Jii is a vector. If you know your basic mechanics, you may wonder why it is not a 3 x 3 matrix. The reason is that Jii only contains the diagonal members (the moments of inertia), which is all you need to specify if your segment-fixed reference frame is aligned with the principal axes. If not, the off-diagonal elements (the deviation moments) can be specified in a property called Jij, which by default contains zeros.

We are eventually going to attach things like muscles, joints, external loads, and visualization objects to our segments. To this end we need attachment points. They are defined in the local coordinate system of the segment. For a given body part it may be a laborious and difficult task to sort out the correct points. Fortunately, good people have done much of the work for you, and, if you construct your model wisely, you can often grab most of what you need from models defined by other people. For now, let us assume that you have sorted out the coordinates of all the points you need on UpperArm, and that you are ready to start adding them. Rather than going through the drill with the object inserter, you can copy and paste the following lines:

```
AnySeg UpperArm = {
  //r0 = {0, 0, 0};
  //Axes0 = {{1, 0, 0}, {0, 1, 0}, {0, 0, 1}};
  Mass = 2;
  Jii = {0.001, 0.01, 0.01};
  AnyDrawSeg drw = {};

  AnyRefNode ShoulderNode = {
    sRel = {-0.2,0,0};
  };
  AnyRefNode ElbowNode = {
    sRel = {0.2,0,0};
  };
  AnyRefNode DeltodeusA = {
    sRel = {-0.1,0,0.02};
  };
  AnyRefNode DeltodeusB = {
    sRel = {-0.1,0,-0.02};
  };
  AnyRefNode Brachialis = {
    sRel = {0.1,0,0.01};
  };
  AnyRefNode BicepsShort = {
    sRel = {-0.1,0,0.03};
  };
  AnyRefNode Brachioradialis = {
    sRel = {0.05,0,0.02};
  };
  AnyRefNode TricepsShort = {
    sRel = {-0.1,0,-0.01};
  };
}; // UpperArm
```



Try loading the model again and have a look at the graphical representation. If you zoom out enough, you should see your points floating around the ellipsoid connected to its center of gravity by yellow pins.

One segment does not make much of a mechanism, so let's define a forearm as well. In the segs folder, add these lines:

```
AnySeg ForeArm = {
  Mass = 2.0;
  Jii = {0.001,0.01,0.01};
  AnyRefNode ElbowNode = {
    sRel = {-0.2,0,0};
  };
  AnyRefNode HandNode = {
    sRel = {0.2,0,0};
  };
  AnyRefNode Brachialis = {
    sRel = {-0.1,0,0.02};
  };
  AnyRefNode Brachioradialis = {
    sRel = {0.0,0,0.02};
  };
  AnyRefNode Biceps = {
    sRel = {-0.15,0,0.01};
  };
  AnyRefNode Triceps = {
    sRel = {-0.25,0,-0.05};
  };
  AnyDrawSeg DrwSeg = {};
}; // ForeArm
}; // Segs folder
```

When you reload the model you may not be able to see that the forearm has been added. In fact it is there, but it is placed exactly on top of the upper arm and since the two segments have similar mass properties, it is impossible to see which is which.

Before we proceed it might be worth thinking a bit about why objects get placed the way they do in the model and how we can control the placement. The first thing to notice is that we are in the process of making a model of a living organism which supposedly will move about changing its position all the time. So there really is no "right" placement of a segment in the model. The second thing to notice is that even if we are able to exercise some control over the placement of objects, then at least we have not done so yet. So this is why the system for lack of better information places both segments at the origin of the global reference frame at load time.

What eventually will happen is that we will define joints to constrain the segments with respect to each other and also drivers to specify how the mechanism will move. When all that is done, these specifications

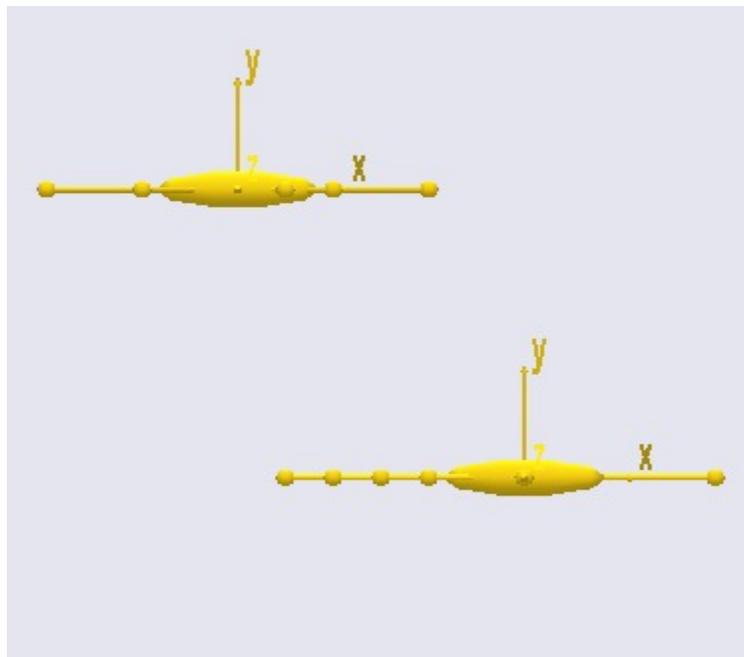
will determine where everything is at every point in time. But we need to go through several steps of definitions and subsequently the system must do some equation solving before everything can fall into its "right" position. So what to do in the meantime? Well, perhaps you noticed that the UpperArm segment we originally created with the object inserter has two properties named `r0` and `Axes0`. These two properties determine the location and orientation of the segment at load time. The `r0`'s are easy because they are simply three-dimensional coordinates in space. So we can separate the two segments at load time like this:

```
AnySeg UpperArm = {
  r0 = {0, 0.3, 0};
  //Axes0 = {{1, 0, 0}, {0, 1, 0}, {0, 0, 1}};
  Mass = 2;
  Jii = {0.001, 0.01, 0.01};
  AnyDrawSeg drw = {};
```

and

```
AnySeg ForeArm = {
  r0 = {0.3, 0, 0};
  Mass = 2.0;
  Jii = {0.001, 0.01, 0.01};
```

This will clearly separate the segments in your model view:



So far so good. But it might improve the visual impression if they were also oriented a bit like we would expect an arm to be. This involves the `Axes0` property, which is really a rotation matrix. Such matrices are a bit difficult to cook up on the fly. The predefined version in the UpperArm segment looks like this:

```
AnySeg UpperArm = {
  r0 = {0, 0.3, 0};
  Axes0 = {{1, 0, 0}, {0, 1, 0}, {0, 0, 1}};
```

If your spatial capacity is really good, you can start figuring out unit vectors for the coordinate system orientation you want and insert them into the `Axes0` specification instead of the existing ones. But there is

corresponding to a given axis and rotation angle. Therefore, we can specify:

```
AnySeg UpperArm = {
  r0 = {0, 0.3, 0};
  Axes0 =RotMat(-90*pi/180, z);
```

When you reload again you will see that the UpperArm is indeed rotated -90 degrees about the z axis as the function arguments indicate. Notice the multiplication of the angle by pi/180. AnyBody identifies the word "pi" as 3.14159... and dividing this with 180 gives the conversion factor between degrees and radians. Angles in AnyScript are always in radians, but anywhere a number is expected you can substitute it by a mathematical expression just like in other programming languages.

In the next section we will look at how joints can be used to constrain the movement of segments and allow them to articulate the way we desire. So if you are up to it, let's continue onward to [Lesson 3: Connecting segments by joints](#).

 *In rigid body dynamics terminology, a "segment" would be called a "rigid body", but to avoid unnecessary confusion between the rigid bodies and the total body model, we have chosen to use "segments" for the rigid parts of the model.

Lesson 3: Connecting segments by joints

Here's an AnyScript file to start on if you have not completed the previous lesson:
[demo.lesson3.any](#).

You can think of joints in different ways. We tend to perceive them as providers of freedom, which is correct compared to a rigid structure. However in dynamics it is often practical to perceive joints to be constraining movement rather than releasing it. Two segments that are not joined (constrained) in any way have $2 \times 6 = 12$ degrees of freedom. When you join them, you take some of these degrees of freedom away. The different joint types distinguish themselves by the degrees of freedom they remove from the connected segments.

A segment without joints is basically floating free in space. When you connect the segments by joints, you bind them together in some sense. But the mechanism as a whole can still fly around in space.

Not knowing where stuff is in space can be very impractical so the first thing to do is usually to ground the mechanism somewhere. Perhaps you remember that the system added these lines somewhere in the top of the AnyScript model:

```
AnyFixedRefFrame GlobalRef = {
  // Todo: Add points for grounding
  // of the model here
}; // Global reference frame
```

This is actually the definition of a global reference frame of the model. You can think of it as a coordinate system fixed somewhere in global space. Otherwise, it is just like a segment in the sense that we can add points to it for attachment of joints and muscles. Lets do just that. Again you can insert the objects with the object inserter or to save time simply cut and paste the following lines into your model:

```
AnyFixedRefFrame GlobalRef = {
  AnyDrawRefFrame DrwGlobalRef = {};
  AnyRefNode Shoulder = {
    sRel = {0,0,0};
  };
  AnyRefNode DeltodeusA = {
```

```

    sRel = {0.05,0,0};
};
AnyRefNode DeltodeusB = {
    sRel = {-0.05,0,0};
};
AnyRefNode BicepsLong = {
    sRel = {0.1,0,0};
};
AnyRefNode TricepsLong = {
    sRel = {-0.1,0,0};
};
}; // Global reference frame

```

The first line, "AnyDrawRefFrame ..." does nothing else than cause the global reference system to be displayed in the graphics window. If for some reason you don't want the reference frame to be visible, just erase this line or make it a comment by prefixing it with "//". It is often nice to have a visualization of the global reference frame, but the current version may be a bit on the large side for the model. Let us reduce the size a little bit and change the color to better distinguish it from the yellow segments:

```

AnyDrawRefFrame DrwGlobalRef = {
    ScaleXYZ = {0.1, 0.1, 0.1};
    RGB = {0,1,0};
};

```

The remaining lines are definitions of points in the global reference frame.

Now that we have the necessary points available, we can go ahead and fix the upper arm to the global reference frame by means of a "shoulder" joint. A real shoulder is a very complex mechanism with several joints in it, but for this 2-D model, we shall just define a simple hinge. We create a new folder to contain the joints and define the shoulder:

```

}; // LowerArm
}; // Segs folder
AnyFolder Jnts = {
    //-----
    AnyRevoluteJoint Shoulder = {
        Axis = z;
        AnyRefNode &GroundNode = ..GlobalRef.Shoulder;
        AnyRefNode &UpperArmNode = ..Segs.UpperArm.ShoulderNode;
    }; // Shoulder joint
}; // Jnts folder

```

A hinge is technically called a revolute joint, and this is what the type definition "AnyRevoluteJoint" means. After that, the definition is just a matter of setting the properties of the joint that make it behave the way we want. Let's have a closer look at each property:

```
Axis = z;
```

The AnyBody system is inherently three-dimensional. This applies also when we are creating a model that will only operate in two dimensions, and it means that a revolute joint must know which axis to rotate about. The property Axis = z simply specifies that the segment will rotate about the z axis of the node at the joint. Does that sound complicated?

Well, a segment is really a reference frame. The nodes on segments are also reference frames, and each reference frame can have its orientation defined by the user. A joint of this type forces the two z axes of the two joined nodes to be parallel. You can control the mutual orientation of the two joined segments by rotating the reference frames of the nodes you are connecting. This is relevant if you want one of the joints to rotate about some skew axis.

The joint connects several segments, and it needs to know which point on each segment to attach to. For this purpose, we have lines like

```
AnyRefNode &GroundNode = ..GlobalRef.Shoulder;
AnyRefNode &UpperArmNode = ..Segs.UpperArm.ShoulderNode;
```

The simple explanation is that these lines define nodes on the GlobalRef and UpperArm to which the joint attaches. Notice the two dots in front of the names. They signify that the GlobalRef and Segs folders are defined two levels up compared to where we are now in the model. If you neglected the two dots, then AnyBody would be searching for the two objects in the Shoulder folder, and would not be able to find them. This "dot" system is quite similar to the system you may know from directory structures in Dos, Windows, Unix, or just about any other computer operating system.

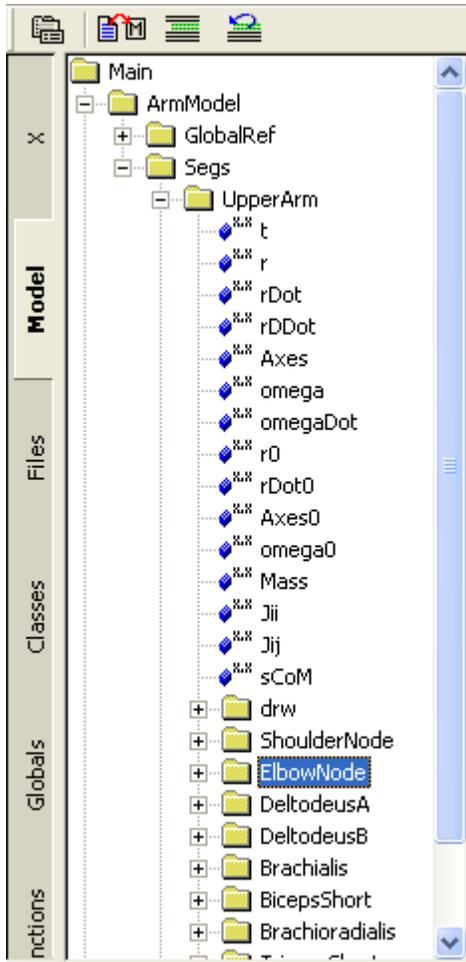
But there is more to it than that. You can see that the Shoulder point on GlobalRef has been given the local name of "GroundNode". This means that, within the context of this joint, we can hereafter refer to the point as "GroundNode". This is practical because it allows us to assign shorter names to long external references.

Another specialty is the '&' in front of the local name. If you have C++ experience, you should be familiar with this. It means that GroundNode is a reference (a pointer) to GlobalRef.Shoulder rather than a copy of it. So if GlobalRef.Shoulder moves around, Shoulder.GroundNode follows with it. Hit F7 to load the model again to make sure that the definition is correct.

We need an elbow joint before we are finished: the elbow. The definition is completely parallel to what you have just seen, but we shall use one of the handy tools to define the references. The skeleton of the elbow joint is as follows:

```
AnyFolder Jnts = {
  //-----
  AnyRevoluteJoint Shoulder = {
    Axis = z;
    AnyRefNode &GroundNode = ..GlobalRef.Shoulder;
    AnyRefNode &UpperArmNode = ..Segs.UpperArm.ShoulderNode;
  }; // Shoulder joint
  AnyRevoluteJoint Elbow = {
    Axis = z;
    AnyRefNode &UpperArmNode = ;
    AnyRefNode &ForeArmNode = ;
  }; // Elbow joint
}; // Jnts folder
```

As you can clearly see, the nodes in the Elbow joint are not pointing at anything yet. In this simple model it is easy to find the relative path of the pertinent nodes on the upper arm and the forearm, but in a complex model it can be very difficult to sort these references out. So the system offers a tool to help you. If you click the model tab in the tree view on the left hand side of the editor window, then the tree of objects in the loaded model appears. Anything that was defined in the model when it was recently successfully loaded can be found in this tree including the two nodes we are going to connect in the elbow. Click to place the cursor just before the semicolon in the &UpperArmNode definition in the Elbow joint. Then expand the tree as shown below.



When you right-click the ElbowNode you can select "Insert object name" from the context menu. This writes the full path of the node into the Elbow joint definition where you placed the cursor. Notice that this method inserts the absolute and not the relative path. Repeat the process to expand the ForeArm segment and insert its ElbowNode in the line below to obtain this:

```
AnyRevoluteJoint Elbow = {
  Axis = z;
  AnyRefNode &UpperArmNode = Main.ArmModel.Segs.UpperArm.ElbowNode;
  AnyRefNode &ForeArmNode = Main.ArmModel.Segs.ForeArm.ElbowNode;
}; // Elbow joint
```

Seems like everything is connected now. So why do we still get the annoying error message:

Model Warning: Study 'Main.ArmStudy' contains too few kinematic constraints to be kinematically determinate.

when we reload the model? The explanation is that we have connected the model but we have not specified its position yet. Each of the two joints can still take any angular position, so there are two degrees of freedom left to specify before AnyBody can determine the mechanism's position. This is taken care of by kinematic drivers.

They are one of the subjects of [Lesson 4: Definition of movement](#).

Lesson 4: Definition of movement

Here's an AnyScript file to start on if you have not completed the previous lesson: [demo.lesson4.any](#).



If you have completed the three previous lessons, you should have a model with an upper arm grounded at the shoulder joint and connected to a forearm by the elbow. What we want to do now is to make the arm move.

How can an arm with no muscles move? Well, in reality it cannot, but in what we are about to do here, the movement comes first, and the muscle forces afterwards. This technique is known as inverse dynamics. We shall get to the muscles in the next lesson and stick to the movement in this one.

Our mechanism has two degrees of freedom because it can rotate at the shoulder and at the elbow. This means that we have to specify two drivers. The natural way is to drive the shoulder and elbow rotations directly and this is in fact what we shall do. But we could also choose any other two measures as long as they uniquely determine the position of all the segments in the mechanism. If you were building this model for some ergonomic investigation, you might want to drive the end point of the forearm where the wrist should be located in x and y coordinates to simulate the operation of some handles or controls. And this would be just as valid a model because the end point position uniquely determines the elbow and shoulder rotations.

For now, let's make a new folder and define two drivers:

```
}; // Jnts folder
AnyFolder Drivers = {
  //-----
  AnyKinEqSimpleDriver ShoulderMotion = {
    AnyRevoluteJoint &Jnt = ..Jnts.Shoulder;
    DriverPos = {-100*pi/180};
    DriverVel = {30*pi/180};
  }; // Shoulder driver

  //-----
  AnyKinEqSimpleDriver ElbowMotion = {
    AnyRevoluteJoint &Jnt = ..Jnts.Elbow;
    DriverPos = {90*pi/180};
    DriverVel = {45*pi/180};
  }; // Elbow driver
}; // Driver folder
```

This is much like what we have seen before. The folder contains two objects: ShoulderMotion and ElbowMotion. Each of these are of type AnyKinEqSimpleDriver. A driver is really nothing but a mathematical function of time. The AnyKinEqSimpleDriver is a particularly simple type that starts at some position at time = 0 and increases or decreases at constant velocity from there. These two drivers are attached to joints, and therefore they drive joint rotations, but the same driver type could be used to drive any other degree of freedom as well, for instance the Cartesian position of a point.

The lines

```
AnyRevoluteJoint &Jnt = ..Jnts.Shoulder;
```

and

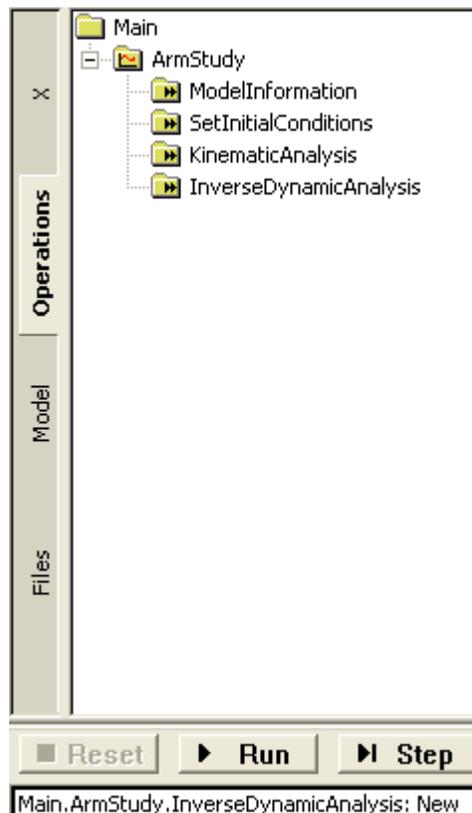
```
AnyRevoluteJoint &Jnt = ..Jnts.Elbow;
```

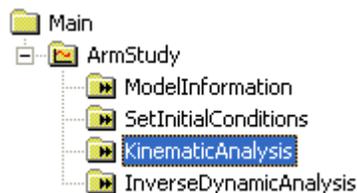
are the ones that affiliate the two drivers with the shoulder and elbow joints respectively. They are constructed the same way as the joint definition in [Lesson 3](#) in the sense that a local variable, Jnt, is declared and can be used instead of the longer global name if we need to reference the joint somewhere else inside the driver. Notice also the use of the reference operator '&' that causes the local variable to be a pointer to the global one rather than a copy. It means that if some property of the globally defined joint changes, then the local version changes with it.

The specifications of DriverPos and DriverVel are the starting value of the driver and the constant velocity, respectively. Since these drivers drive angles, the units are radians and radians/sec.

Try loading the model again by hitting F7. If you did not mistype anything, you should get the message "Loaded successfully" and no complaints about lacking kinematic constraints this time.

This is good news, because you are now actually ready to see the model move. If you look closer at the pane in the bottom of the main frame, you will notice that it now contains the root of a tree in its upper left cell. This is the place where the AnyBody system places your studies, and from this window you can execute them, i.e., start analyses and calculations.





Try expanding the ArmStudy root. You will get a list of the study types that the system can perform. "Study" is a common name for operations you can perform on a model. When you click one of the studies, the buttons on the middle, lower part of the panel come to life. Try clicking the KinematicAnalysis study. With the buttons, you can now execute various types of analysis. The panel contains three buttons:

- **Run.** This button starts the highlighted study and runs it until the end, usually producing some sort of motion in the model. When Run has been pushed, it changes name to Break. If you push it in this state, it pauses the running operation. F5 is a shortcut to this function to Run and Break.
- **Step.** This button advances the operation one step. What a step is depends on the type of operation, but it is typically a time step in a dynamic analysis. (F6 is the shortcut key for Stepping)
- **Reset.** This puts the operation back to its initial position. You must reset before you can start a new analysis, if you have stopped it in the middle. (F4 is the shortcut for resetting operations)

All these functions are also available from the Main Frame toolbar and the menu Operation.

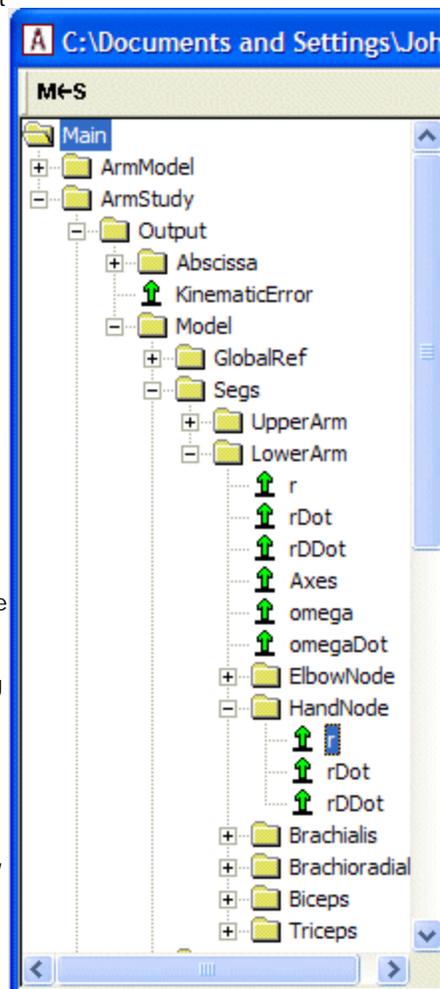
Do you have a Model View window open? This is the one where you can see the model graphically. If not, open one with Window->New model view from the pull down menus at the top of the screen. Now, try your luck with the KinematicAnalysis study and the Run button. What should happen is that the model starts to move as the system runs through 101 time steps of the study.

Since we have no muscles so far, kinematic analysis is really all that makes sense. A kinematic analysis is pure motion. The model moves, and you can subsequently investigate positions, velocities, and accelerations. But no force, power, energy or other such things are computed. These properties are computed by the InverseDynamicAnalysis, which is actually a superset of the KinematicAnalysis.

Try the Reset button, and then the Step button. This should allow you to single-step through the time steps of the analysis. When you get tired of that, hit the Run button, and the system completes the remaining time steps.

The analysis has 101 time steps corresponding to a division of the total analysis time into 100 equal pieces. The total time span simulated in the analysis is 1 sec. These are default values because we did not specify them when we defined the ArmModelStudy in the AnyScript model. If you want more or less time steps or a longer or shorter analysis interval, all you have to do is to set the corresponding property in the ArmModelStudy definition. When you click "Run", all the time steps are executed in sequence, and the mechanism animates in the graphics window.

So far, the model is merely a two-bar mechanism moving at constant joint angular velocities. There is not much biomechanics yet. However, the system has actually computed information that might be interesting to investigate. All the analysis results are available in the ArmModelStudy branch of the tree view. You can expand the tree as



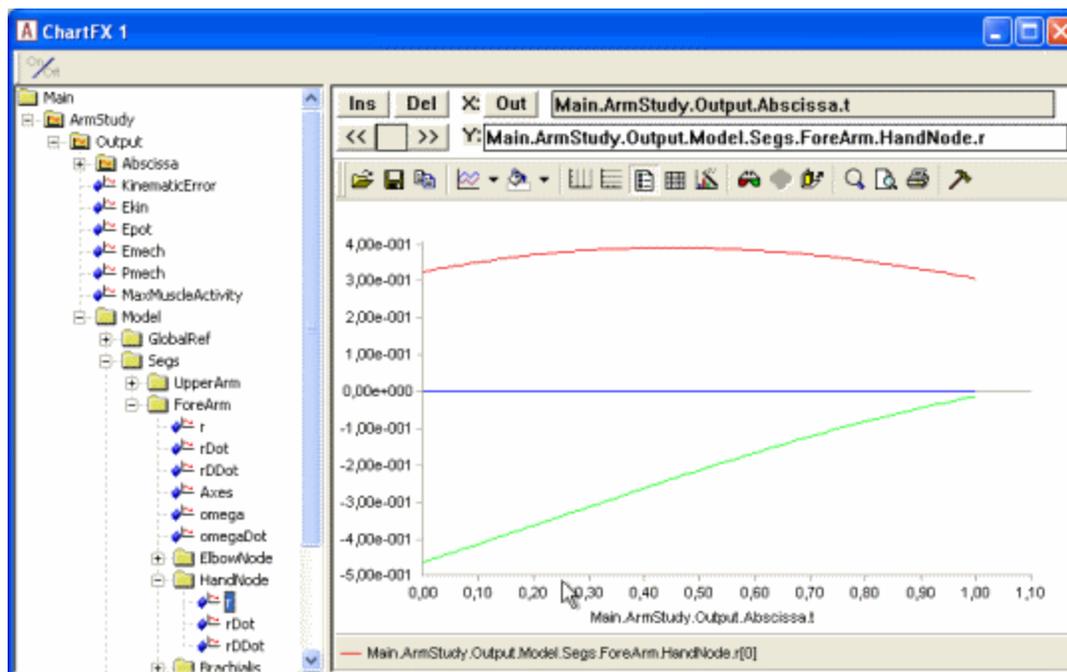
shown in the figure to the right.

Directly under the ArmModelStudy branch you find the Output branch where all computed results are stored. Notice that the Output branch contains the folders we defined in the AnyScript model: GlobalRef, Segs, and so on. In the Segs folder you find ForeArm, and in that a branch for each of the nodes we defined on the arm. Try expanding the branch for the HandNode. It contains the field 'r' which is the position vector of the node. We might want to know the precise position of the HandNode at each time in the analysis, for instance if we were doing an ergonomic study and wanted to know if the hand had collided with anything on its way.

If you double-click the 'r' node, the position vector of the hand node for each time step is dumped in the message window at the bottom of the screen. So you get the information you wanted, but perhaps not in a very attractive way. But we can do much better than that. AnyBody has special windows for investigating results. You open them from the pull-down menus by choosing Window -> ChartFX 2D (new).

This gives you a new window structured just like the editor window with a tree view to the left, but with an empty graphics field instead of the large text editor field to the right. The graphics field is for graphing results.

The tree in this window is much like the tree in the editor window except that some of the data have been filtered out, so that you mainly see the parts of the tree that are relevant in terms of results or output. You can expand of the tree in the chart window through ArmStudy and Output until you come to the HandNode. When you pick the property 'r', you get three curves corresponding to the development of the three Cartesian coordinates of this node during the analysis. Try holding the mouse pointer over one of the curves for a moment. A small label with the global name of the data of the curve appears. All data computed in AnyBody can be visualized this way.



So far, we have only the kinematic data to look at. Before we can start the real biomechanics, we must add some muscles to the model.

This is the subject of [Lesson 5: Definition of muscles and external forces](#).

Lesson 5: Definition of muscles and external forces

Here's an AnyScript file to start on if you have not completed the previous lesson: [demo.lesson5.any](#).

We have seen that models in AnyBody can move even though they do not have any muscles. This is because we can ask the system to perform a simple kinematic analysis that does not consider forces. However, things don't get really interesting until we add muscles to the model.

Skeletal muscles are very complicated mechanical actuators. They produce movement by pulling on our bones in complicated patterns determined by our central nervous system. One of the main features of AnyBody is that the system is able to predict realistic activation patterns for the muscles based on the movement and external load.

The behavior of real muscles depends on their operating conditions, tissue composition, oxygen supply, and many other properties, and scientists are still debating exactly how they work and what properties are important for their function. In AnyBody you can use several different models for the muscles' behavior, and some of them are quite sophisticated. Introducing all the features of muscle modeling is a subject fully worthy of [its own tutorial](#). Here, we shall just define one very simple muscle model and use it indiscriminately for all the muscles of the arm we are building.

As always, we start by creating a folder for the muscles:

```
AnyFolder Muscles = {
}; // Muscles folder
```

The next step is to create a muscle model that we can use for definition of the properties of all the muscles.

```
AnyFolder Muscles = {
  // Simple muscle model with constant strength = 300 Newton
  AnyMuscleModel MusMdl = {
    F0 = 300;
  };
}; // Muscles folder
```

Now we can start adding muscles. If you want the model to move, you basically need muscles to actuate each joint in the system. Remember that muscles cannot push, so to allow a joint to move in both directions you have to define one muscle on each side of the joint in two dimensions. If you work in three dimensions and you have, say, a spherical joint, then you may need much more muscles than that. In fact, it can sometimes be difficult to figure out exactly how many muscles are required to drive a complex body model. It is very likely that your career in body modeling will involve quite a few frustrations caused by models refusing to compute due insufficient muscles.

Let's add just one muscle to start with. These lines will do the trick:

```
AnyFolder Muscles = {
  // Simple muscle model with constant strength = 300 Newton
  AnyMuscleModel MusMdl = {
    F0 = 300;
  };
  //-----
  AnyViaPointMuscle Brachialis = {
    AnyMuscleModel &MusMdl = ..Muscles.MusMdl;
    AnyRefNode &Org = ..Segs.UpperArm.Brachialis;
    AnyRefNode &Ins = ..Segs.ForeArm.Brachialis;
    AnyDrawMuscle DrwMus = {};
  };
}; // Muscles folder
```

that it goes from its origin to insertion via a number of predefined points. The via-points are the AnyRefNodes defined in the second and third property lines. If you have a muscle that goes in a straight line from origin to insertion, then you can just define two points like we have done here. If you have a more complicated muscle path, then all you need to do is to add the points in between the origin and insertion.

The physiological behavior of the muscle is defined by the first property

```
AnyMuscleModel &MusMdl = ..Muscles.MusMdl;
```

You can see that it points right back to the muscle model we started out by creating. Notice the two leading dots. Finally, the line

```
AnyDrawMuscle DrwMus = {};
```

ensures that the muscle is visible in the graphics window. Lets have a look at it. If you have the Model View window (you know, the one with the rendering of the model in it) open, then just hit F7. If you don't have the Model View window open, choose Window -> Model View (new) from the pull down menus at the top of the main frame. You should see a thick, red line connecting the muscle's origin and insertion points. There are other ways to visualize muscles, but we shall save that for the [dedicated the muscle tutorial](#).

Notice that the muscle's position on the body might be a little strange because we have not yet positioned the segments relative to each other by a kinematic analysis.

All the other muscles are defined in the same way:

```
//-----
AnyViaPointMuscle Brachialis = {
  AnyMuscleModel &MusMdl = ..Muscles.MusMdl;
  AnyRefNode &Org = ..Segs.UpperArm.Brachialis;
  AnyRefNode &Ins = ..Segs.ForeArm.Brachialis;
  AnyDrawMuscle DrwMus = {};
```

```
};
//-----
AnyViaPointMuscle DeltodeusA = {
  AnyMuscleModel &MusMdl = ..Muscles.MusMdl;
  AnyRefNode &Org = ..GlobalRef.DeltodeusA;
  AnyRefNode &Ins = ..Segs.UpperArm.DeltodeusA;
  AnyDrawMuscle DrwMus = {};
```

```
};
//-----
AnyViaPointMuscle DeltodeusB = {
  AnyMuscleModel &MusMdl = ..Muscles.MusMdl;
  AnyRefNode &Org = ..GlobalRef.DeltodeusB;
  AnyRefNode &Ins = ..Segs.UpperArm.DeltodeusB;
  AnyDrawMuscle DrwMus = {};
```

```
};
//-----
AnyViaPointMuscle Brachioradialis = {
  AnyMuscleModel &MusMdl = ..Muscles.MusMdl;
  AnyRefNode &Org = ..Segs.UpperArm.Brachioradialis;
  AnyRefNode &Ins = ..Segs.ForeArm.Brachioradialis;
  AnyDrawMuscle DrwMus = {};
```

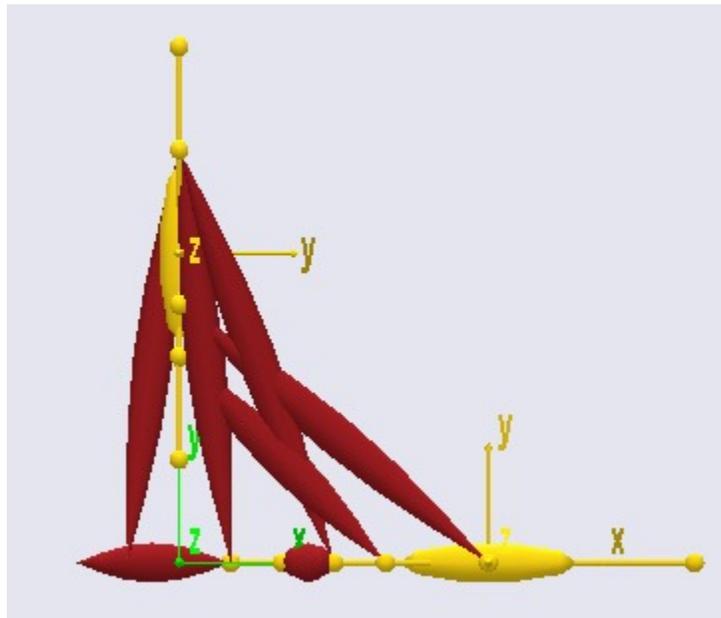
```
};
//-----
AnyViaPointMuscle BicepsShort = {
  AnyMuscleModel &MusMdl = ..Muscles.MusMdl;
  AnyRefNode &Org = ..Segs.UpperArm.BicepsShort;
  AnyRefNode &Ins = ..Segs.ForeArm.Biceps;
  AnyDrawMuscle DrwMus = {};
```

```

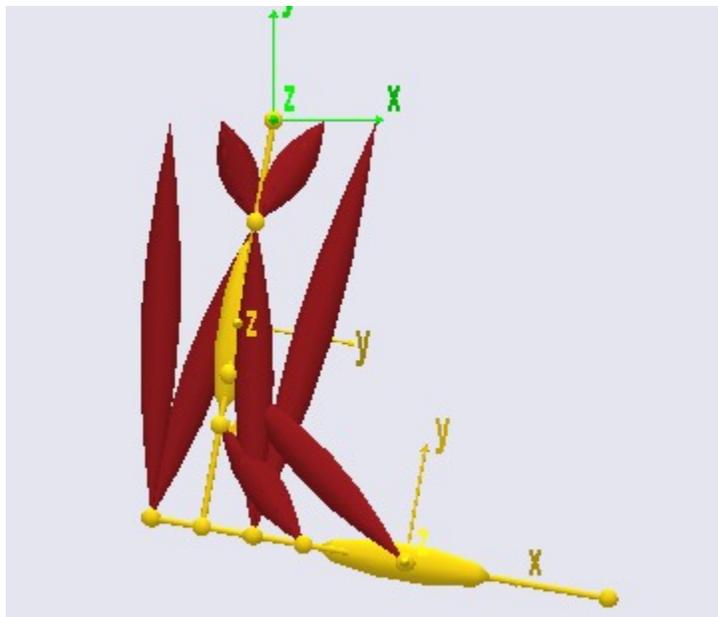
};
//-----
AnyViaPointMuscle TricepsShort = {
  AnyMuscleModel &MusMdl = ..Muscles.MusMdl;
  AnyRefNode &Org = ..Segs.UpperArm.TricepsShort;
  AnyRefNode &Ins = ..Segs.ForeArm.Triceps;
  AnyDrawMuscle DrwMus = {};
};
//-----
AnyViaPointMuscle BicepsLong = {
  AnyMuscleModel &MusMdl = ..Muscles.MusMdl;
  AnyRefNode &Org = ..GlobalRef.BicepsLong;
  AnyRefNode &Ins = ..Segs.ForeArm.Biceps;
  AnyDrawMuscle DrwMus = {};
};
//-----
AnyViaPointMuscle TricepsLong = {
  AnyMuscleModel &MusMdl = ..Muscles.MusMdl;
  AnyRefNode &Org = ..GlobalRef.TricepsLong;
  AnyRefNode &Ins = ..Segs.ForeArm.Triceps;
  AnyDrawMuscle DrwMus = {};
};
};

```

Try adding the data and viewing the result by reloading. You should get a picture more or less as what you see below:



The model does not seem to be correctly connected at the elbow. The ArmStudy actually contains a default operation for getting the elements ordered with respect to each other. It is the SetInitialConditions study in the tree at the upper left corner of the Main Frame. Try clicking it, then hit the Run button, and the segments fall into position as shown below.



We now have enough muscles in the model to start computing the muscle forces that can drive the motion. But there is one more detail to take care of, and it is both important and slightly intricate. The bottom line is: There must be something for the muscles to drive - some load to carry. We have not added any exterior forces to the model yet, but that is not the problem. You remember, perhaps, from [Lesson 2](#) that each segment has a mass. Additionally, the ArmModelStudy is equipped with a standard gravity of -9.81 units in the global y direction. This means that gravity actually provides the external force the analysis needs to make any sense.

What is the problem then? Well, unless you specify otherwise, drivers, like the ones we added to the elbow and shoulder joints, act like motors. This means that they provide whatever moment or force that might be necessary to make the motion happen. Although it would be practical, few of us have motors built into our joints. Instead, we have very efficient muscles so we want to leave the task of providing force in the model to them. The way to do that is to set a property called Reaction.Type for the driver to zero. This is how it's done for the shoulder:

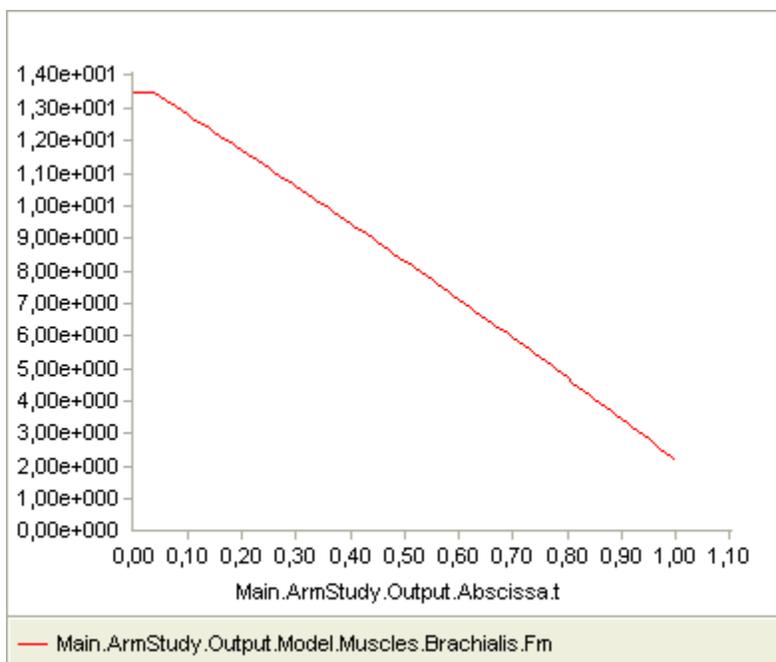
```
AnyKinEqSimpleDriver ShoulderMotion = {
  AnyRevoluteJoint &Jnt = ..Jnts.Shoulder;
  DriverPos = {-100*pi/180};
  DriverVel = {30*pi/180};
  Reaction.Type = {Off};
}; // Shoulder driver
```

This additional line makes sure that the driver provides the motion but not the moment. Why is AnyScript made that way? Why would anyone ever want to model a joint with a motor in it? The explanation is that AnyScript models for ergonomic studies often comprise machinery that the body of the model is connected to. And this machinery can have motors that provide moment or force input to the system. Why is the motor then switched on by default? Well, models under development often do not have enough muscles to move. Such models will not work before the last muscle is added unless they have motors in the drivers, and it is practical to be able to run an analysis now and then during development to check that the model works correctly.

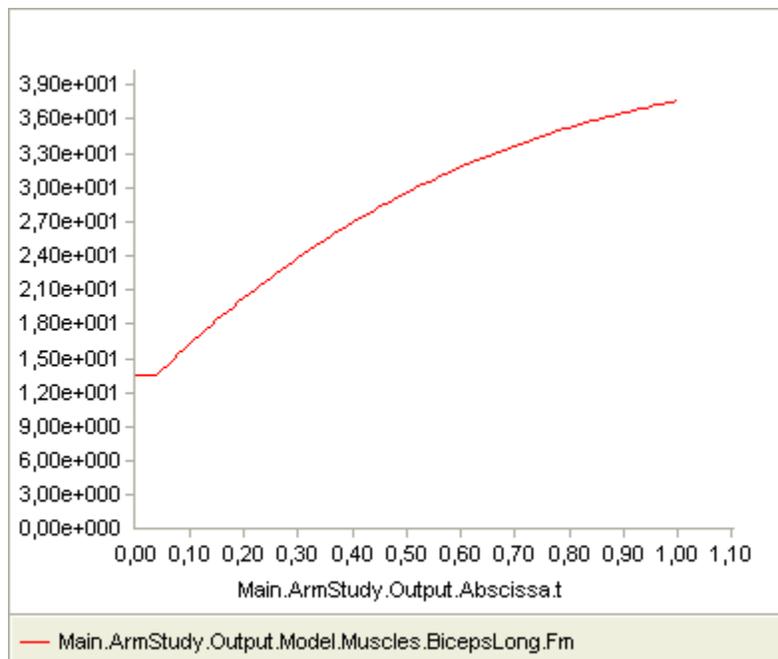
As you can see, the single Off is encapsulated in braces, {Off}. This is because it is a vector. A driver by default has several components and hence all the data in the driver is vector quantities. For semantic reasons this applies even when the driver only controls one degree of freedom as it does here.

Add a similar line to the definition of the elbow driver and we are ready to compute muscle forces. Click the

InverseDynamicAnalysis in the study tree at the bottom left of the screen and then the Run button, and watch the model move. It should look exactly like in the kinematic analysis, however, during this analysis, the AnyBody system computes all muscle and joint forces in addition to a whole lot of other useful information. To see it, you once again have to open a ChartFX window (if you don't have the one we used previously open) by means of the menu Window -> ChartFX 2D (new) in the pull down menus in the top of the main frame. In this new window, expand the ArmStudy -> Output -> Model -> Muscles branch. You should see a list of all the muscles appearing. Each of them can be expanded to reveal the data inside. Let us expand the brachialis muscle and investigate its force variation over the movement. You should see a node named Fm. If you click it, you should get a curve like the one shown below:



Notice that the force in the muscle drops as the movement proceeds. This is quite as expected, because the moment arm of the gravity about the elbow gets smaller as the elbow flexes, and less muscle force is therefore needed to carry it. If you look at the muscle force in the BicepsLong, you see a different pattern:



This muscle grows in force during the movement. That is because it is influenced by the movement of two joints, namely the shoulder and the elbow. In addition, it collaborates both with DeltoidusA on shoulder flexion, and with the other elbow flexors, and these muscles all have to level their work in relation to each other.

This might sound like there are heuristic rules built into AnyBody. This is not the case. AnyBody distributes the work between the muscles in a very systematic way: It solves an optimization problem to actuate muscles so that the maximum relative load on any muscle is minimized. This corresponds to postponing muscle fatigue as far as possible, and it causes muscle to collaborate as much as they can. This sometimes involves development of antagonistic muscle forces, i.e., forces that appear to contradict the movement but in fact relieve weaker muscles of load. Muscle synergy and the occasional presence of antagonists is well known from many experiments, and the minimum fatigue criterion used in AnyBody reproduces this behavior.

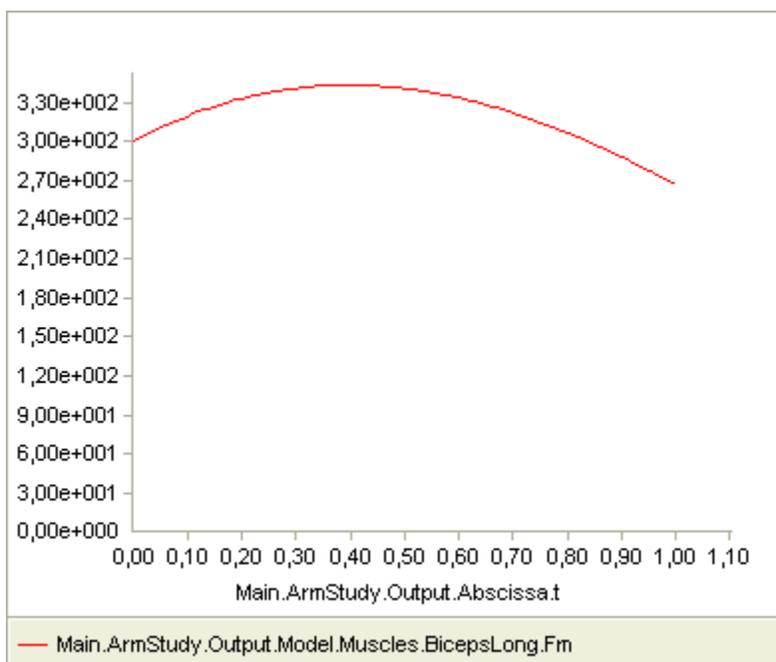
Now that we have the analysis going, we might want to investigate the model's behavior in different situations. A typical example could be to see how it carries an external load in addition to gravity. Let us imagine that the model is performing a dumbbell curl where it carries some load at the hand. We start by attaching a node to the forearm at the position of the palm. Add this definition to the ForeArm section:

```
AnyRefNode PalmNode = {
    sRel = {0.27,0,0};
};
```

The next step is to add an external force. We make a folder for this purpose:

```
AnyFolder Loads = {
    //-----
    AnyForce3D Dumbbell = {
        AnyRefNode &PalmNode = ..Segs.ForeArm.PalmNode;
        F = {0,-100,0}; // Force in Newton
    };
}; // Loads folder
```

That's all there is to it. Now you can analyze how the model will react to a downward force of 100 N (approximately 10 kg dumbbell weight). If you reload, rerun, and investigate the BicepsLong force again, you should see this:



The muscle force is obviously much larger than before, and the development is also different. It now reaches a maximum during the movement and drops off again.

Applied forces do not have to be constant. They can change with time and other properties in the model. Please refer to the [tutorial on forces](#) for more details.

There are infinitely many studies that could be made using even a simple model like this one, and you are encouraged to experiment a little or a lot. To get reliable results, however, would take at the very least an individual definition of the muscles with a realistic strength for each of them, and a more detailed modeling of the deltoid's origin-insertion path in the shoulder; it can be a comprehensive job to define a realistic body model which is exactly why most users would probably start out using [the body model available from the AnyBody Research Project](#).

This tutorial, being of introductory nature, will instead skip to a new subject: How can we add realistic geometries of bones and other elements to our model?

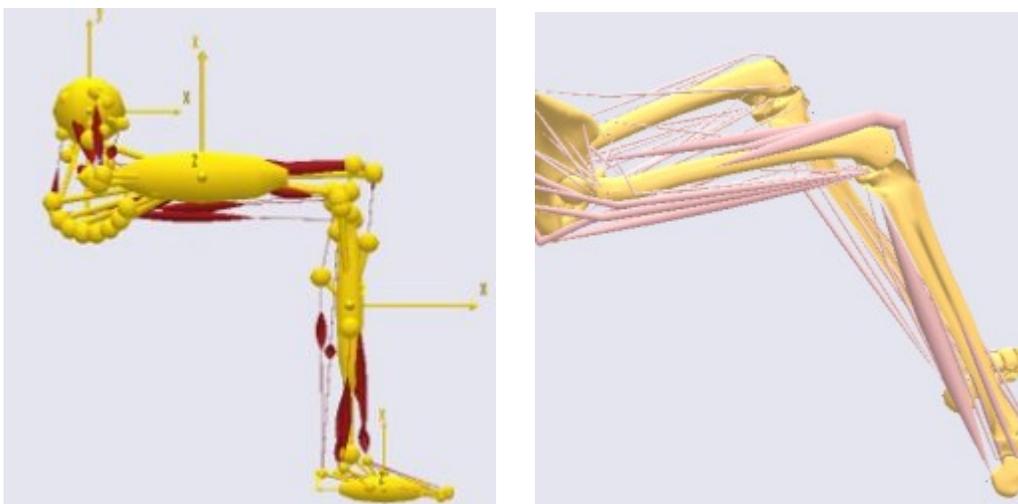
Now, let's continue to [Lesson 6: Adding real bone geometrics](#)

Lesson 6: Adding real bone geometrics

Here's an AnyScript file to start on if you have not completed the previous lesson: [demo.lesson6.any](#).

So far, the graphics of the model you have developed is what we can call a stick figure representation. This is a straightforward way of seeing the model and it reflects the mechanics very vividly, but it does not look

very physiological. You may be wondering how you can add cool bones and other geometries that will impress your colleagues and look good in your presentations. You may want to put your model into an environment such as a room, a treadmill, or a bicycle to illustrate the purpose of the model.



However, there may be other reasons than mere aesthetics why it can be advantageous to work with real geometries. When attaching muscles, for instance, a real bone geometry gives you an instant visual feedback on where the muscle is located in the organism as illustrated by the two pictures above.

Adding geometric models such as bones is fortunately very simple. All you need is a file with a 3-D graphical representation of the bone or other component you may wish to add. The format of the file must be STL ascii. STL is a very simple graphical file format that basically contains triangles. Virtually any CAD system you can think of can save geometry on STL format, so if you have your geometry described on IGES, STEP, DXF or any other usual type, just run it through your favorite CAD system and convert it to STL. STL comes in two varieties: ascii and binary. AnyBody needs an ascii file, so please make sure to choose that option if you create your own STL files in a CAD system.

The bone models you see on the pictures above are a bit elaborate for a short tutorial, so we shall start with something a little simpler. What we want to do now is to add a dumbbell geometry to the arm model we have just created. You can find a file to use [here](#). Right-click the link, choose "save as", and put the file in the directory where you have placed the arm model.

The dumbbell should be added to the forearm, so the first thing to do it to add a reference to the STL file we just saved to the definition of the forearm:

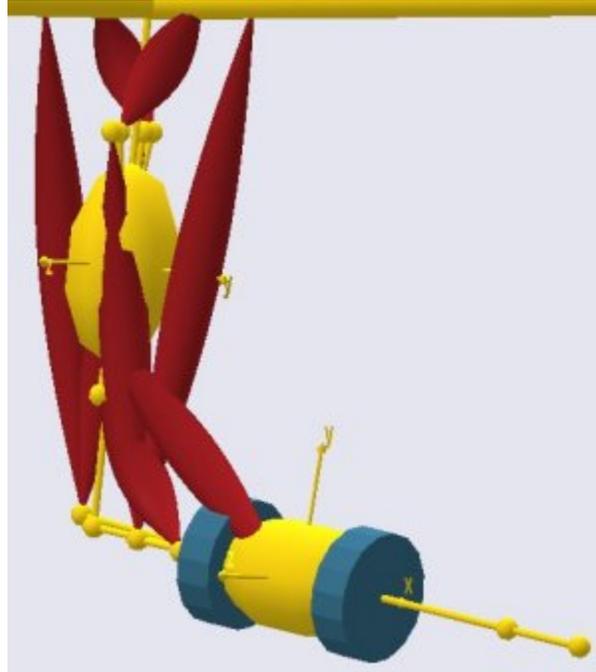
```
AnyDrawSeg DrwSeg = {};
AnyDrawSTL DrwSTL = {
  FileName = "dumbbell.stl";
};
}; // ForeArm
```

Try reloading the model again. You will probably see nothing but grey the Model view. A closer investigation of the problem would reveal that the entire arm model is actually situated inside the dumbbell handle. This is because the STL file was created in millimeters, where the arm model is in meters. Rather than going back to whatever CAD system was used and scale the dumbbell model down 1000 times, we can add the scale definition to AnyScript in the following way:

```
AnyDrawSTL DrwSTL = {
  FileName = "dumbbell.stl";
```

```
ScaleXYZ = {0.001, 0.001, 0.001};
};
```

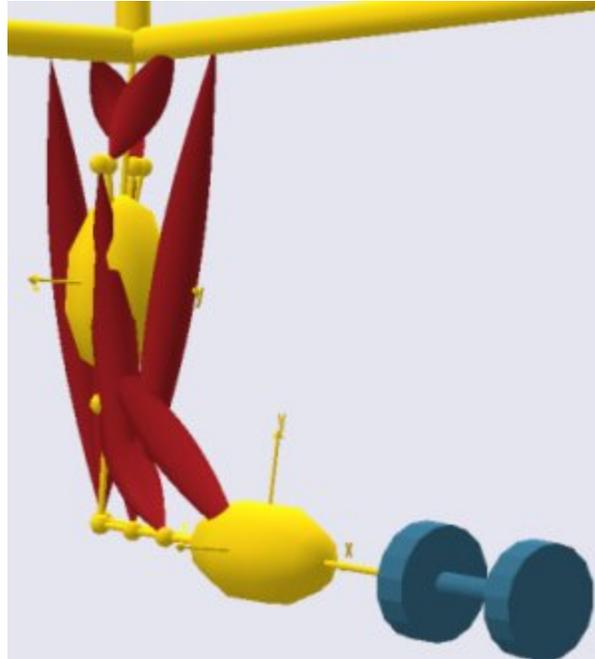
When you reload the model, the picture you get should be similar to what you see below. The dumbbell is visible now and has the right size, but it is sitting at the center of gravity of the lower arm rather than at the hand, and it is not oriented correctly.



The fact is that, when you attach something to a segment, it is positioned at the segment's origin which is usually the same as the center of mass. However, you can also attach stuff to points, so moving the dumbbell to the hand is simply a question of moving the reference to it from the ForeArm segment to the PalmNode that we defined previously. Block the entire AnyDrawSTL folder with the mouse and cut it out. Then re-insert it under the PalmNode like this:

```
AnyRefNode PalmNode = {
  sRel = {0.27,0,0};
  AnyDrawSTL DrwSTL = {
    FileName = "dumbbell.stl";
    ScaleXYZ = {0.001, 0.001, 0.001};
  };
};
AnyDrawSeg DrwSeg = {};
}; // ForeArm
```

On reload, this produces a new picture with the dumbbell attached at the right location, but it is still not oriented correctly.



We want to rotate the dumbbell 90 degrees about the y axis. We could do that by going back to the CAD system and modifying the dumbbell STL file, but an easier option is to rotate it directly inside AnyScript.

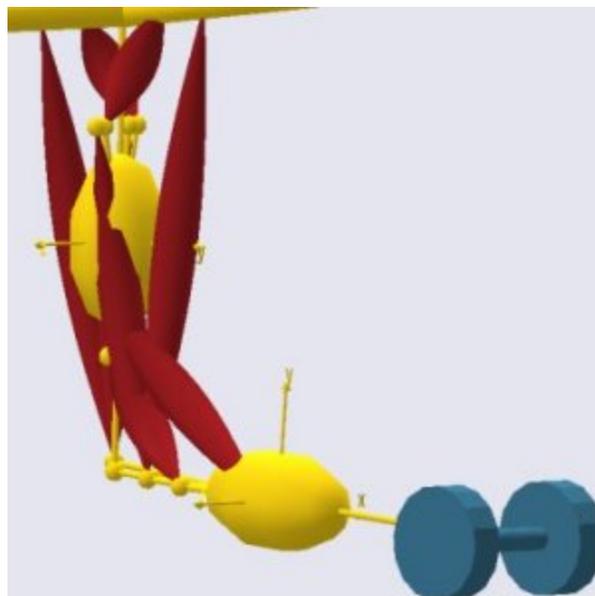
A geometrical object that you insert gets the same orientation as the coordinate system it is attached to. In this case the dumbbell is attached to PalmNode. Nodes are actually reference frames with the ability to be positioned and oriented relatively to other reference frames, for instance a segment or another node. We have already positioned nodes by means of the member vector sRel and relative orientation happens similarly with the member matrix ARel, the relative rotational transformation matrix. We wish to rotate the dumbbell 90 degrees about the local y axis and hence write:

```
AnyRefNode PalmNode = {
  sRel = {0.27,0,0};
  ARel = RotMat(90*pi/180, y);
  AnyDrawSTL DrwSTL = {
    FileName = "dumbbell.stl";
    ScaleXYZ = {0.001, 0.001, 0.001};
  };
};
```

As a final cosmetic touch, you may want to change the color of the dumbbell. This can be done by adding the property RGB to the STL file reference:

```
AnyDrawSTL DrwSTL = {
  FileName = "dumbbell.stl";
  ScaleXYZ = {0.001, 0.001, 0.001};
  RGB = {0.2,0.4,0.5};
};
```

The RGB property specifies the blend of colors Red, Green, and Blue in that order for displaying the STL geometry. The combination above produces a dull blue shade.



This completes the Getting Started with AnyScript tutorial. The final result of the efforts is in demo.arm2d.any.

Interface features

This tutorial deals with the interface features of the AnyBody Modeling System. Before trying your luck with this tutorial, please complete the [Getting Started with AnyScript tutorial](#).

Much of the interface works like other types of windows software; you can copy and paste data, and you can arrange the various windows as you would expect. But AnyBody does computations that no other computer system is capable of, and this calls for some special features.

We need something to work on. Please [download this file](#), save it in a working directory of your choice, and load it into the AnyBody Modeling System.

The squat problem

The file you have loaded is a squat example. It is a 2-D model and contains only a single leg with eight muscles. The strength and mass of the single leg correspond roughly to two ordinary legs.

The arm of the model is used for balance. It does not have any muscles, and it has no explicit driver attached, but if you run the kinematic analysis or the inverse dynamic analysis on the model you will see that the arm moves to maintain the balance of the model. This is because the model has a driver on the position of the collective center of mass requiring it to be directly above the contact point with the ground, which the model accommodates by movement of the arm.

This tutorial consists of the following lessons:

- [Lesson 1: Windows and workspaces](#)
- [Lesson 2: Editor Window Facilities](#)
- [Lesson 3: The Model View Window](#)
- [Lesson 4: The Chart View](#)



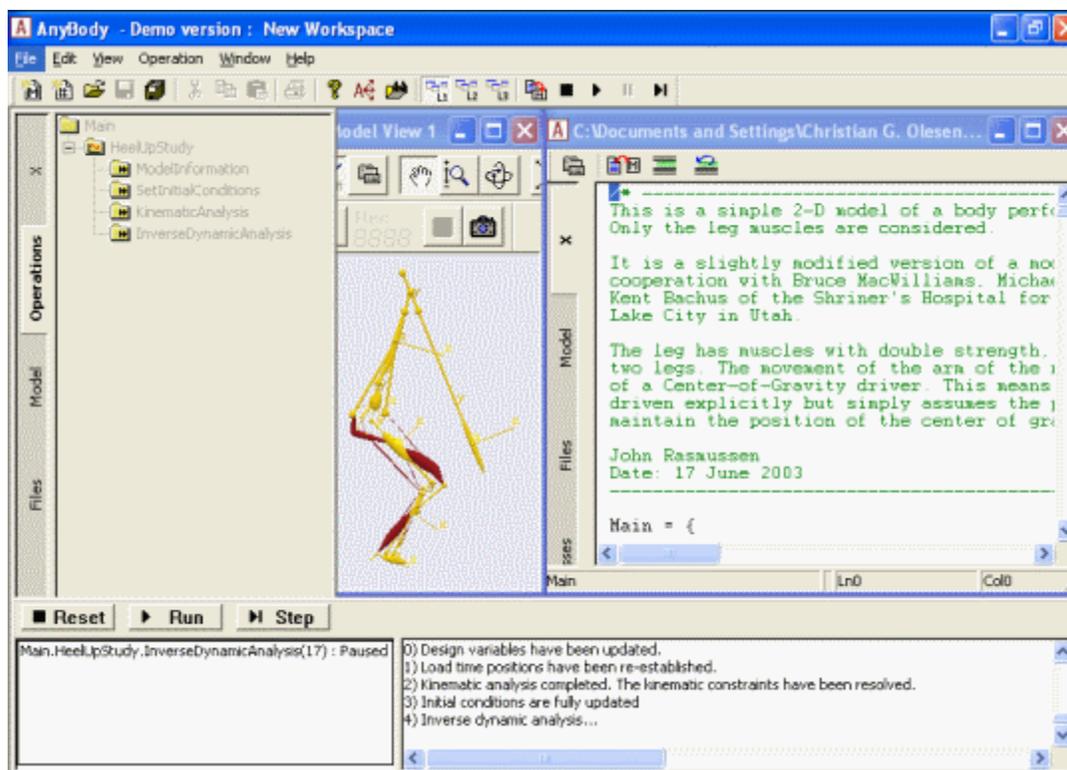
- [Lesson 5: The Command Line Application](#)

Let us quickly proceed to the first lesson: [Windows and workspaces](#).

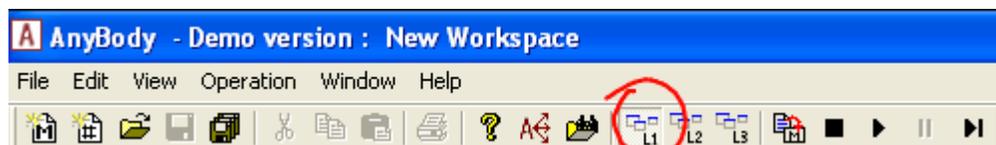
Lesson 1: Windows and workspaces

When you work with a model like this, you are likely to initially go through a series of model refinements, subsequently conduct a number of investigations, and finally extract data for further processing or reporting. This may be a process going on over a longer period where you start and stop the AnyBody Modeling System several times, and you want to quickly come back to the windows layout fitting the task at hand. This section is about how to control your windows layout.

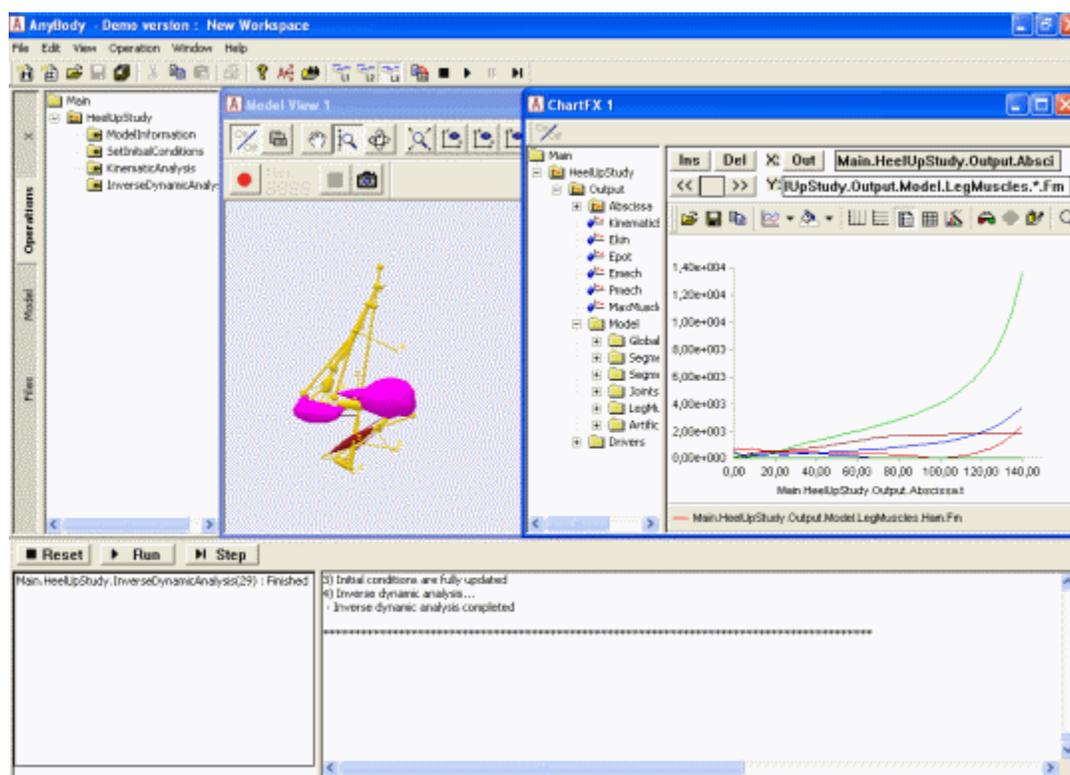
When you start the AnyBody Modeling System, load the model, and open a model view window, you will get the standard layout of windows in the AnyBody workspace. It looks like this:



This layout is standard because it gives you a little bit of everything. But it may not be what you want for a particular task. You may also find yourself doing a number of basically different tasks for which different windows layouts are convenient and being annoyed about having to change layout every time you change task. Therefore, the system offers you three different user layouts that you can set up as you like and switch between. If you look at the top of the main window, you will notice that the button, L1, is pressed in.



This indicates that you are now working in the first of the three user-defined layouts. Each layout can contain a different user-defined window setup, and you can switch between them by a single mouse click. Try running the HeelUpStudy.InverseDynamicAnalysis and open a ChartFX window to investigate the results. Perhaps you want to simultaneously see the Model View window, the Chart window and the AnyScript code, while you are not particularly interested in the Operations window at the bottom of the screen. You might arrange the windows as show below.



Suppose you have very carefully set this window layout up and want to keep it for later use after you have worked with another layout. How can that be done? Simple, you just press the L2 button. This will give you a fresh layout to work on, and you can always go back to what you had by pressing L1 again. Whichever layout you create under one of the L1, L2, and L3 buttons is kept for later use.

Workspaces

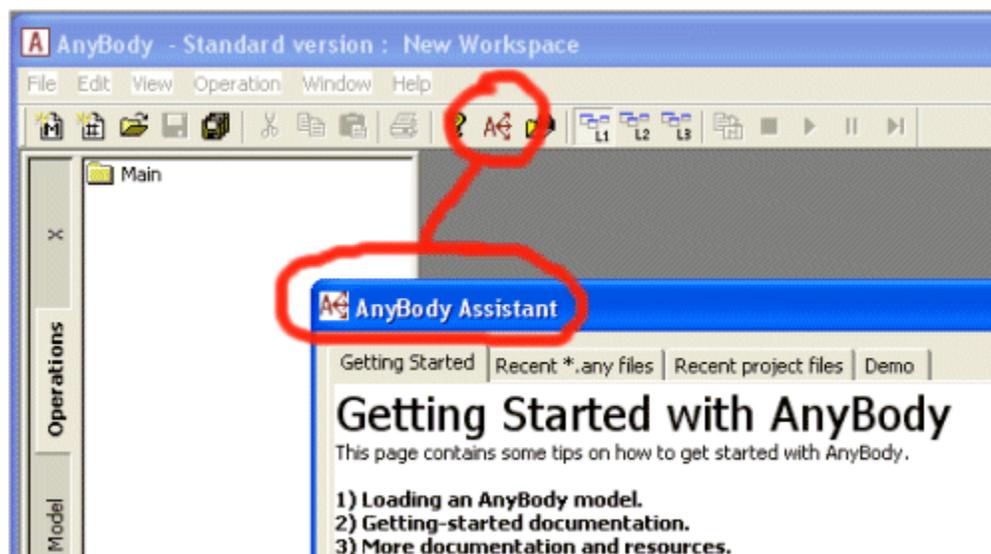
So, how do you preserve all the windows layouts when you have invested much time in setting them up and have to shut your computer down for the night? The answer is to save the workspace. A workspace file is a description of the state of your user interface. Notice the title of the main window:



It says "New Workspace" because you did not load a workspace when you started, and you have not yet saved the one you have created. Click File-> Save Workspace as..., pick a directory and a suitable name, and save the workspace. Then exit AnyBody, and start the system again.

When you have re-started, click File->Load Workspace..., browse your way to the workspace file you just saved, and load it. You will get the windows layout back that you had when you started. You can also find a workspace file in Windows Explorer and double-click it. The workspace files have the extension .anyws.

In addition, you can conveniently find recent workspaces in the AnyBody Assistant dialog box, please see the picture below. In the Recent Project files tab, you will find recent workspaces and main files listed. A complete list of recently uses AnyScript files is found in the Recent *.any files tab.



Window properties

Each window is equipped with a number of properties that are saved with the workspace. This set of properties is often updated in newer version of AnyBody in order to make the workspace storage of your working environment as good as possible and in order to match new functionality added to the windows.

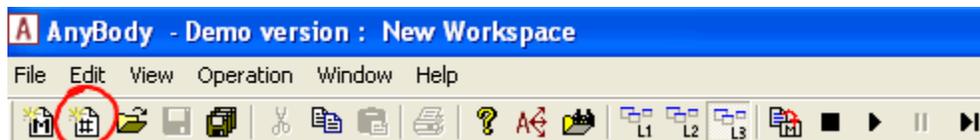
Some of these properties can be accessed and set by the user. This can be done from the Main Frame menu item Windows -> GUI Properties. Selecting this item opens a the Properties Window that show the properties of the current window. Some windows, where frequent access to the properties may be needed, for instance the Model View and AnyChart View, have a button on thier toolbar for easy access to the

properties. Look for a button looking like this  on the toolbar of a window.

[In the next lesson we shall proceed to have a closer look at the individual window types, and why not start with the Editor Windows.](#)

Lesson 2: The Editor Window

We need something to work on. Let us create a blank file and type something into it using the editor. The way to do that is to click the "New Include" button on the toolbar:



This brings up a new editor window with an empty file, and we can go ahead typing anything we want. The first thing you have probably noticed about the AnyScript editor is that it recognizes the predefined class names and highlights them automatically. It does this all the time as you are typing, and it is a great help to avoid misspellings that might later lead to annoying syntax errors.

Syntax Highlighting

When you start typing something, the writing color is black. This is the standard color in the editor for things that have not been recognized. For instance, if you start defining a segment, you may type (try it!):

```
AnySe
```

And the text remains black until you type the last character of the reserved word:

```
AnySeg
```

at which point the text becomes blue. This can be a great help if you are not quite sure about the name of a particular object. You can try typing the different forms of the name, and when you hit the right one, the text turns blue. The editor similarly recognizes comments. If you precede the AnySeg class name with a double-slash, the entire line turns green:

```
// AnySeg
```

Please notice that similar to C, C++, Java, and JavaScript you can turn entire blocks of code into a comment by encapsulating it into a pair of `/* */` delimiters. Another easy way to temporarily remove and re-activate several lines from the file is to block the text in question and use the two buttons  in the toolbar of the Editor window. This automatically places or removes double slashes in front of each line in the block.

Please also notice the so-called Documentation Comments. This is comments using the following syntactical forms: `/// ...`, `/** ... */`, `///< ...`, and `/**< ... */`. The Documentation Comments are related to a given object in the model and these comments are treated specially so the information can be accessed more conveniently after loading the model and thereby help the user of a model to understand the model without reading the code. In the editor, the Documentation Comments do however have the same color as other the normal comments. The Documentation Comments' form is similar to other source code systems like JavaDoc, Doxygen, and others.

Automatic Indentation

When developing software that is hierarchical it is customary to indent the code according to the hierarchical level of each line. This greatly improves the legibility. In the AnyScript editor we have decided that the standard indentation for each level is two spaces. The editor automatically keeps track of where you are in the code as defined by the start and end braces, and it helps you make the right indentations as you type. Let us continue the segment definition we started above. Remove any leading double slashes and proceed to type

```
AnySeg Segment1 = {
```

and hit the Return key to change line. Notice that the editor automatically indents the next line by two

You are not forced to accept this. You can easily backspace to the beginning of the line and start your typing there, if you like that better. You might write something like:

```
AnySeg Segment1 = {
Mass = 1.0;
```

The editor will discover that you did not like its suggested indentation, so the next line you type will begin at the same character as Mass, and you may proceed to finish the definition of the segment by typing:

```
AnySeg Segment1 = {
Mass = 1.0;
Jii = {0.1,0.01,0.1};
};
```

Auto format

Perhaps you decide at this point that the indentation is better after all. (If you do not decide at this point, you surely will when you have written a few hundred lines and are trying to balance your start and end braces.) So, how can you restore the default indentation? Well, the AnyScript editor has a very nice feature called Auto format. It allows you to block a part of the code or the entire file and indent it in one simple step.

Try highlighting the block you have written, and press Alt-F8. You should get this result:

```
AnySeg Segment1 = {
  Mass = 1.0;
  Jii = {0.1,0.01,0.1};
};
```

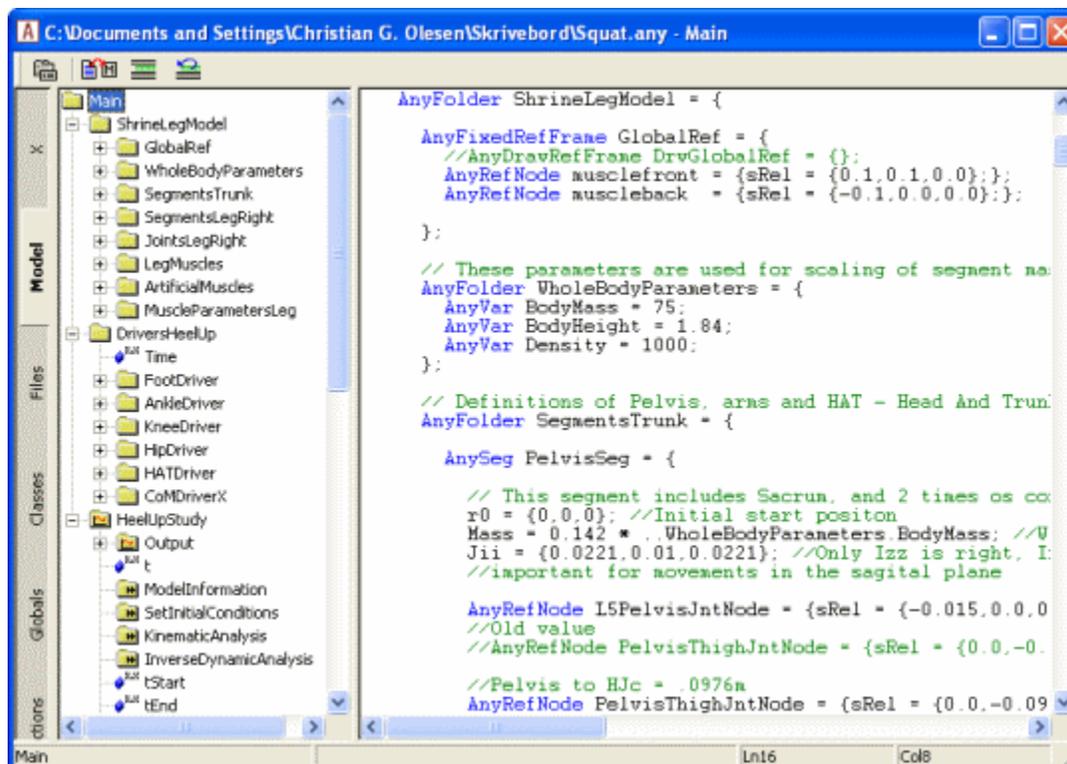
This facility is also available in through the pull-down menu Edit->Format Indentation.

If you are ever in a situation where the model will not load and you suspect that you have forgotten a brace somewhere, simply block the entire file and apply Auto format to it. You will usually be able to see by a few glances where the error is located.

You can also manually control the indentation of a block of lines. A highlighted block of text can be indented or unindented in steps of two spaces by pressing Tab or Shift-Tab.

Tree Views

The structure of an AnyScript model is hierarchical. This means that it is obvious to represent the loaded model as a tree, and the system makes extensive use of this representation in all its different window types. If you still have the squat model from the previous lesson open, go to the main file and load it (key F7). You should see a tree at the left hand side of the editor window as in the figure below.



What you see here is the Model Tree, which is the main tree view of AnyBody showing all objects in the loaded model in the structure they are created in the AnyScript code. The Model Tree is in principle available in many of AnyBody's windows, but some of the information is filtered out in some window types to make the tree view practical for specific purposes such as browsing output or operations in the model.

The Editor windows have the complete unfiltered Model Tree, and they can take up a significant space in the Editor window. Therefore, they are by default collapsed to maximize the space for editing and an unfiltered Model Tree is also available on the Main Frame, which is sufficient for most purposes. Multiple Model Trees can, however, be handy when working with large models and browsing for information in different places of the structure; this is the reason for having the option of opening a Model Tree in the Editor windows. Moreover, the Model Trees in the Editor have to options for interaction with the code of the particular Editor Window, which is not available from the Main Frame Model Tree. You can collapse the tree again after opening it by clicking the X tab on the left hand side of the tree.

We shall not go into details about the functionality in the Model Tree, but notice that right-clicking an object in the Model Tree give you access to these functions. There are two categories of these functions:

1. Interaction with the AnyScript code such as inserting object name into the code at the place of the cursor
2. Class Operations that are operations associated with the AnyScript classes. These cannot be explained in detail here because they follow the classes, but there are a couple of very basic Class Operation that is available to all objects.

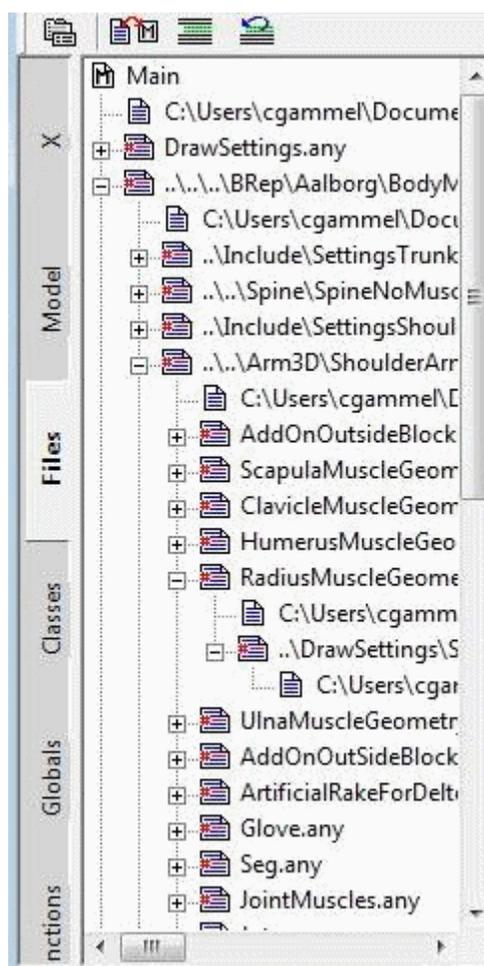
In particular notice the Class Operation called Object Description that comprise much practical information for the given object, including the Documentation Comments made by the AnyScript programmer making the model. The Object Description is very useful when browsing the model because it contains active links, which for instance can bring you to the code with single click. The Object Description is considered to be the most fundamental operation in the Model Tree so it will be activated when you double-click any node in the tree.

The Model Tree offers you several options to go from the tree to associated places the AnyScript code. There are, however, also options to go the opposite way, i.e. from the code to the Model Tree. Try right-clicking the code. You will then get a pop-up menu with several editor options. One of these is "Locate in Model Tree". It will probably be greyed, i.e. disabled, because you have not selected anything that can be related to the tree. But if you try highlighting an object name in the code it should become active. Selecting this will bring you to the specific object in the Model Tree. In some cases, there is not a single clear one-to-one correspondence between the code location and the Model Tree. This happens if the code, you look at, is in an include file that have been included several times in the model. In such cases, the Editor will provide you with a list of options to select from.

As you can see, there are also other tree views available. Clicking the Files tab will give you an overview of the model's include file structure. Models in AnyScript are often divided over several files where one main file links to other files, which link on to other files and so on. The links are realized by means of include statements in the AnyScript code:

```
#include "includefile.any"
```

The File Tree is very unimpressive in this model because it does not have any include files, but below you see a File Tree from a more complicated model:



The leaves in the tree are marked by two different icons. The icon with the little red # sign points to a place in the model with an include statement. If you double-click such a line you will be taken to the position of the include statement. If you click the + to the left of the icon, the branch folds out, and you see another icon below without the # sign. If you click this icon, the include file itself opens up in an editor window.

The third tab in the tree view is named Classes. It gives you access to a tree of the predefined classes in the system. From this tree you can insert templates of new objects. This eliminates much of the need to remember the syntax of each object and saves you many lookups in the reference manual. The use of the Classes Tree is described in the [Getting Started with AnyScript tutorial](#).

There are a couple of more tree views. These contains global objects that are available to your code. Global AnyScript constants are listed in one tree and global AnyScript function in another.

Find and Replace

No editor is complete without a find and replace function. The function in the AnyScript editor is not much different from what you find elsewhere. It is accessible through the Edit menu or by the keyboard shortcuts

Ctrl-F for find

Ctrl-H for find and replace.

F3 repeats the previous find operation.

Support for External Editors

Some users have very strong preferences when it comes to editors. The AnyBody Modeling System allows you to use any text editor you like to author your models as long as it saves the files on an ascii text format.

The Main file must be open in the AnyBody Modeling system initially to allow compilation. Once you have compiled it, the system remembers the current Main file, and it will re-compile it every time you press F7. This means that you can edit and save any Main or include file by means of an external editor and compile it from inside the AnyBody Modeling System.

So what happens if you have a file open in an AnyBody Editor Window, and you are simultaneously editing it in an external editor? Well, every time you press F7 to compile the model, the system will attempt to save any changed files to pass them on to the compiler from the disk during the compilation. But before the system saves the file, it checks if the file has been updated from elsewhere, for instance from an external editor, and the system will ask you if it is supposed to load the newer file into the AnyBody Editor Window.

- If you answer yes, the new file is loaded and used in the compilation.
- If you answer no, the old file is saved and used in the compilation, overwriting whatever you have saved from the external editor.

[Let us venture to have a closer look at the Model View](#)

Lesson 3: The Model View Window

The Model View window is the system's graphical representation of the model. You can open a Model View window by the Window->Model View (new) command.

The Model View displays a special type of model elements that we usually call "Draw Objects". These are the objects you can attach to the segments, muscles, nodes, surfaces and such on the model. Most classes in AnyScript have corresponding draw classes, and the library of draw classes is constantly being extended and improved.

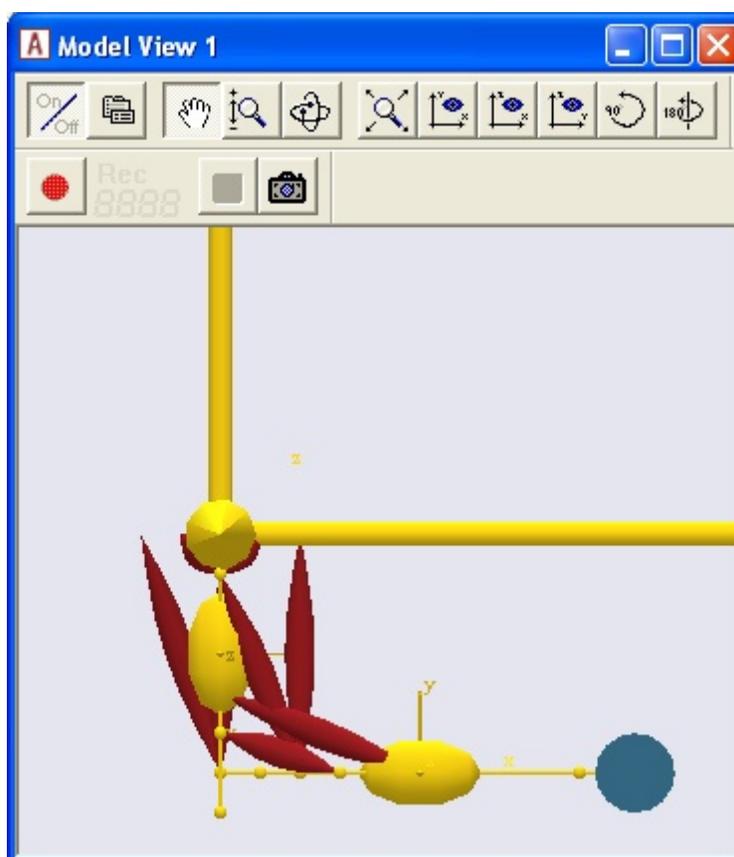
When active, the Model View updates the model as the computation proceeds. The update can involve the elements moving on the screen or colors or shapes changing to reflect the state of the model such as, for instance, muscle forces.

If the model is not too big and the computer is not too slow, the computation runs fast enough to create a dynamic animation in real time or close to that. However, for many larger models, the computation is too slow to give you a dynamic impression of the model's movement. The model view then provides the opportunity to save the individual frames for subsequent processing into a video animation that you can play at any speed you like.

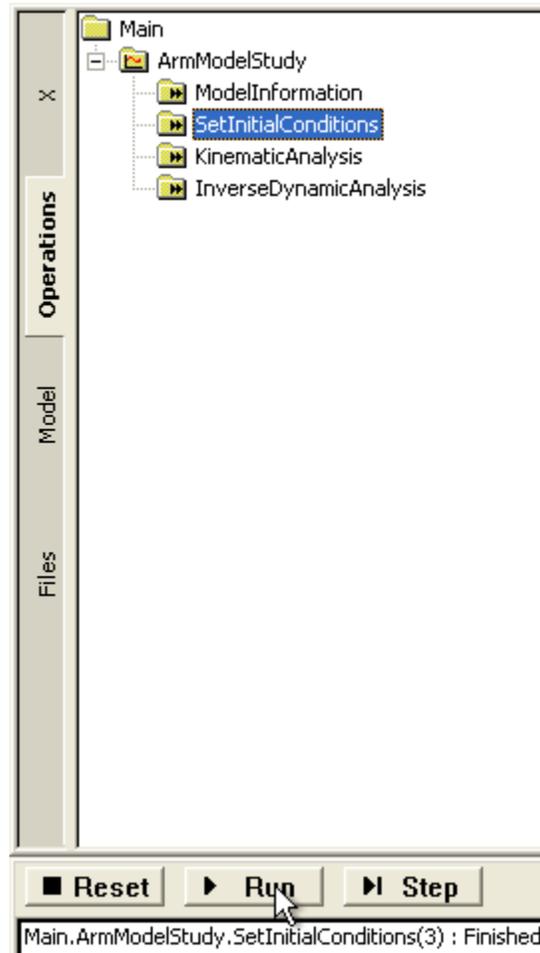
This lesson looks into the functionality of the Model View, and even though you can probably use it intuitively, you may also pick up a useful trick or two you did not know about.

As usual, we need a model to work on. For this tutorial you can pick any model you may have, or you can download the familiar dumbbell example here: demo.arm2d.any. You will also need the accompanying STL file: [dumbbell.stl](#).

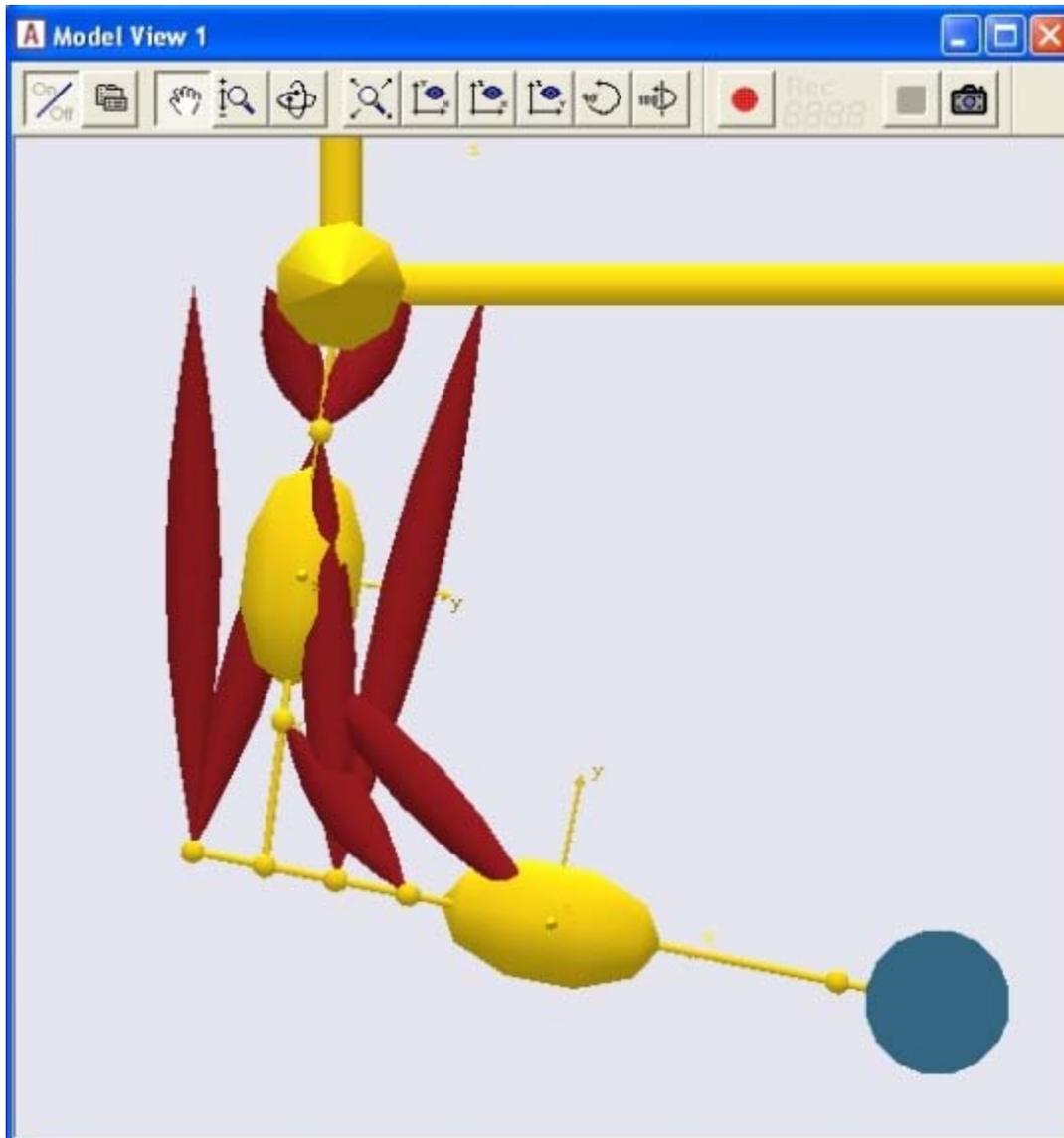
Load the model into the AnyBody Modeling System and click Window -> Model View (new). You should get a window looking like this:



- The model is centered in the window, and you should be able to see all its elements. When you open a new Model View, the window automatically applies a Zoom All function that shrinks the view until all elements are visible.
- The model is not necessarily assembled correctly. All the segments at load time are positioned where they are defined in the AnyScript model. These positions rarely comply with the kinematical constraints such as joints. In fact, you might want to assemble the model above correctly by running the SetInitialConditions operation in the ArmStudy at the lower left corner of the screen.



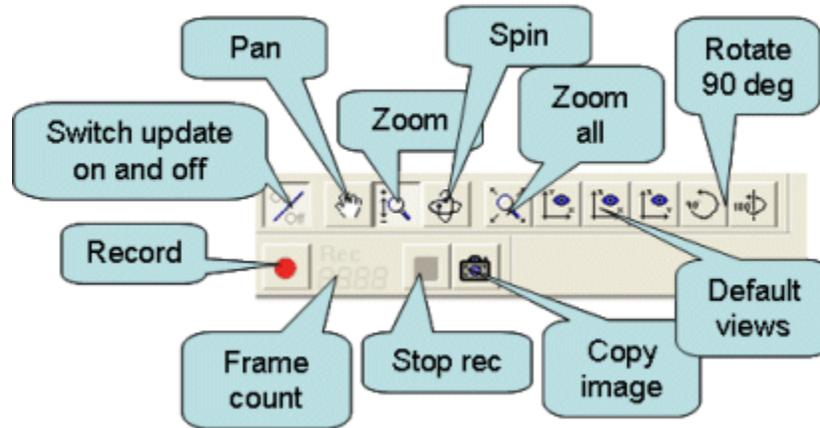
This resolves the kinematical constraints and puts the model into the position defined by its drivers at time step 0. It produces the picture shown below.



Notice that we are looking at the model directly from the side. The default viewing direction is the xy plane. This coincides well with the [International Society of Biomechanics](#) standard of letting the sagittal plane coincide with the global xy plane.

The Toolbar

The Model View has its own toolbar with following button functions:



- **On/Off:** This button switches automatic update of the window on and off. When switched off, the window does not update when the model is moving, and it is not possible to rotate, scale and pan the view. The advantage of switching the update off is that it makes the analysis run faster, especially on computers without a separate graphics processor.
- **Properties** : Button that opens the properties window (equivalent to menu item Windows -> GUI Properties). In the properties, you have options for setting properties more specifically. We shall not go into details about these options here, see below.
- **Pan tool:** Selecting this tool causes the cursor to change shape to a hand. When you drag the mouse over the screen with the left button down, the picture moves with it.
- **Zoom tool:** When this tool is active, the cursor resembles a small magnifying glass. When you drag the mouse over the picture with the left button down, it zooms in or out for upward or downward movements respectively.
- **Spin tool:** This tool allows you to spin the model dynamically on the screen by dragging the mouse with the left button down. The function is very intuitive and you will soon get the hang of it. It works like the model is attached to an imaginative sphere centered on the screen. When you hold down the left mouse button, you are grabbing the surface of the sphere and spinning it with the movement of the mouse.
- **Default views:** These three buttons represent predefined viewing directions: the xy plane (standard), the yz plane, and the xz plane respectively.
- **Zoom all:** This button refits the view to contain all the drawing elements.
- **Record:** This button starts video frame capturing explained in more detail below.
- **Frame count:** This panel displaying the number of captured frames during a recording.
- **Stop recording:** This button stops a video frame capturing session. The function is explained in detail below.

Model View Properties

The Model View properties accessible to the user contains three groups:

1. View point settings that are also set by the typical interaction with Model View. Through Pan, Zoom and Spin operations. These settings in the Properties be set directly or they can be grapped for use in a camera implemented into your model. The view point definition in the properties of Model View is using the AnyScript class AnyCameraModelView. This is done to enable easy exchange of view point properties between model and Model View. The individual properties is introduced in the AnyScript Reference Manual.
2. Viewer properties that control viewer behavior.
3. Scene properties that control general scene properties, such as back ground color, that are not given in the model definition.

Recording video

You may want to save a video file of your simulation for a presentation or simply to be able to show a large model running in real time. The model view provides the opportunity to save the individual graphics frames for subsequent processing into a video animation that you can play at any speed you like.

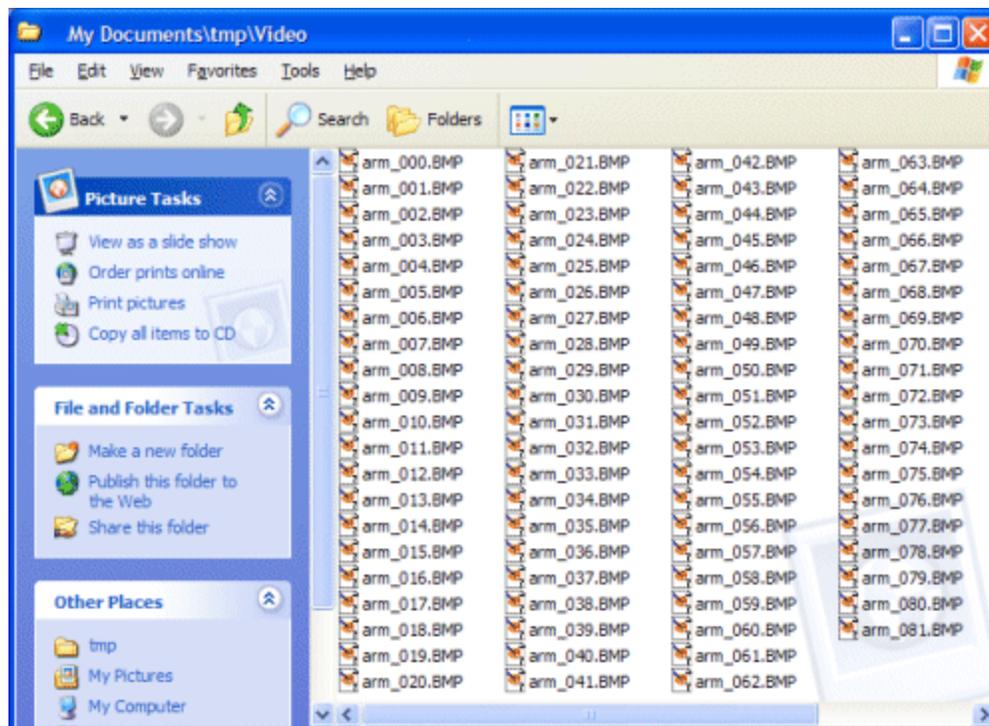
The function works much like a video tape recorder in the sense that you can push the red record button any time you like, and what happens in the window is subsequently saved for further processing. Let's see how it works. Try clicking the record button. A file manager will pop up and request you to select a location and a naming of the files you make. The name you select will be appended with _nnn where nnn is the frame number of each image. You can also select the image type, and jpeg is usually a good choice to limit the size of the images on the disk.



You will notice that the frame counter lights up, the "Rec" letters flash, the record button becomes inactive indicating that you cannot push it twice, and the stop button becomes active indicating that you can push it.

Everything that takes place in the window will now be recorded. Try spinning the model around **a little** with the mouse and notice how the frame counter adds up. Notice that the system is intelligent enough to not record anything when nothing is happening. This means that you are in no hurry when you have pushed the Record button. The system only grabs frames when the picture actually changes. This happens either when you manipulate the picture manually as you did here, or when an analysis is running and producing new pictures as it proceeds. If you record an analysis with 100 time steps, then you will get 100 frames saved.

When you have 50-100 frames, push the "Stop recording" button. The system will ask you whether you really want to save the frames. If you answer no, they will be erased. If you save the frames you will be left with a bunch of image files like this:



The AnyBody Modeling System does not provide a video editing facility to process these files into an AVI, MPEG or similar video file format. However, many really good and cheap utilities are available for this

purpose. We at AnyBody Technology use a very good and inexpensive tool called VideoMach available from <http://www.gromada.com/>.

Size matters

Regardless of how videos are processed, they are rather data intensive, and it is a really good idea to plan the recording well. Depending a little on the image format, the size of the frames you are saving is proportional to the area of the Model View. This means that it is more rational (and usually gives a better result) to resize the shape of the Model View to the animation you want in the end, than it is to change the size or crop the video afterwards.

[The next lesson deals with the two different Chart Views for investigating analysis results.](#)

Lesson 4: The Chart Views

The AnyBody Modeling System has two different window types for graphing results:

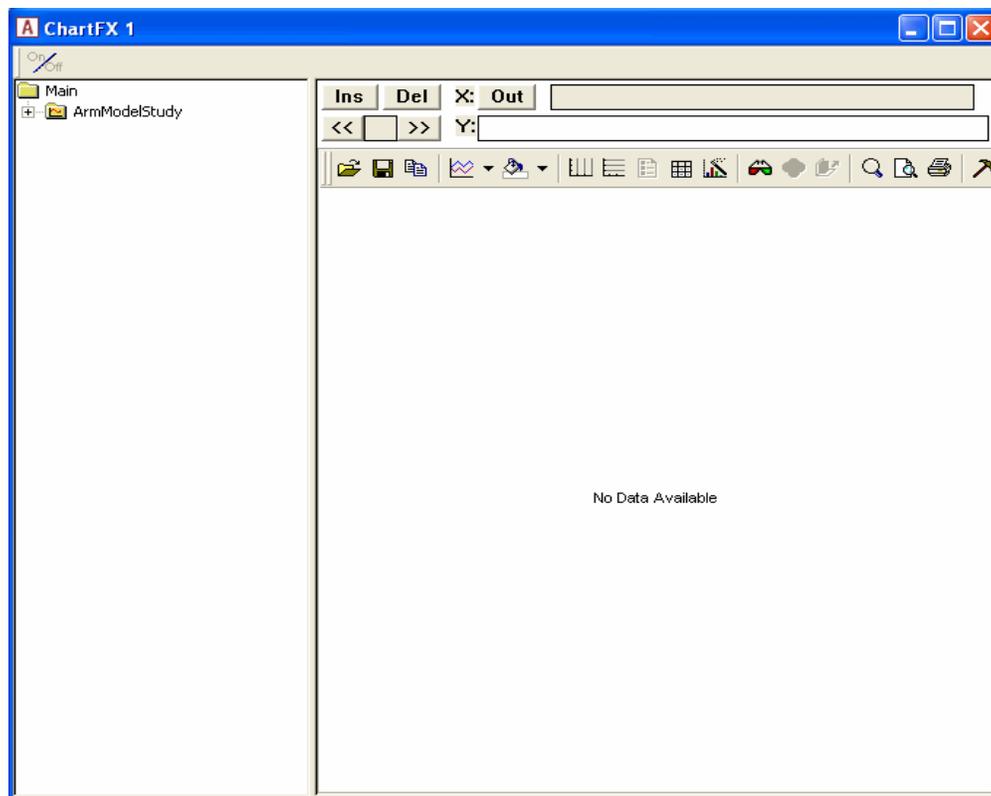
The ChartFX View and the AnyChart View. The former gives you a large gallery of different graph types to choose from and has useful features for interfacing with other windows applications such as the option to copy data on many different formats. However, this view is restricted to two-dimensional graphs.

The AnyChart View gives you the opportunity to make three-dimensional surface plots. It is based on the AnyScript drawing object class also called AnyChart and this reuse of functionality allows you to make identic charts in the AnyChart View and inside the model scene, i.e., in Model View. AnyChart is still a fairly simple chart option, but its functionality is being extended in future version of AnyBody.

The ChartFX View

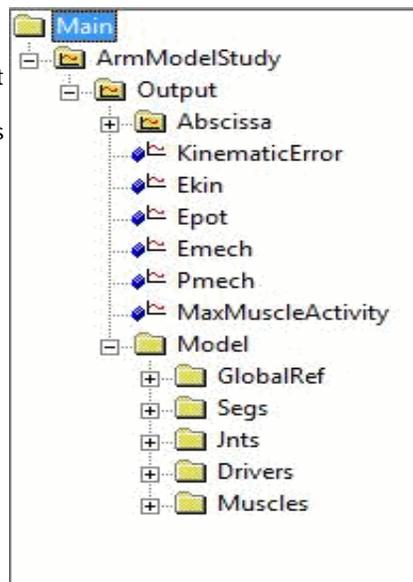
Do you still have the demo.Arm2D.any model loaded? If not, try loading it in and we'll play a little with it and see how results can be investigated.

Please load the model and run the ArmStudy.InverseDynamicAnalysis. Then open a ChartFX View by clicking Window -> ChartFX (new). You will get a window like this:



Notice that the window like all other windows in the AnyBody Modeling System is divided into a tree pane on the left and the actual data area to the right. If you play around a bit with the tree you will soon see that it resembles the trees from most of the other window types, but that some stuff is missing. This is because the tree is filtered, and it requires a further explanation:

The AnyBody Modeling System contains a special type of data called output data. This is essentially what comes out of a computation. Output data is organized in series with one item for each time step of the analysis, so the output data is not available until an analysis has been performed. The tree in the Chart View has been filtered such that you only see the output data. This makes browsing a bit less confusing. However, the tree retains its basic structure, so to get to useful data you normally have to expand the tree through Main.ArmStudy.Output.Model. Notice that the other option next to Output is Abscissa. The standard Abscissa in an InverseDynamicAnalysis is time, so if you expand the Abscissa branch and click the 't' variable, you will get a straight line with slope 1 because you are plotting time against time.



Global output data

Directly under output you also find some data pertaining to the "global" properties of the model:

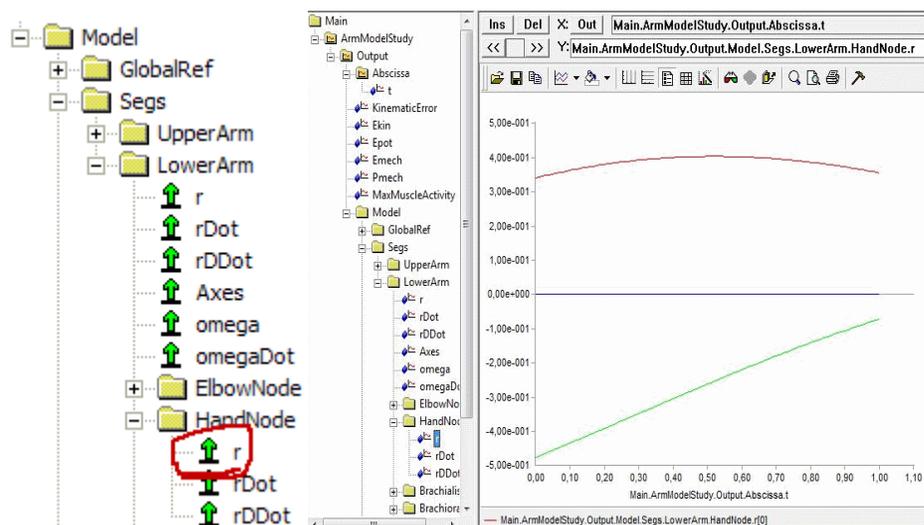
- Ekin - the total kinetic energy of the system
- Epot - the total potential energy of the system
- Emech - the total mechanical energy of the system, i.e. the sum of potential and kinetic energies
- Pmech - the mechanical power of the system

Try clicking Ekin, Epot, and Emech in turn. You will notice that Epot and Emech are very similar. This is because the movement in this model is relatively slow, so the kinetic energy remains small throughout the simulation and has little influence.

The **KinematicError** is not very interesting unless something is wrong with the analysis. It stores the error in the kinematic analysis as a measure of how far the kinematic constraints of the problem are from being satisfied. Normally this should be zero or very close to zero. If it is not, information about the development of the kinematic error may help you determine the cause of the problem.

Finally, the **MaxMuscleActivity** is the a measure of the overall effort of the body model but it requires further explanation, so we shall get to it a little later.

Time-dependent data



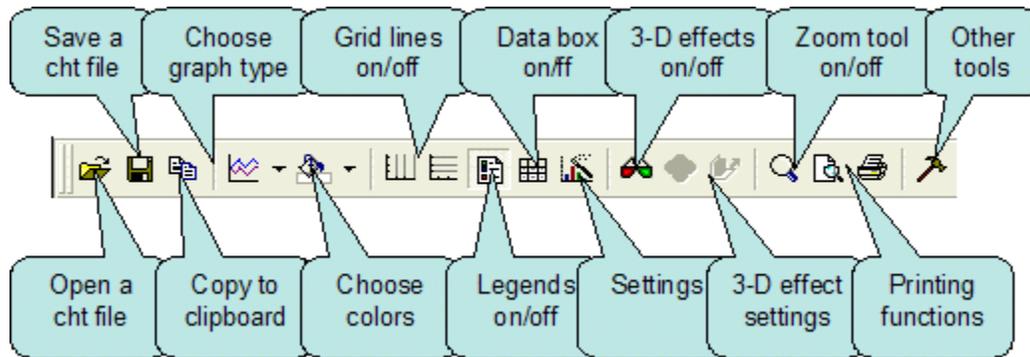
The predominant way of looking at data is as a function of time or rather time steps. If you expand the Model branch into the Segs section, you can investigate the movement of the "hand" of the model as shown in the figure above.

Expand the tree until you get to the HandNode object as shown to the left. Then click the r property. This displays three curves on the screen corresponding to the x, y, and z coordinates of the handnode as the arm moves. The z coordinate is zero because it is a 2-D problem. By the way, the color codes of the chart view are red, green and blue in that order, so red is for x, green is for y, and blue is for z.

Let us look as more complex data. Most users of musculoskeletal analysis are interested in muscle forces. In this model we can find the muscles in the tree by expanding the nodes Main.Model.Muscles. Take the first muscle, brachialis, and click the Fm property.

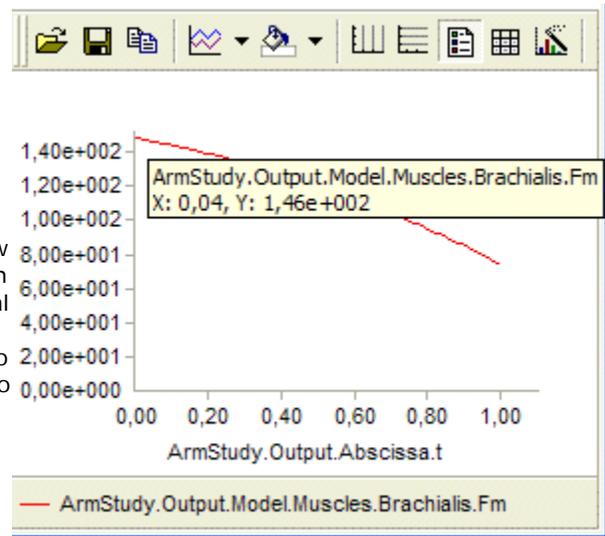
Fm is the muscle force, and as you can see, the brachialis force declines as the arm moves. Not all of the muscle data items in the tree contain any reasonable results. It depends a bit on the muscle model in question. But the muscle force, Fm, and the active state, Activity, are always available. Please refer to the [Muscle Modeling tutorial](#) for more information.

Detailed data investigation

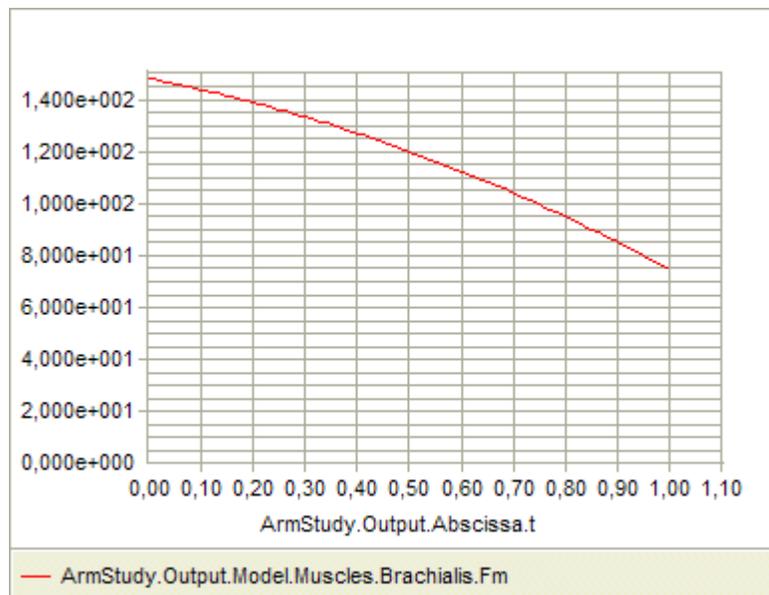


Having an item graphed you may want to investigate the results a little closer, and the toolbar above the graph gives you different options for doing so.

However, the first thing you might notice is that if you hold the mouse pointer still above the curve for a short moment, a small box will pop up and give you the name of the data series and the value of the closest data point. In the example to the right you can see how the little box informs you that the curve passes through point (0.04; 1.46e+002). Please notice that the decimal commas are because this picture is made on a computer with a European language setting. Notice also that the Chart View uses 'x' and 'y' to designate the two axes regardless of which parameters are actually being graphed.



To facilitate studying of the details of the data you can switch on the grid lines horizontally, vertically, or in both directions simultaneously, and you can edit the properties of the x and y axes to display the grid lines as closely as you desire as shown below.

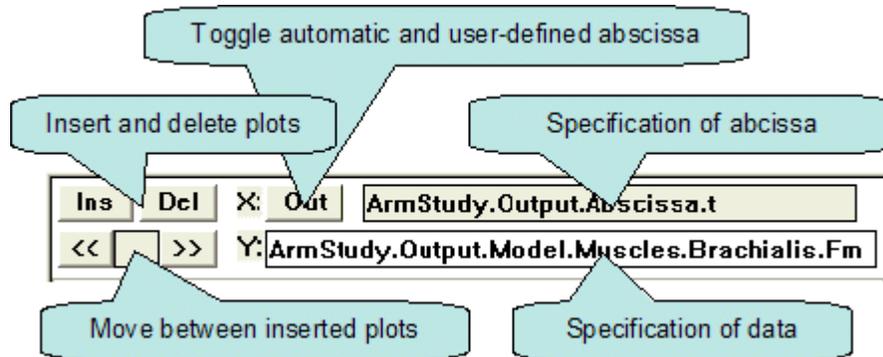


In some cases you can have curves with complicated shapes that you may want to investigate in details. The zoom tool is handy for that. When you press the toolbar button with the little magnifying glass, zoom mode switches on, and you can select an area of the chart for closer investigation by dragging the mouse. You can zoom again on the zoomed area and go as close to the detail you are interested in as you like. The zoom mode remains active until you click the magnifying glass again. This resets the view to the original area.

To investigate the data in even more detail you can switch the data box on by clicking the appropriate button on the toolbar. This gives you a spreadsheet-like box at the bottom of the screen, and you can investigate the numbers behind the graphs in detail. You can even double-click the numbers and edit them. Of course, that would be cheating...

The specification line

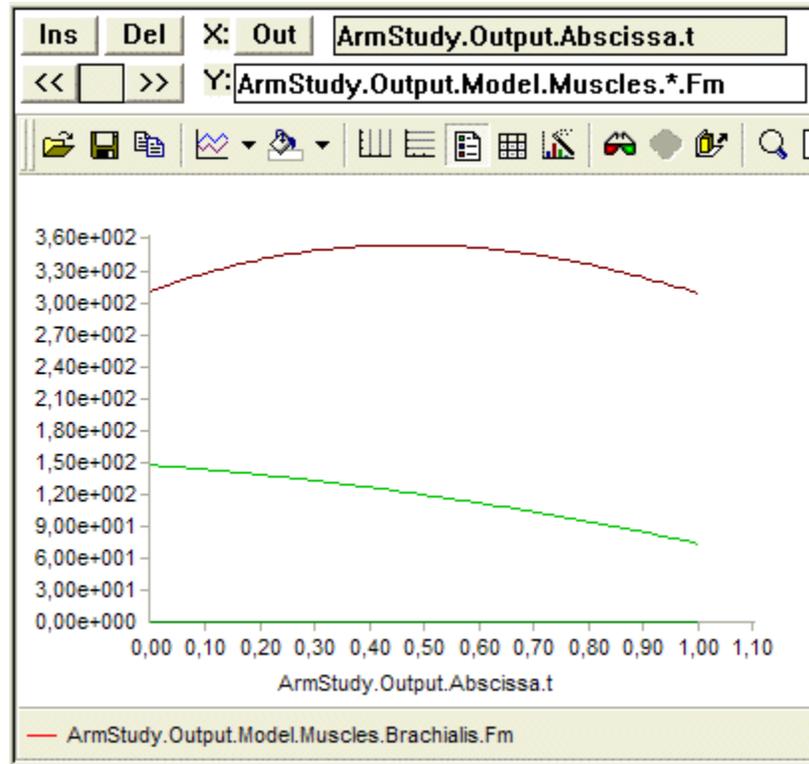
Above the toolbar in the chart view you find a specification panel. It is useful for several applications that are a bit more advanced. With the specification panel you can specify plotting of a family of curves, you can specify your own abscissa, and you can save and recall plot specifications.



You may want to look at several curves at a time. The secret to doing that is the Y data specification line. This line can to some extent parse the specification string. This means that you can compose the string with any number of wild characters such as you may know from file name specifications in Windows, Unix and other operative systems. If you, for instance, replace "brachialis" the data specification with '*' like this:

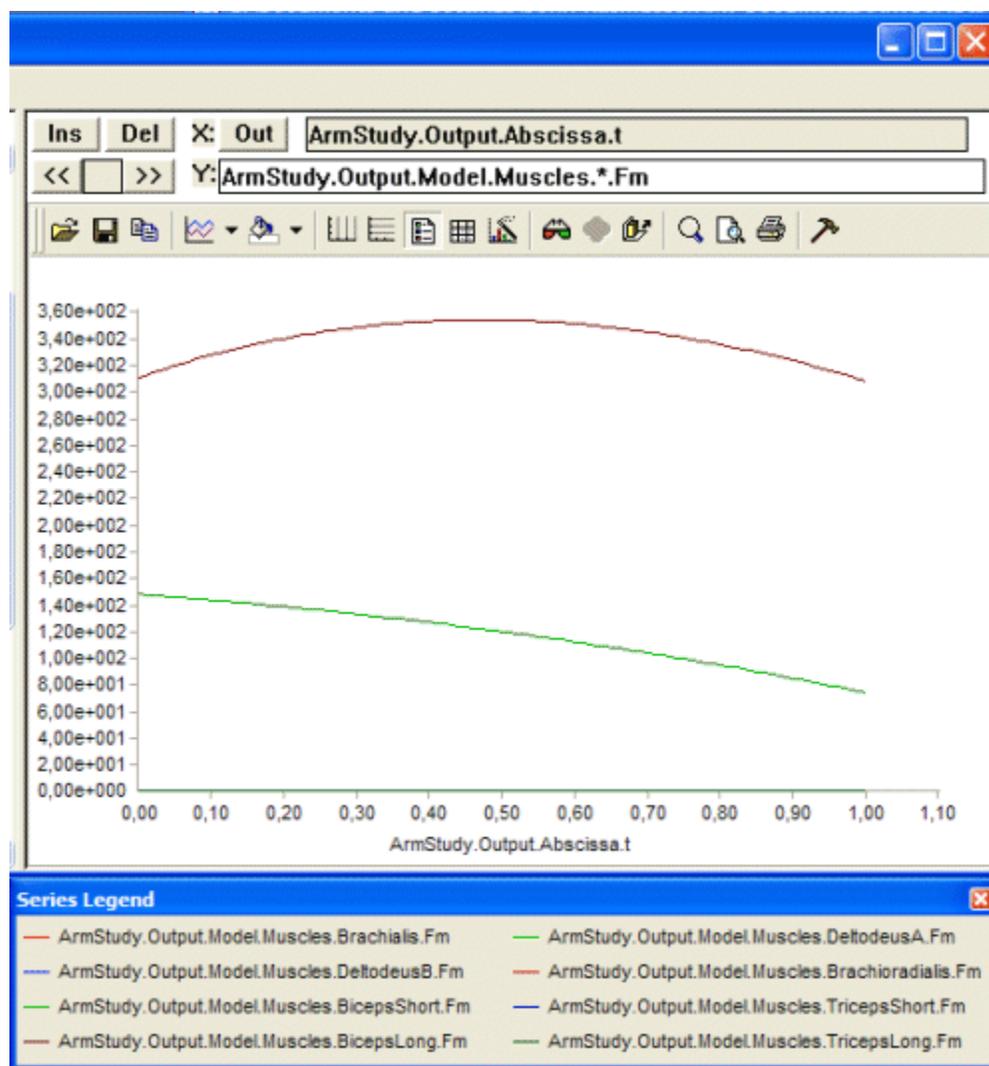
```
ArmStudy.Output.Model.Muscles.*.Fm
```

then you will get all the muscle force curves plotted simultaneously. as shown below:



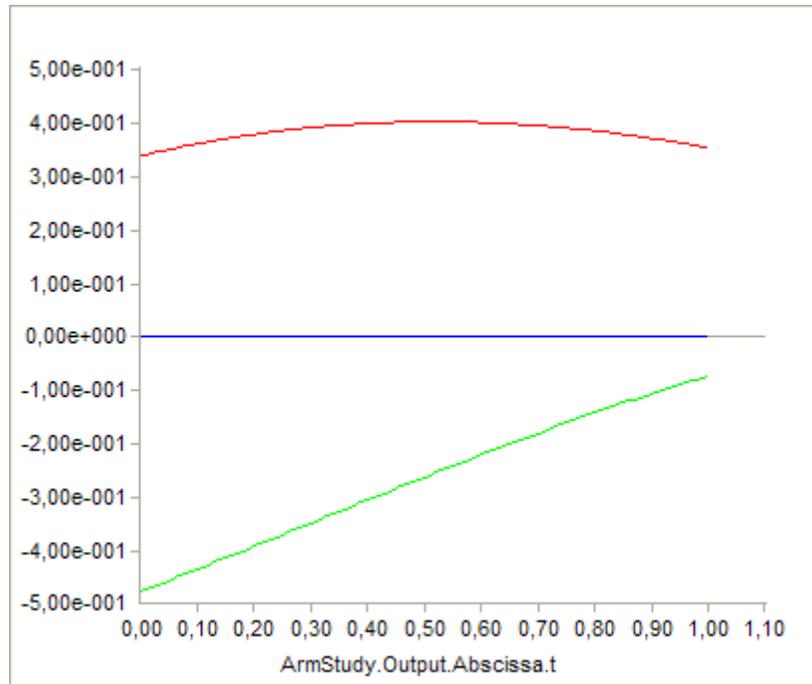
We have eight muscles in this model, so why do you only see two curves? The explanation is that all the muscles in this model have the same strength, so they team up in groups where all the muscles pull exactly the same. This model has three groups. The brown curve at the top, the green curve in the middle, and another green curve of inactive muscles on the x axis. So several curves are hidden under each of the curves you can see.

As you can see, the legend box at the bottom of the window only shows one muscle. This is because the muscle names are rather long, and the box simply does not have room for more. However the box is dockable, and you can place it anywhere you like, including in its own window outside the Chart View, and you can resize it until it fits the legends you want to display, for instance as shown below:



User-defined abscissa

The default abscissa in the chart view is time. However, you can in principle plot data against any scalar property the system has computed. Let us imagine that the dumbbell curl study we are looking at is an ergonomic investigation of the effort of lifting the weight to different heights. In that case, it might be more relevant to plot the muscle force as a function of the height of the hand. The way to do so is simply to replace the `ArmStudy.Output.Abcissa.t` specification in the X specification line. Let us start by finding the position of the hand. If you browse down the tree through `Main.Model.Segs.LowerArm.Handnode.r`. You will get three graphs:



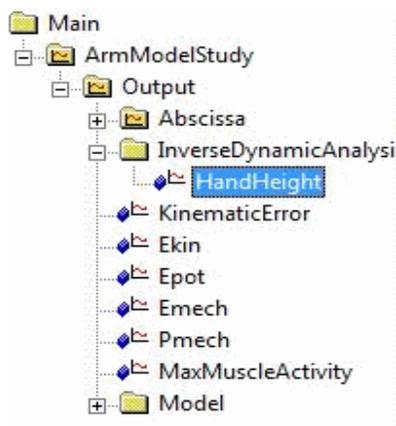
The three graphs (of which one is constant zero) is because the hand node position is a vector with three coordinates. We want to extract the height, which is the y coordinate, and use it as the abscissa. But the abscissa obviously cannot be a vector, so we must construct a scalar variable containing the y coordinate of the hand node in the AnyScript model. The way to do so represents a very useful and slightly subtle trick, and requires a bit of explanation.

At the beginning of this lesson you learned that the system automatically defines a group of variables containing the output from the analysis. But you can also define your own output variables. The only difference between an output variable and an ordinary AnyVar is that the values of output variables get stored for each time step.

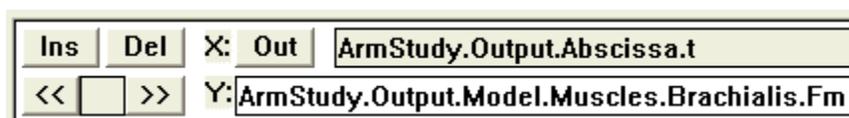
So how can we make the system perceive a given variable as an output variable? The answer is that any variable defined inside an operation in a study is a user-defined output variable. Now we are getting to the point of the case at hand: We can define the y coordinate of the HandNode as a variable in the InverseDynamicAnalysis operation in the study and subsequently use it as the abscissa of the Chart View. Here's what to do:

```
AnyBodyStudy ArmStudy = {
  AnyFolder &Model = .ArmModel;
  RecruitmentSolver = MinMaxSimplex;
  Gravity = {0.0, -9.81, 0.0};
  InverseDynamicAnalysis = {
    AnyVar HandHeight = Main.ArmModel.Segs.LowerArm.HandNode.r[1];
  };
};
```

As you can see, the new code is an addition to the existing (implicitly defined) InverseDynamicAnalysis object. The result is that the model now contains a scalar output variable called HandHeight containing the y coordinate of the handle. Try adding that piece of code to the model, reload, and run the InverseDynamicAnalysis. You should now have the following section in the tree in the Chart View:



As you can see, the tree has been extended with the new variable we have defined. The next step is to use this variable as the abscissa.



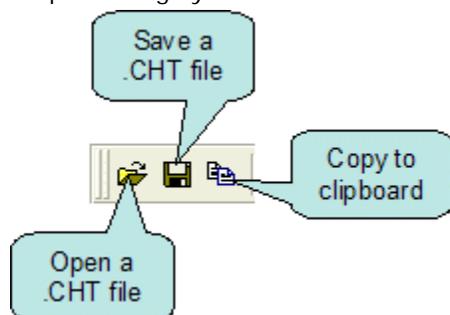
Notice the first line of the panel above. It holds the time specification, but it is grayed out, and you cannot write anything in the field. To be able to change this line, first click the "Out" button. "Out" means that this is where to click if you want to select a new abscissa among the output variables. Clicking the button changes its name to "Auto" and ungrays the line. Now you can place the cursor by clicking somewhere on the formerly gray line and subsequently browse your way in the tree to the HandHeight variable and click it. This places the variable in the X specification, and it is now used as the abscissa of the graph.

Stacking graphs

As you have seen, getting the specifications of a graph completely right can sometimes require a some amount of clicking around in the tree and in the specification panel. So some way to save your carefully selected plot specifications can be handy. The specification panel allows you to put your carefully selected graphs on a stack and to recall them when you want them back. Whenever you click the "Ins" button the current graph is inserted into the stack and given a number. By means of the "<<" and ">>" buttons you can scroll back and forth between the plots you have saved. The "Del" button removes the current graph from the stack.

Exporting data

You are almost bound to want to save your data in various ways. Perhaps you want to save a graph for inclusion in a report you are writing. Perhaps you desire to save the chart on a compact format for later review without having to run the AnyBody analysis again. Perhaps you want to export the data to a text file for processing by statistical software. Or perhaps you want to paste the data into a spreadsheet to make customized combinations of data for presentation in customized graph types.



The Chart View has its own file format that you can save and load. The files have extension .CHT, and they are very compact and easy to store and exchange. You Open and Save .CHT files with the first two buttons on the toolbar. A stored .CHT file can be sent to other AnyBody users, and they can load it in and investigate the results you have produced. Please notice that a loaded .CHT file is only computational data. It has no connection to the model that generated the output data, and you do not get the model loaded when you load

the .CHT file.

.CHT files are a convenient way of storing analysis data because they can subsequently be reformatted and displayed in other ways than you initially planned, for instance a stacked column diagram or a pie chart instead of curves.

Data can also be exported from the Chart View via the clipboard. The "Copy to clipboard" icon on the toolbar gives you the opportunity to copy the present chart on different formats:

- As a bitmap picture. The picture will have screen resolution, so the quality depends on the size of the Model View. For maximum quality, maximize the AnyBody Modeling System main frame on your desktop and maximize the Chart View inside the main frame.
- As a vector-based windows meta file. This type of file has infinite resolution, so you can scale it up and down without loss of quality. However, this requires that the application into which you intend to import the file supports vector graphics.
- As a windows object. This option is currently not active.
- As a text. This option copies the graphed numbers to the clipboard on text format, and you can subsequently paste them into a spreadsheet or a text editor. Pasting into a spreadsheet can be very useful because it allows you to use the data in subsequent processing such as statistical analysis.

A word of caution regarding the the text option: Different countries have different conventions for decimal numbers. Some use a point as decimal separator, and some use a comma. The numbers copied to the clipboard from the Chart View follow the nationality settings for decimal point or comma. When you subsequently paste the numbers into a spreadsheet it is important that the spreadsheet follows the same conventions. If the numbers coming out of the Chart View for instance use decimal comma and the spreadsheet receiving them expects number with decimal points, then the spreadsheet will interpret the numbers you paste in as text rather than numbers.

The AnyChart View

AnyChart is AnyBody's alternative for making charts. AnyChart is special compared to ChartFX in the way that AnyChart uses the AnyScript class called AnyChart to make the visualization. The AnyScript class AnyChart is a draw object that can be used in the AnyScript code to make charts in the Model View of the model. The AnyChart View wraps the features of the AnyChart class into a window in the AnyBody GUI. Currently, AnyChart processes only simple charting features, and therefore AnyChart and ChartFX still lives side-by-side in the system.

AnyChart collects all its properties as described for the AnyChart class in the AnyScript Reference Manual. In contrast to ChartFX, all these properties are saved in workspace files, so AnyChart Views are generally reestablished better, when introduced into workspaces.

AnyChart is AnyBody's only tool for showing 3-D surfaces. One main difference between AnyChart and ChartFX is that AnyChart allows you to define two Abscissa axes. AnyChart is mainly used in conjunction with parameter studies and optimization. Please refer to the [Parameter Studies and Optimization tutorial](#) for a demonstration of these features.

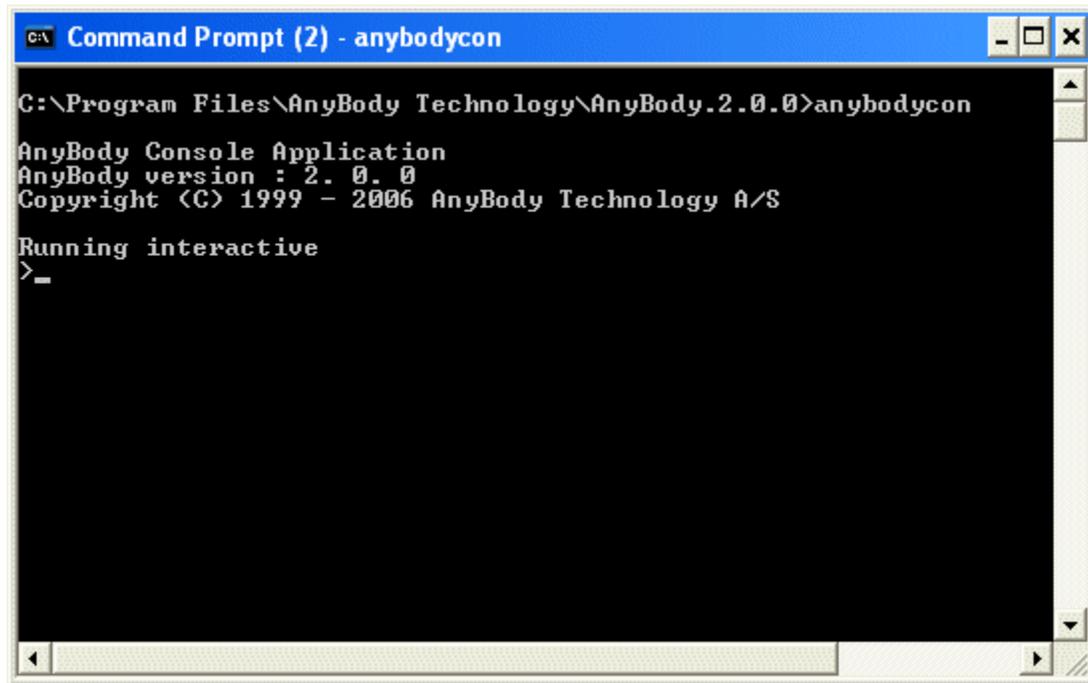
AnyChart also introduces multiple series in the same chart. The primary mechanism of selecting values to be depicted in the chart is the same as for ChartFX, but with multiple series you can add several selections together in the same chart.

One additional small difference between the charts is AnyChart's selection line also that allows you select elements of vectors, matrices, and higher order tensors. Like in AnyScript code, [] bracket can be used to select subelements.

The next interface lesson is concerned with a part of the system that really has a minimum interface: [The command line version](#).

Lesson 5: The Command Line Application

The AnyBody Modeling System comes with a command line version included. It is named AnyBodyCon.exe ("Con" for console application), and you will find it in the directory where you install AnyBody. The command line version is - as the name indicates - a version of the AnyBody Modeling System with the user interface stripped off. This means that it is executed from a DOS command prompt or - more importantly - by a batch file or another software application.



```

C:\Program Files\AnyBody Technology\AnyBody.2.0.0>anybodycon

AnyBody Console Application
AnyBody version : 2.0.0
Copyright (C) 1999 - 2006 AnyBody Technology A/S

Running interactive
>_

```

As you may suspect from that introduction, the command line version is mostly designed for technical users wishing to set up their own data processing application by piecing different types of software together.

The console application can either work interactively and accepts commands that you type in response to its command prompt, or it can take its input from a file containing macro commands. Let us try the interactive mode. We need a model to work on, so please download and save [Demo.outputfile.any](#) in some working directory.

Here's a tricky part: AnyBodyCon does currently not have any commands for changing the working directory after it has been started. Therefore, it must be started in a way so that it can find the model files you intend to load. You can basically do this in two ways from a DOS prompt:

1. You change directory to wherever you saved `Demo.outputfile.any` and from here you run the console program using its full path, e.g. `"C:\Program Files\AnyBody Technology\AnyBody.3.0\AnyBodyCon.exe"`.
2. You open AnyBody with a `/d` argument that sets the working directory of console. You can either change the directory to the place of AnyBodyCon.exe first or you can use the full path from anywhere, e.g. `"C:\Program Files\AnyBody Technology\AnyBody.3.0\AnyBodyCon.exe" /d "c:\...\My Documents"`

Naturally, you can add the path of AnyBodyCon.exe to the path of your DOS command prompt environment, but be aware that this can cause confusion in case of multiple installations of AnyBody. We shall cover this issue of using DOS PATH in more details in a separate section later in this lesson.

You are now ready to use the console application. The application is rather primitive. It only

understands eight different commands. You also always get help by using the 'help' command or by calling AnyBodyCon with /? argument. The latter approach will give you the full help including descriptions of the possible program arguments. The table below contain a description of the commands accepted by the AnyBody console.

Command name	Functionality
load "filename.any"	Example: load "demo.outputfile.any" This command loads an AnyScript model into the system and compiles it. Don't forget to put the filename between double quotes.
operation <op.name>	Example: operation Main.ArmStudyInverseDynamicAnalysis This command sets the active operation. This is what you must do as the first thing after you load a model. All the remaining commands except exit require an active operation to work on.
run	Example: run This command takes no arguments. It simply runs the active operation.
step	Example: step This command takes no arguments. It performs a single step of the active operation.
reset	Example: reset This command takes no arguments. It resets the active operation.
print <object>	Example: print Main.ArmModel.Jnts.Shoulder.Pos This command prints the value of a single variable. If the variable is a folder, it just lists the names of the element of the folder.
printdown <object>	Example: printdown Main.ArmModel.Jnts This command recursively prints the values of all elements in an entire folder.
exit	Example: Exit This command exits anybodycon.exe and returns to the dos command prompt.

Now let us try the console application. Start AnyBodyCon.exe from the command prompt and issue the command sequence:

```
load "demo.outputfile.any"
operation Main.ArmStudy.InverseDynamicAnalysis
run
exit
```

nearly as interesting as running the Windows version of the AnyBody Modeling System. So why bother?

Well, the command line version of the AnyBody Modeling System faithfully performs all the computations you ask it to through the command line. But what good does it do you, and how can you access the results? You could issue print or printdown commands and have the results listed on the screen. It would give you a whole lot of probably completely useless numbers to look at.

A more clever way to use the command line version is to insert AnyOutputFile objects into the AnyScript model. If you load the demo.outputfile.any model you have just worked on into the Windows version of the AnyBody Modeling System, you will notice that it contains two definitions of AnyOutputFile objects inside the ArmStudy.

```
// The study: Operations to be performed on the model
AnyBodyStudy ArmStudy = {
  AnyFolder &Model = .ArmModel;
  RecruitmentSolver = MinMaxSimplex;
  Gravity = {0.0, -9.81, 0.0};

  AnyOutputFile OutFile1 = {
    FileName = "out1.csv";

    AnyVar MaxAct = .MaxMuscleActivity;

    AnyFloat TestTensorConst = {
      {1, 2, 3},
      {1, 2, 3}
    };

    AnyFloat TestTensor = {
      {
        {1, 2, 3},
        {1, 2, 3}*2,
        {1, 2, 3}*3,
        {1, 2, 3}*MaxAct
      },
      {
        {1, 2, 3},
        {1, 2, 3}*2,
        {1, 2, 3}*3,
        {1, 2, 3}*MaxAct
      }
    };
  };

  AnyOutputFile OutFile2 = {
    FileName = "out2.csv";
    Search = {"ArmModel.Muscles.*.Act*", "ArmModel.Muscles.*.Ft"};
    SepSign = ";";
  };
};
```

Furthermore, if you open a file manager and look at the contents of the directory where you are running the problem, you will notice that two new files have been generated: out1.csv and out2.csv. They are comma-separated files with a semicolon as separator between numbers as defined in the AnyOutputFile above.

If you have software on your computer that is associated with csv files, such as Microsoft Excel, then you can double-click any of the two files and open it. You will notice that it contains columns of data dumped from the analysis. The precise nature of the data is defined in the file's header, and it has been determined by the variables defined inside the corresponding AnyOutputFile object. Please refer to the reference manual for further information.

As you can see, the command line version can produce output data that can be formatted according to your desire and processed further by other types of software. But the really great thing about the console application is that you can execute it from other software such as Matlab or Visual Basic and as such build it into an integrated system for large-scale biomechanical data processing such as response surface-based optimization. Instead of typing the commands into the application by hand, you can store them in a macro file. Such files usually have the extension ".anymcr". The command line application can be given such a file as its command line argument, and it will perform the commands in it. Don't forget to make "exit" the final command of the macro file if you want the application to end after processing the macro file.

You are now ready to let the command line application be a part of a system for biomechanical data processing of your own design.

Path specification

As mentioned earlier, you can add the path of AnyBodyCon.exe to the path environmental variable for your DOS prompt to ease the call to AnyBodyCon.exe from anywhere. This you can do from the DOS prompt with a statement such as

```
path c:\Program Files\AnyBody Technology\AnyBody.3.0\;
```

or

```
path %path%;c:\Program Files\AnyBody Technology\AnyBody.3.0\;
```

if you want to add the AnyBodyCon.exe's path to the existing path definition. Notice that you cannot have any space between ';' and the following path "c:\..." and that you can see the resulting path by simply calling the internal path command again without arguments.

These statements will only take effect until the current DOS prompt is closed, but you can also add the path of AnyBodyCon.exe permanently to the path for all DOS prompts. In Windows XP for instance, you do this from Control Panel -> System under the Advanced tab. You should however be aware that multiple versions of AnyBody may be installed on the computer at the same time, and therefore, multiple versions of AnyBodyCon.exe may exist in different locations. Thus, your path specification not only make it easy to call AnyBodyCon.exe; it will also specify which version that will be used. This can make unclear which one you are actually using if you need several of them.

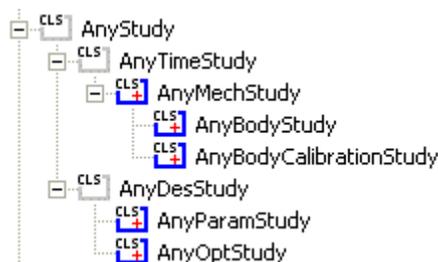
To be in full control with multiple installations of AnyBody, you can define aliases by the following procedure

1. Make a directory with .bat files or shortcut to the AnyBodyCon.exe version you will need. Name the bat-files properly, so you can recognize the different version, e.g. AnyBodyCon201.bat and AnyBodyCon30.bat. The bat files contain a single statement, the call of AnyBodyCon.exe with its full path.
2. Add this directory to the permanent path of the DOS prompt.
3. You can now call the different versions of AnyBodyCon via the bat files, so the bat file names are working as aliases for the real exe files.

A study of studies

Studies are AnyBody's mechanism for specifying "things to do to the model" in the sense that a study executes the model and gives you results to investigate afterwards. The study or studies is what you see organized in a tree in the frame at the bottom of the screen when you have loaded a model.

AnyBody's family of study classes looks like this:



where the classes with blue icons are the ones you can actually define. In this tutorial we shall focus on `AnyBodyStudy` and `AnyBodyCalibrationStudy`, while [a separate tutorial](#) is dedicated to `AnyParamStudy` and `AnyOptStudy`.

The `AnyBodyStudy` and Studies in general

A study is really just a folder. It is a pair of braces between which you can place some specifications. Whatever you put between the braces becomes part of the study. As every object, a study has some predefined properties that you either can set, must set, or cannot touch.

When you create a new model by means of the menu File -> New Main, the system automatically inserts an `AnyBodyStudy` for you (please do it and save the file under some relevant name). It looks like this:

```
// The study: Operations to be performed on the model
AnyBodyStudy MyStudy = {
  AnyFolder &Model = .MyModel;
  RecruitmentSolver = MinMaxSimplex;
  Gravity = {0.0, -9.81, 0.0};
};
```

It contains all the things you formally need. Let's start with the two last lines. They read

```
RecruitmentSolver = MinMaxSimplex;
Gravity = {0.0, -9.81, 0.0};
```

As you can see, they are simply assignments of values to variables. The two variables shown here have no type definitions in front of them. This is because they are predefined properties of the `AnyBodyStudy` object. The value of `RecruitmentSolver` tells the system which solution algorithm to use for muscle recruitment, and `Gravity` is a specification of the vector of gravitational acceleration affecting the model. The system assumes that you want to work with the y axis being vertical in space. If you prefer otherwise, simply change the direction of `Gravity` to reflect your choice. Please go ahead and load the model if you have not already done it by pressing F7 or the  icon.

An `AnyBodyStudy` has many more predefined properties that you can play with. You can get an overview of these using the Model Browser. The Model Browser is opened from the menu Windows -> Model Browser, whereafter you can find the study in the Model Tree. Alternatively, you can, as with all objects in the model, dump the contents of a study in the message window. This is done simply by finding the study in any Model Tree view, right-clicking it and selecting Dump. This produces a whole lot of output in the Output Window.

Most of the properties deal with solution methods, tolerances, and other stuff that is necessary or handy for advanced users. For a description of each property, please refer to the AnyScript Reference manual. A few of the properties, however, are necessary to know even for casual users:

tStart	This is the time at which the study begins. In almost every case, this would be zero. Using a non-zero value of tStart is sometimes used to restrict the study to a subset of the time it was originally developed for or if the model is driven by measured data which does not begin at $t = 0$.
--------	---

tEnd	Ah, you guessed it already. This is the time at which the study ends. Contrary to tStart, this often has to be set by the user. The standard value is tEnd = 1.0, and if you want your study to span any more or less time, you have to set tEnd manually. A very common modeling mistake is to define data-based drivers such as the AnyKinEqInterPolDriver with a time span exceeding the interval from 0 to 1 and then wondering why only a small part of the movement interval gets simulated. In this case, the user must manually specify tEnd to correspond with the end of the driver time span.
nStep	AnyBody analyzes movement in discrete time steps, and nStep specifies how many steps the system should use to come from tStart to tEnd. The steps are equidistant, and since tStart is always the first analysis time, and tEnd the last, the interval gets divided into nStep-1 equal intervals. The default value is nStep=100, which for most purposes is a very fine resolution. If you have a large and time-consuming model, it might be a good idea to manually set nStep to a smaller number.

The first line of the study reads

```
AnyFolder &Model = .MyModel;
```

Notice that the first word of that line is a type definition: "AnyFolder". The predefined properties we have just discussed need no type definition because the study already knows them. They are already defined and merely get new values by the assignments we may specify. So the type definition at the beginning of this line indicates that this property is an addition to the study; something that was not known already. This is an important point to understand about studies: You can add almost anything to a study and the study does not need to know its type in advance.

The significance of adding something to a study is that whatever you add becomes a part of what the study executes. This particular line defines a variable called "Model" and sets it equal to .MyModel. If you look at the beginning of the AnyScript file, you will see that MyModel is really the folder containing the entire model the system has generated for you (we refer to it as .MyModel with a leading dot because it is one brace up compared to where it is referenced from). This means that the entire model comes under influence of the study. Instead of this line, we could simply have pasted the entire contents of the braces defining the MyModel in at this place, and in some sense, this is precisely what we have done. The ampersand '&' in front of "Model" means that Model does not get replicated inside the study. Instead, the '&' means that the study merely contains a pointer to MyModel. The concept of pointers should be very familiar to you if you have any experience in C, C++, or Java programming. If not, simply think of a pointer as a handle to something that's defined elsewhere. Whenever you access it, you are actually handling what it is pointing to.

Instead of including the entire model, we could have chosen to point to some of the sub folders of MyModel. This would mean that the study would work on just a subset of the model, and it can be very relevant in some cases. One of the more important examples is for calibration of muscles as we shall see in the forthcoming lesson on [Calibration Studies](#).

The elements of a study

When you define an AnyBodyStudy, regardless of what you include between the braces of the study, the result is four standard operations that appear in the study tree. They each represent something you can do to the model elements the study is pointing at:

- ModelInformation dumps statistics of the mechanical system and is mainly a model debugging tool.
- SetInitialConditions reads the values of whatever drivers you have included in the study and puts the model in the position of these drivers at time tStart. This is done in a multi-step process: The model is initialized into the initial positions from load time, and the kinematics is subsequently solved in a few steps (more details can be found in the [reference manual](#)). This is particularly useful for inspection of the specified initial positions when having problems with the initial configuration of the mechanism.
- KinematicAnalysis. A kinematic analysis is a simulation of the movement of the model without

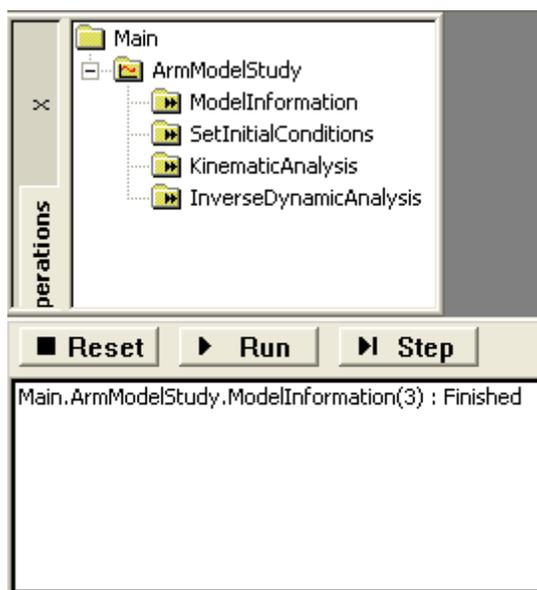
calculation of any sort of forces. This means that you can run KinematicAnalysis as soon as you have the movement defined uniquely. You don't need any muscles in the model for this one.

- InverseDynamicAnalysis. This is a simulation of the forces involved in the given movement or posture and whatever can be derived from them. The InverseDynamicAnalysis uses the KinematicAnalysis as a subroutine, so this requires a correctly defined movement or posture as well as the muscles or motors necessary to drive the model.

Each of these studies, when executed, assembles the output they generate in the Output section under the study's tree.

Running operations

You execute operations through the wide, narrow control pane that's usually located at the bottom of the screen. This is usually referred to as the Operation Window.



The lower portion of this pane is just the message window where the system writes various messages and dumps object properties when you double-click them as we did before with the entire study. The left of the upper fields is a filtered version of the tree you can find on the left side of just about any window in the AnyBody Modeling System. Rather than presenting all the objects of the model, this tree only comprises the studies. If you expand a study, you will find its operations, which typically are: SetInitialConditions, KinematicAnalysis, InverseDynamicAnalysis, and MuscleCalibrationAnalysis.

You pick an operation by clicking it once. This highlights its name, and you can now execute it with the Run or Step buttons in the right hand field. The "Run" button starts the study and it will run until it comes to its end or encounters an error. Once you press the run button, it changes its name to "Break", and pressing it in that state breaks the current analysis process.

The "Step" button takes one step at a time, What a step is exactly depends a little on the type of operation. For KinematicAnalysis, InverseDynamicAnalysis, and MuscleCalibrationAnalysis, a step is one time step of the movement. For SetInitialConditions, a step is one of the several distinct operations necessary to put the model into its initial state. We shall return to that subject in the next lesson.

The "Reset" button returns the model to its initial state after it has gone through a sequence of time steps. You must press "Reset" before you can rerun the model.

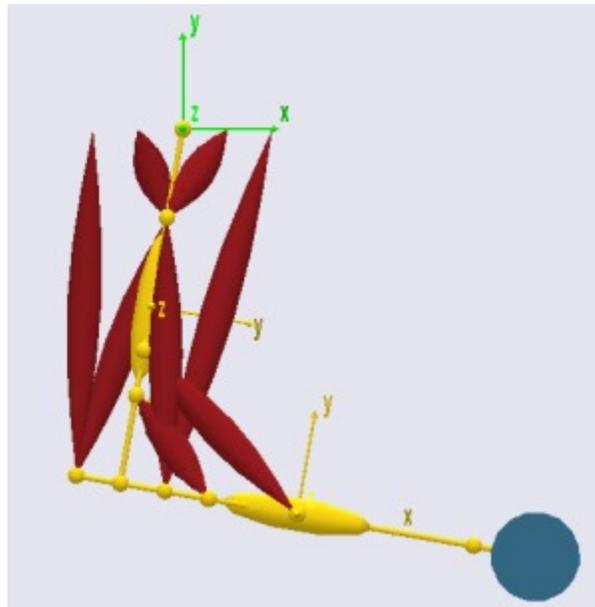
In the following lessons we shall look in more detail at the different operations in an AnyBodyStudy and finally also at the AnyBodyCalibrationStudy.

- [Lesson 1: ModelInformation](#)
- [Lesson 2: SetInitialConditions](#)
- [Lesson 3: KinematicAnalysis](#)
- [Lesson 4: InverseDynamicAnalysis](#)
- [Lesson 5: AnyBodyCalibrationStudy](#)

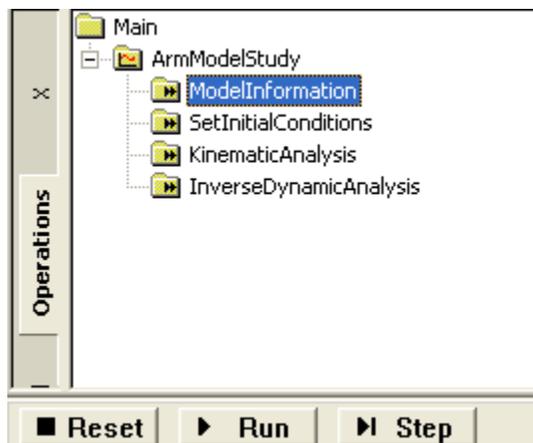
We need a model with a bit more substance than the template we created above. If you do not already have our trusted arm model stored somewhere, [please download it here](#), save it to your disk, and load it into AnyBody. We are then ready to proceed to [Lesson1: ModelInformation](#).

Lesson 1: Model Information

In this lesson we are presuming that you have the arm2d.any file loaded into AnyBody. If you do not have the model on file, please download and save a copy from this link: [arm2d.any](#). It should look like this when you have loaded the model and opened a Model View:



The mechanics of this model is fairly simple in the sense that it only has two segments and two revolute joints. However, in more realistic models with dozens of segments connected by many joints of different types it can be very difficult to maintain the overview of the model. Making a model move requires a balance between the number of kinematic degrees of freedom and the number of constraints, and it can be difficult to get it completely right. This is where the ModelInformation operation comes in. Let us go ahead and try it on the arm2d model. Expand the study tree and locate the ModelInformation operation:



When you press the run button you will see a whole lot of text scrolling over the message pane below the study tree. You can scroll up and down using the vertical slider bar, but it is probably easier to maximize the window and move the divider bar up a little. At this point, if you scroll up a bit you will come to a line of asterixes where the output from the ModelInformation operation starts. The first section looks like this:

```
*****
Model Information: (Operation: Main.ArmStudy.ModelInformation):
```

```
-----
0) Contents:
1) List of segments
2) List of joints and kinematic constraints
3) List of reaction forces
-----
```

This is obviously a table of contents and it introduces the different sections you can find further down. The first of these looks like this:

```
-----
1) List of segments:
0: Main.ArmModel.Segs.UpperArm
1: Main.ArmModel.Segs.ForeArm
```

```
Total number of rigid-body d.o.f.: 12
-----
```

This section is a table of the segments in the model. In a simple model like arm2d where all the segments are defined next to each other, this might seem a little unnecessary, but larger models typically have the segment definitions divided over many different folders and files, and it can be helpful to see a compiled list of all of them. AnyBody models are always in three dimensions and a rigid segment in three dimensional space has six degrees of freedom, i.e. three spatial movements and three rotations. Thus, the ModelInformation operation multiplies the number of segments by 6 and reports the total number of rigid-body degrees of freedom, in this case $2 \times 6 = 12$. To enable the system to figure out where everything is in space we must provide 12 constraints. This is what the next section helps us do:

```
-----
2) List of joints and kinematic constraints:
Joints:
0: Main.ArmModel.Jnts.Shoulder (5constr., 1coords.)
1: Main.ArmModel.Jnts.Elbow (5constr., 1coords.)
Total number of joint coordinates: 2
```

```
Drivers:
```

0: Main.ArmModel.Drivers.ShoulderMotion (1constr.)
 1: Main.ArmModel.Drivers.ElbowMotion (1constr.)

Other:
 - none!

Total number of constraints:

Joints: 10
 Drivers: 2
 Other: 0
 Total: 12

This section counts the kinematic constraints. The sum of constraints must add up to the number of degrees of freedom in the model, i.e. 12. You can see in the last line of the section above that this indeed the case. Further up we can see how the 12 constraints come about. $2 \times 5 = 10$ of them come from the two revolute joints in the model for the shoulder and elbow. A revolute joint leaves only one degree of freedom between the two reference frames it connects, so it has five constraints. With two of these we have two degrees of freedom left in the model because $12 - 2 \times 5 = 2$. These remaining degrees of freedom after the joints have been added are also called the joint coordinates. The remaining part of the section must specify this number of additional constraints.

The usual way of providing constraints for the joint degrees of freedom is by means of drivers. In our case we have simply added two drivers directly to the two joints as the list shows. However, it does not have to be like that. We have to provide as many constraints as we have joint coordinates but the constraints need no address the joint coordinates directly. For instance, we could also have driven the x and y coordinates of a point on the forearm.

There is also a section called "Other". This is for constraints that are neither any of the predefined joint types nor driver functions. Such constraints are very frequent in more complex models because the AnyScript language allows for user-defined joints and other constraints to mimic complex behaviors movement patterns between different joints. This, however, is an advanced topic that we shall postpone for now.

The final section of the output has the following form:

 3) List of reaction forces:

0: Main.ArmModel.Jnts.Shoulder.Constraints.Reaction(5 active of 5 reactions)
 1: Main.ArmModel.Jnts.Elbow.Constraints.Reaction(5 active of 5 reactions)
 2: Main.ArmModel.Drivers.ShoulderMotion.Reaction(0 active of 1 reactions)
 3: Main.ArmModel.Drivers.ElbowMotion.Reaction(0 active of 1 reactions)

Total number of active reaction and driver forces: 10

The fact that the reaction and driver forces add up to the same number as the joints and kinematic constraints is no coincidence. In a straightforward model like this one, joints usually provide the same number of reactions as kinematic constraints. This is also how it is in real life in most cases, because the mechanical joints we have in our surroundings enforce their kinematic constraints by reaction forces. But it is not always like that in the body. A knee, for instance, can roughly be approximated as a hinge joint (many physiologists will disagree here) but the internal load-carrying mechanisms in the knee are not like they are in a mechanical hinge. Instead knee reactions are provided by a complicated interplay between unilateral joint surfaces, ligaments, and muscles. So AnyBody allows for the definition of joints that only provide kinematic constraints but not the associated reaction forces. In fact, the system also allows the opposite: Reaction forces without kinematic constraints. For an in-depth discussion of some of these issues, please refer to the [tutorial on mechanical elements](#). For now, the bottom line is that counting reactions can sometimes be tricky, and the ModelInformation operation is helpful in this respect.

A few special cases are:

1. The number of reaction and driver forces is less than the number of rigid body degrees of freedom in the model as it is the case here. This leaves some reactions to be provided by other elements, and these elements are usually the muscles in the model.
2. If the number of reaction and driver forces is equal to the number of rigid body degrees of freedom, then the model is (usually) capable of balancing itself, and there is no use for muscles. In fact, if you add muscles to such a mechanism, the muscles will end up doing nothing.
3. If the model has more reaction and driver forces than rigid body degrees of freedom then it is statically indeterminate. This usually means that there is something wrong with the model. Mechanically it is equivalent to the model having multiple different ay of balancing itself and having no way of determining which is the correct one. Even though AnyBody is capable of computing the forces in such a model you will often find the solutions oscillating between the infinitely many possibilities between time steps. Models like these should in general be avoided.

Let us investigate what happens if we make some changes in the model. Let us initially remove one of the drivers in the model leaving it kinematically indeterminate:

```
AnyFolder Drivers = {
    //-----
    //     AnyKinEqSimpleDriver ShoulderMotion = {
    //         AnyRevoluteJoint &Jnt = ..Jnts.Shoulder;
    //         DriverPos = {-100*pi/180};
    //         DriverVel = {30*pi/180};
    //         Reaction.Type = {Off};
    //     }; // Shoulder driver

    //-----
    AnyKinEqSimpleDriver ElbowMotion = {
        AnyRevoluteJoint &Jnt = ..Jnts.Elbow;
        DriverPos = {90*pi/180};
        DriverVel = {45*pi/180};
        Reaction.Type = {Off};
    }; // Elbow driver
}; // Driver folder
```

When you load the model again you will see the message:

Model Warning: Study 'Main.ArmStudy' contains too few kinematic constraints to be kinematically determinate.

When you load the model, the system automatically discovers that there seems to be less kinematic constraints than required. In this situation it might not be possible to assemble the mechanism and it is almost certainly not possible to run a kinematic analysis. Running the ModelInformation operation produces this output:

```
-----
1) List of segments:
0: Main.ArmModel.Segs.UpperArm
1: Main.ArmModel.Segs.ForeArm

Total number of rigid-body d.o.f.: 12
-----
2) List of joints and kinematic constraints:
Joints:
0: Main.ArmModel.Jnts.Shoulder (5constr., 1coords.)
1: Main.ArmModel.Jnts.Elbow (5constr., 1coords.)
Total number of joint coordinates: 2
```

Drivers:

0: Main.ArmModel.Drivers.ElbowMotion (1constr.)

Other:

- none!

Total number of constraints:

Joints: 10

Drivers: 1

Other: 0

Total: 11

The ModelInformation operation allows you to investigate in detail how many constraints are missing and which ones they may be. Let us shift the missing driver back in:

```
//-----
AnyKinEqSimpleDriver ShoulderMotion = {
    AnyRevoluteJoint &Jnt = ..Jnts.Shoulder;
    DriverPos = {-100*pi/180};
    DriverVel = {30*pi/180};
    Reaction.Type = {Off};
}; // Shoulder driver

//-----
AnyKinEqSimpleDriver ElbowMotion = {
    AnyRevoluteJoint &Jnt = ..Jnts.Elbow;
    DriverPos = {90*pi/180};
    DriverVel = {45*pi/180};
    Reaction.Type = {Off};
}; // Elbow driver
```

... and try something else:

```
//-----
AnyKinEqSimpleDriver ShoulderMotion = {
    AnyRevoluteJoint &Jnt = ..Jnts.Shoulder;
    DriverPos = {-100*pi/180};
    DriverVel = {30*pi/180};
    Reaction.Type = {On};
}; // Shoulder driver

//-----
AnyKinEqSimpleDriver ElbowMotion = {
    AnyRevoluteJoint &Jnt = ..Jnts.Elbow;
    DriverPos = {90*pi/180};
    DriverVel = {45*pi/180};
    Reaction.Type = {On};
}; // Elbow driver
```

What we have done here is to switch the reaction forces in the two joint drivers on. This is equivalent to imbedding motors into the joints, and it means that the system will obtain enough reaction forces to carry the loads without help from any muscles, corresponding to the statically determinate situation 2 listed above. Loading the model does not bring about any warnings, but if you run the InverseDynamicAnalysis you will get the following message for each time step:

'ArmStudy': The muscles in the model are not loaded due to kinetically over-constrained mechanical system.

And running the ModelInformation operation will give the following feedback:

```
-----
3) List of reaction forces:
0: Main.ArmModel.Jnts.Shoulder.Constraints.Reaction(5 active of 5 reactions)
1: Main.ArmModel.Jnts.Elbow.Constraints.Reaction(5 active of 5 reactions)
2: Main.ArmModel.Drivers.ShoulderMotion.Reaction(1 active of 1 reactions)
3: Main.ArmModel.Drivers.ElbowMotion.Reaction(1 active of 1 reactions)
```

```
Total number of active reaction and driver forces: 12
-----
```

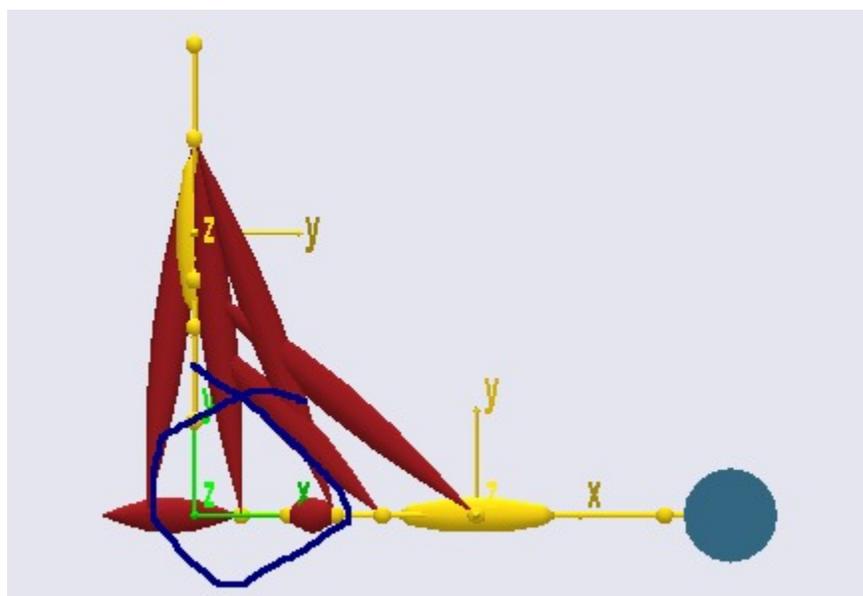
- indicating that the model is precisely statically determinate with 12 reactions corresponding to the 12 rigid body degrees of freedom.

Having familiarized ourselves with the ModelInformation study, let us proceed to SetInitialConditions in the [next lesson](#).

Lesson 2: Setting Initial Conditions

Before we look at the SetInitialConditions study, let us just notice that when the model is loaded, the segments of the model are positioned in space according to their definition in terms of the r0 and Axes0 properties in each segment's definition. These are called the load-time positions.

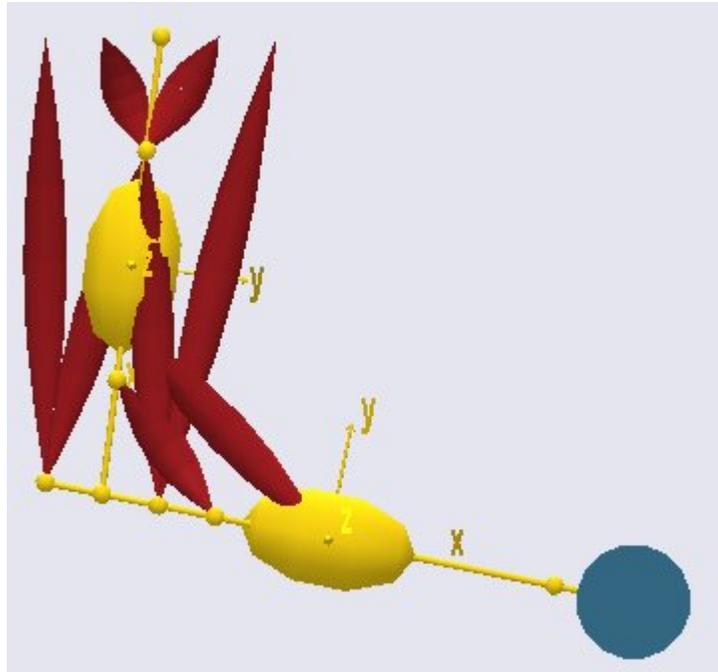
In the figure below, the user has tried to position the forearm and the upper arm approximately at the right positions and angles at load time. This is always a good idea, but it is almost impossible to get them completely in place, and it is not necessary. Indeed, in more complicated models, you can often find the segments and muscles in a big mess at load time. Typically, you will want to see what the model looks like when it has been assembled correctly for time step 1. This is what the SetInitialConditions operation is for.



The load-time positions of segments in a simple arm model. Notice that the forearm and upper arm do not meet correctly at the elbow joint.

When you run the SetInitialConditions operation, it will attempt to put the model in the position it has at

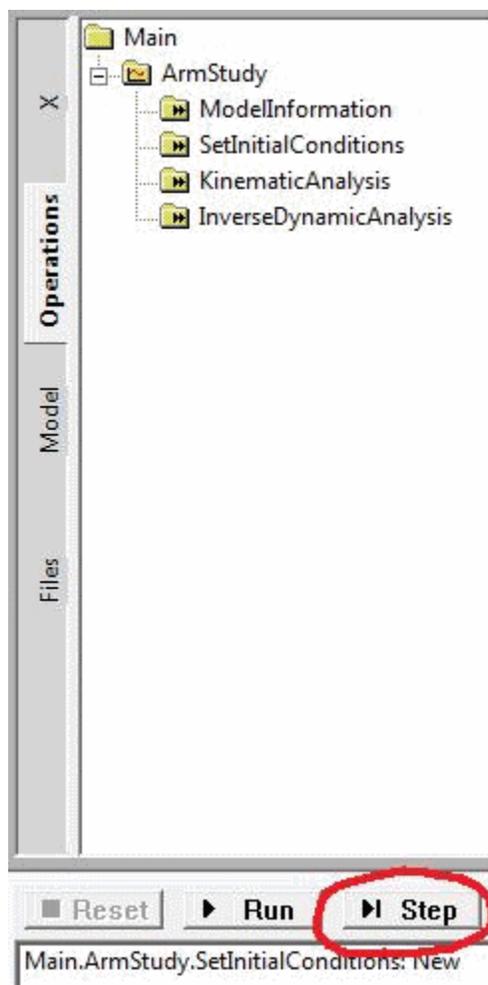
not do it automatically when you load the model. Running the SetInitialConditions operation produces a correctly assembled arm:



The arm correctly assembled at the elbow by SetInitialConditions.

Here's a more detailed explanation: The system must perform a kinematical analysis to connect the model correctly at the joints. This requires that the model is kinematically determinate. Another way of expressing that is that there must be the correct number of - and relationship between joints and drivers in the model. It usually takes some iterations in the model development to get it right. During these iterations it is useful to be able to load the model and see a picture of it, and this is why the loading simply positions the segments where the user placed them.

Instead of simply running the SetInitialConditions operation, you can also single-step through it to see what it does. This is done by clicking the "Step" button instead of the "Run" button.



Picking the step button.

The first step re-establishes the load-time conditions. This means that it positions the model as it was when you loaded it. This is useful for identification of kinematic problems. The second step positions the segments honoring the joints. The third does not seem to do much, but it is used for positioning muscles wrapping over surfaces. It is just not visible in this simple model.

The SetInitialConditions study can be thought of as the first step of a kinematic analysis, which will be the subject of [the next lesson](#).

Lesson 3: Kinematic Analysis

The KinematicAnalysis operation has a short and a very long explanation. The short explanation is that it makes the model perform whichever movement you have imposed on it by the drivers you have defined in the model. And it only does the movement. There is no calculation of forces involved, and the system does not even have to be properly balanced to be subjected to KinematicAnalysis. However, it does have to be kinematically determinate, but that concept is definitely a part of the longer explanation.

So, brace yourself, and let's venture on to...

The long explanation

An AnyBody model is really a collection of rigid segments. You can think of them as a bunch of potatoes floating around in space. Technically, each potato is called a "rigid body", but the term "body" can be misinterpreted in the context of a body modeling system like AnyBody, so we call them "segments".

When a segment flows around in space, it can move in six different directions. We call them degrees of freedom and usually think of them as movement along the three coordinate axes and rotation about the same axes. We call these movement directions "degrees of freedom" and an unconstrained segment in space has six degrees of freedom. If we have n segments in the model, the model will have a total of $6n$ degrees of freedom unless some of them are constrained somehow. The purpose of the kinematic analysis is to determine the position of all the segments at all times, and this requires $6n$ pieces of information about the positions to resolve the $6n$ degrees of freedom. The pieces of information are mathematically speaking equations. So kinematic analysis is about solving $6n$ equations with $6n$ unknowns.

A usual way of constraining degrees of freedom (or adding equations to the system) is to add joints to the model. When you join two segments they lose some of their freedom to move independently. They become constrained to each other. Consider two segments joined at their ends by a ball-and-socket joint. They are now under the constraints that the x , y and z coordinates of the joined points must be the same. In other words, a ball-and-socket joint adds three constraints or three equations to the system.

If you add enough joints to the system to provide all $6n$ constraints, then it might be mathematically possible to solve the equations and find the position of all the segments. But the result would not be very exciting because the system would not be able to move. Usually a body model will have enough joints to keep the segments together but few enough to let the model move. After all, movement is what most higher organisms do. So where do the remaining constraints or equations come from? They are the drivers. When the joints have eaten up their part of the degrees-of-freedom, enough drivers must be added to resolve the remaining unknowns in the system up to the required number of $6n$. When the AnyBody Modeling System performs the KinematicAnalysis operation, these drivers are taken through their sequences of values, and the positions of all the segments are resolved for each time step by solving the $6n$ equations.

When the model is set up in such a way that it has $6n$ equations and these equations can be solved, then it is said to be kinematically determinate. Usually this is necessary to perform the kinematic analysis. We say "usually" because there are a few exceptions where the system can be solved even when the number of equations is different from $6n$. There are also some cases where the system cannot be solved even though there are $6n$ equations available. Both cases are connected with redundant constraints.

If you define two or more constraints that in some way constrain exactly the same degrees of freedom in the same way, then they are redundant. For instance, you might by mistake repeat the definition of a joint. You will then have two joints that work exactly the same, and the equations provided by those two joints will be redundant. You will see them when you count constraints, but they will not have much effect.

The AnyBody Modeling System can sometimes cope with models that have too many constraints as long as those constraints are not conflicting, i.e. some of them are redundant. But it is a good rule to make sure that you have the same number of degrees-of-freedom and constraints.

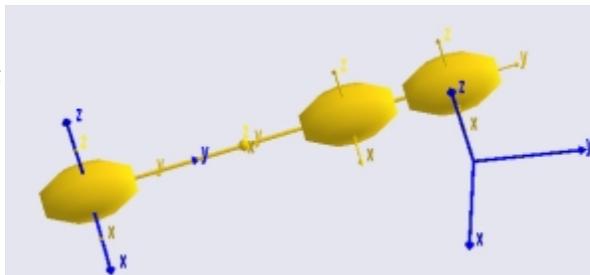
If you have too many constraints and they are incompatible, then the system is kinematically over-determinate. If you have too few constraints, or some of the constraints are redundant, then the system may be kinematically indeterminate. Both cases are likely to prevent the KinematicAnalysis operation to complete.

Actually, even when you have a kinematically indeterminate system, the KinematicAnalysis can fail. This is actually very easy to picture. Sometimes the segments of the model may be configured such that they cannot reach each other, or in such a way that they interlock. The real world is full of that sort of mechanisms: Car doors that get stuck or refuse to close, locks that will not unlock, or stacked glasses that wedge inseparably into each other. Computer systems that model the real world will have them too, and just like the real world it can sometimes be difficult to find out what the problem is.

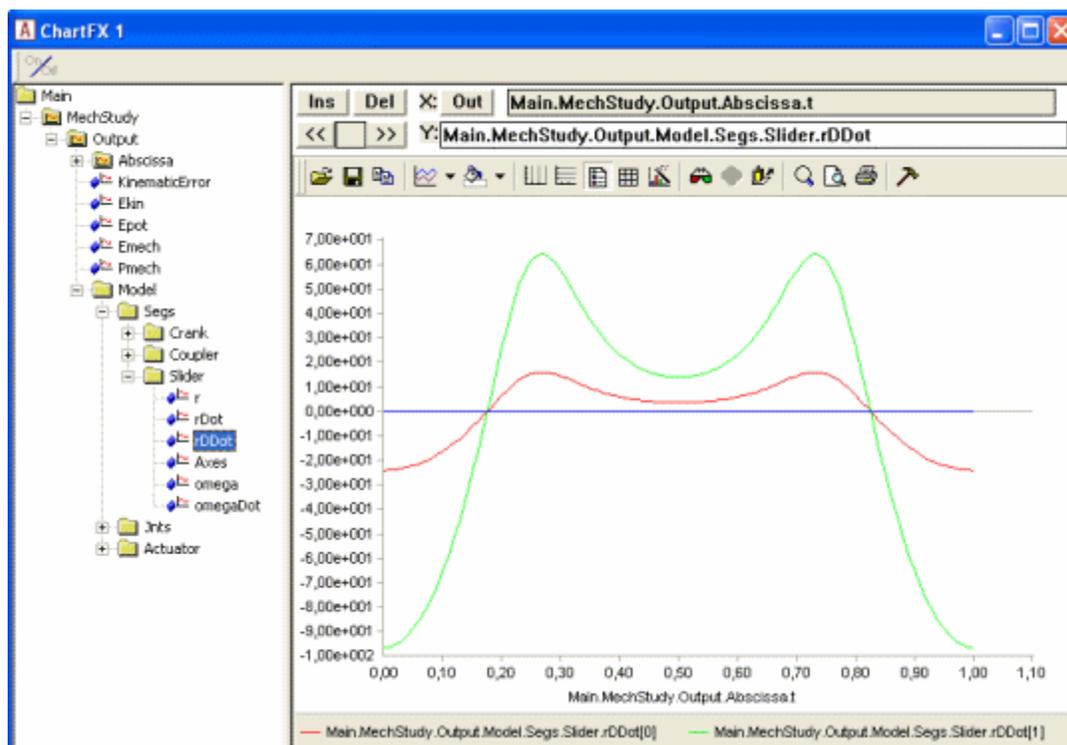
Running kinematic analysis

Now that you know the basics of kinematic analysis, let us look at how it is performed. We need an example to work on, and this one will serve the purpose: [demo.SliderCrank3D.any](#)

When you load it and open a [Model View](#) you will see that this is a very simple mechanism comprising only three segments. They are not yet connected correctly at their joints, but they will be if you run the KinematicAnalysis operation. Go to the Study tree, pick KinematicAnalysis and click the run button. You will see the model assemble and start moving.

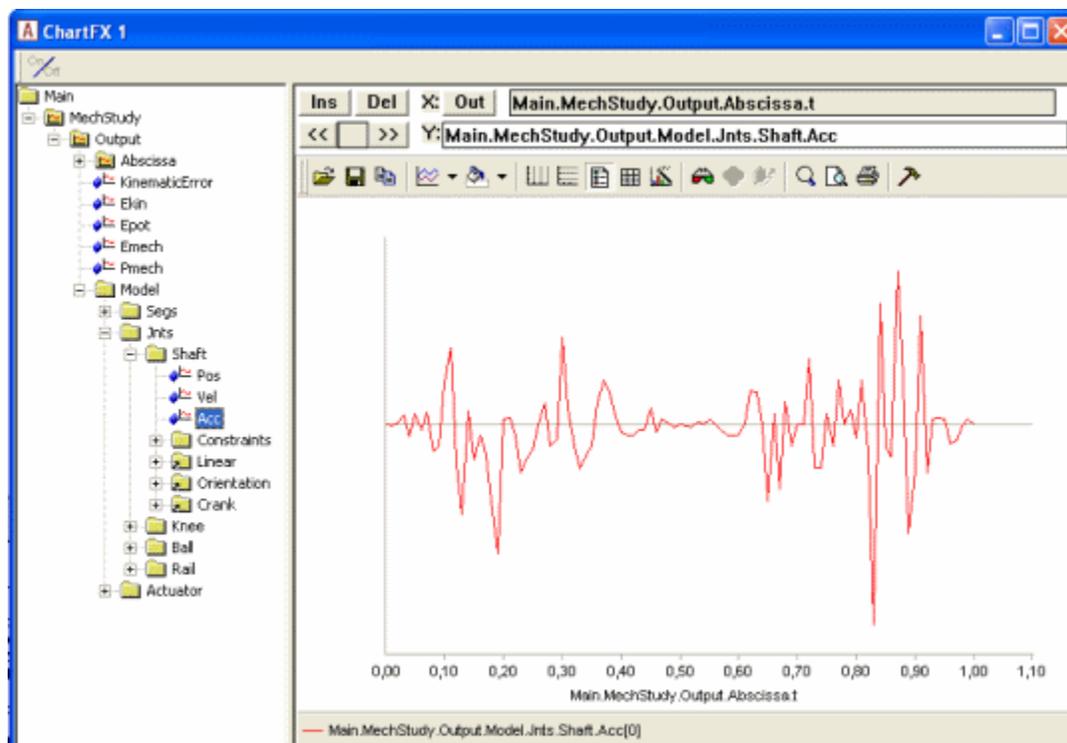


The KinematicAnalysis is precisely an analysis. It assembles data when it runs, and you can subsequently investigate those results in the [ChartFX](#) view. Pick Window -> ChartFX (new) to open it. The kind of results you can get from the KinematicAnalysis study is everything that has to do with positions, velocities, and accelerations. You may expand the tree until you reach the Slider segment, and you can chart its acceleration by choosing the rDDot property.

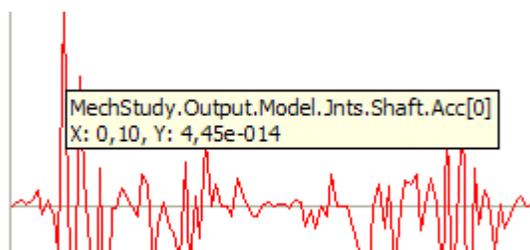


Notice the naming of the positional properties: r is position, $r\dot{}$ is velocity, and $r\ddot{}$ is acceleration. "Dot" or "DDot" are reflections of the mathematical custom of designating differentiation with respect to time by a dot over the symbol. So velocity would be ' r ' with a dot over, and acceleration would be ' r ' with two dots. Try browsing around the tree and look up the various available data.

You may encounter some strange looking results like this one:



Why would anything in a smoothly running model behave like this? The answer lies in the ordinate axis. You will notice that it has no values on it, and if you hold the mouse over a point on the curve a small window will pop up and show you the value:



You can see that the value is $4.45e-14$. For all practical purposes this is zero, and this is also why there are no values on the ordinate axis. What you see here is really zero augmented by numerical round-off errors.

Final remarks

Notice that kinematic analysis determines velocities and accelerations in addition to positions. The position analysis is by far the more challenging because the equations are nonlinear, whereas solution for velocity and acceleration involves linear equations once the positions have been determined. Please notice also that due to the very general approach used by the AnyBody Modeling System, it handles closed kinematic chains. This is crucial in biomechanics where closed chains occur very frequently, for instance in bicycling, gait, and whenever the model grabs something with both hands.

Although the kinematic analysis is useful in its own right for lots of purposes, it is also the first step of the InverseDynamicAnalysis operation, the subject of [the next lesson](#).

Lesson 4: Inverse Dynamic Analysis

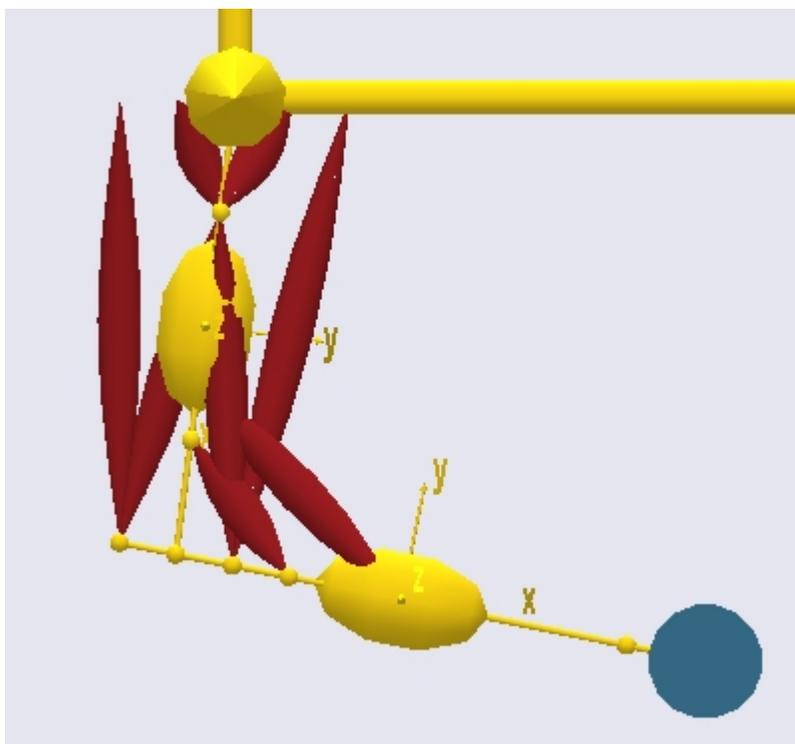
Inverse dynamic analysis is at the heart of what the AnyBody Modeling System does. An InverseDynamicAnalysis operation is like the KinematicAnalysis, except it is augmented with calculation of forces in the system.

Computing forces in a rigid body mechanical system is more difficult than it may seem. In principle, resolving forces is a question of setting up the equilibrium equations and solving them. But in mechanism analysis in general and biomechanics in particular, there are several complications. The system may very easily become statically indeterminate, which means that there are not enough equilibrium equations available to resolve the forces in the system. Another complication is caused by the muscles in the system because they can only pull. This constrains the space of possible solutions and adds a fair bit of mathematical complexity to the problem.

So the basic requirement to the InverseDynamicAnalysis solver is that it must be able to cope with

- Statically indeterminate problems
- Unilateral forces elements.

The fact that a mechanical system involving multiple muscles usually has too few equilibrium equations is not just of mathematical interest. The physical interpretation is that infinitely many different sets of forces can balance the mechanism. Have a look at the example we have been using in many of the tutorials, the simple arm performing a dumbbell curl:



To simplify a little, let us consider just the elbow joint. The model has six muscles spanning the elbow. Four of these are flexors and can work against the gravity on the dumbbell. In principle, only one flexor is necessary provided it is strong enough, so having four flexors available gives all sorts of possibilities for different force combinations. Technically, infinitely many different muscle force combinations can balance the exterior load in a system like this. This is the essence of static indeterminacy.

For use in this tutorial, a slightly modified version of the model is provided here: [demo.diffmusarm2D.any](#). Please download it, save it, and load it into the AnyBody Modeling System.

How does a real human body handle this situation? Actually, not a lot is known about how the human body distributes force between redundant muscles. Compared to other scientific achievements, such as charting the human genome, it may seem like a simple matter to figure out how much a given muscle is pulling on a bone. But it is far from simple.

- Measuring force in the first place is not easy. It is always based on measurement of a deformation of something.
- Measuring force in the human body is almost impossible because it requires insertion of measurement devices into the body. This is subject to obvious ethical restrictions, and even if a harmless measurement device could be inserted, it would be difficult to rule out the possibility that it would influence the function of the body and thereby the results.
- Measuring muscle force is possibly the most difficult of all because it involves very large forces in soft tissues.
- Even if we could measure a muscle force, it could only be done for particular situations, and it may not reveal the overall strategy behind the body's recruitment of muscle forces.

So what do we know about muscle forces in the human body? Well, the following is generally agreed on:

- Although infinitely many different muscle activation patterns can produce a given movement and balance given exterior forces, the recruitment is not random. For repeated movements there seems to be a consistent pattern of muscle activation. In other words, it seems to be based on some rational criterion.
- When several muscles are spanning a joint, they tend to collaborate. Although it may be enough to activate one or a few muscles, the body tends to use all the available muscles.
- In many movements it can be observed that some muscles seem to work against the movement or the exterior load. These are called antagonistic muscles.
- Large muscles provide more force than small muscles.

With the possible exception of the antagonistic muscles, all of this indicates that the body is trying to make the best of its resources. In fact, it is also known that idle muscles quickly lose their strength. Similarly, muscles that are exercised will build up strength. This is really the body's way of making the best of its resources, and it leads to the suspicion that the recruitment of muscles is also based on some sort of optimality criterion. The interesting point is that if the insufficient system of equilibrium equations is augmented with an optimality criterion involving muscle forces, then the problem can have a unique solution. This is precisely the basis of muscle recruitment in the AnyBody Modeling System.

The basic optimality assumption in the AnyBody Modeling System is that the body attempts to use its muscles in such a way that fatigue is postponed as far as possible. This leads to the idea of minimizing maximum muscle activity.

Before we proceed, let us investigate the concept of muscle activity. In the AnyBody Modeling System, muscle activity is defined as muscle force divided by strength. Simple as that may seem, activity depends on our definition of muscle strength. You may think of muscle strength either as a constant property of a muscle or as something that changes with the operational conditions of the muscle. For instance, it is well known that muscle strength decreases with contraction velocity, so that muscles contracting quickly have less strength than muscles contracting slowly. This only depends on the kind of muscle model you choose, and it does not change the fact that the AnyBody Modeling System will recruit muscles according to the following criterion:

Minimize

$$\begin{aligned} & (\text{maximum muscle activity}) \\ & + e1 * (\text{sum of activities}) \\ & + e2 * (\text{sum of squared activities}) \end{aligned}$$

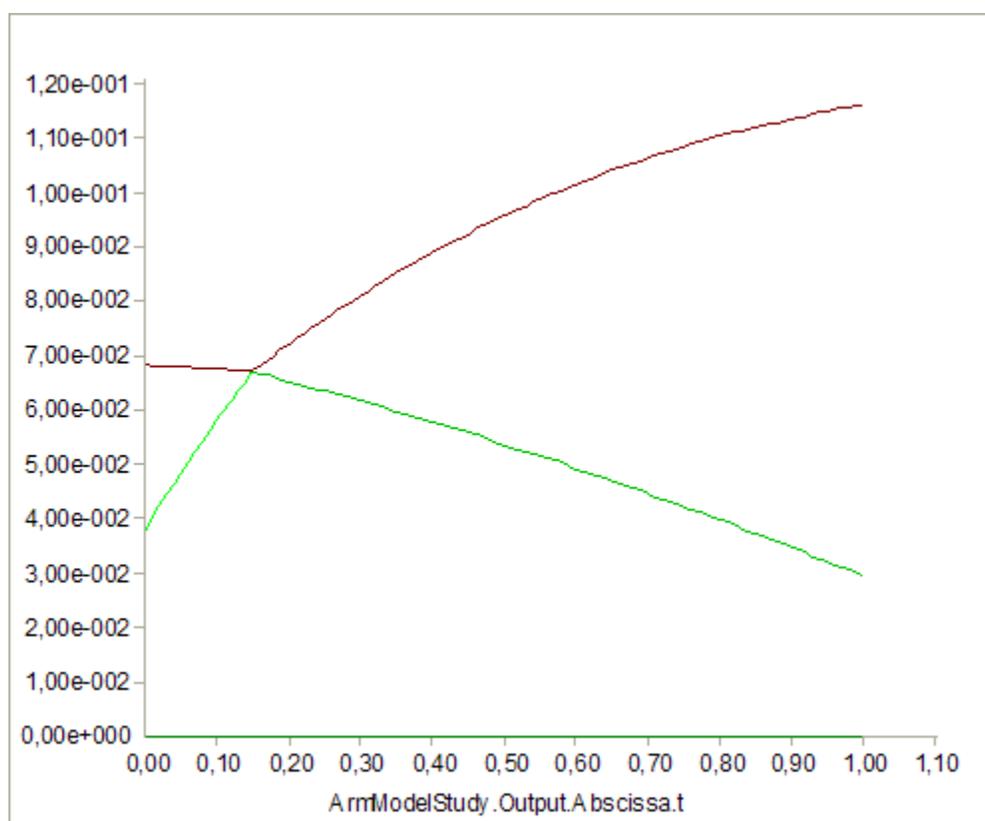
Subject to

- Equilibrium equations fulfilled
- Muscles are not allowed to push

In the standard setup of InverseDynamicAnalysis operations in the AnyBody Modeling System, e_1 and e_2 are both zero. This means that the system is minimizing the maximum muscle activity in each time step. Let us have a look at the consequences of that. Have you loaded [demo.diffmusarm2D.any](#) into the system yet? If not, please do it now, and run the InverseDynamicAnalysis. Open a ChartFX View, and browse your way through the output tree to the muscles. Expand any muscle, click "Activity", and replace the muscle's name in the specification line with an asterisk like this:

```
ArmModelStudy.Output.Model.Muscles.*.Activity
```

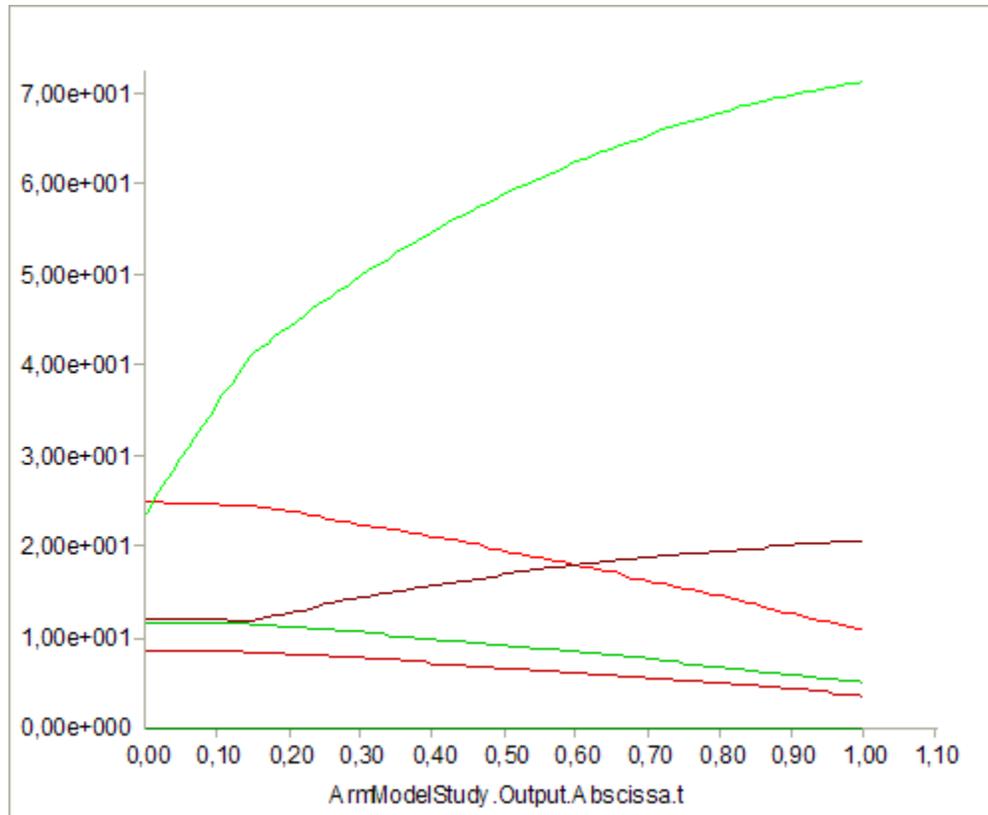
You should get the picture shown below:



Although we have eight muscles in the model you see only a few curves. The explanation is that, in the absence of e_1 and e_2 in the problem formulation above, the system minimizes the maximum activity of any muscle and this causes the muscle activity curves to fall on top of each other. So each curve you see is really several curves covering each other. However, since the muscles have different strengths, the common activities lead to different muscle forces. If we similarly plot the muscle forces by means of the Specification line:

```
ArmModelStudy.Output.Model.Muscles.*.Fm
```

we will get this result:

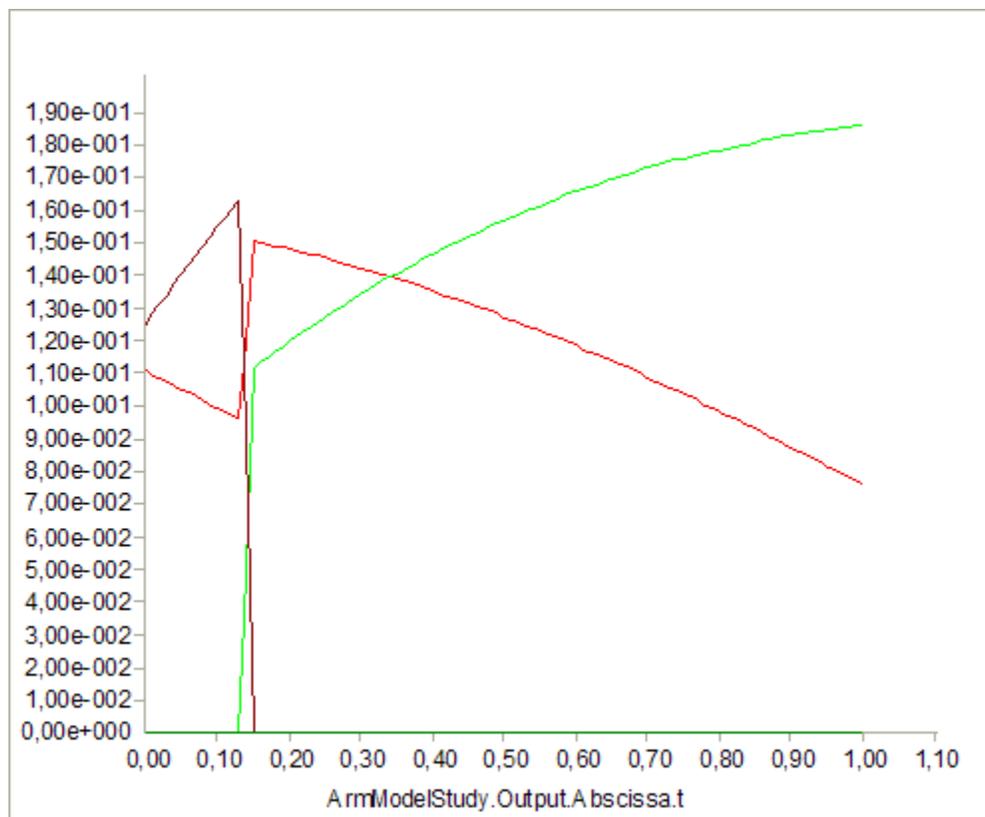


So the very systematic activation pattern becomes much more complex when viewed as muscle forces. Let us for a moment return to the activities again. They appear to range between approximately 0.30 and 1.20. These are direct measures of the load of the muscles. A load of 1.0 corresponds to the muscle working at its ultimate strength. In this case it appears that the muscles are about 20% overloaded when the dumbbell approaches the end of its movement. One of the advantages of the min/max criterion we are using here is that it guarantees that there is no other muscle recruitment that would lead to a smaller maximum activity. In other words, this criterion exploits the organism to its maximum potential and causes the muscles to collaborate maximally. This is a reasonable strategy for an organism trying to survive in a competitive environment.

But let us take a look at the consequence of increasing the value of $e1$. The name of $e1$ in AnyScript is `RecruitmentLpPenalty`. It is a member of the `AnyBodyStudy` class, so we can assign a value to it. Add the red line to the AnyScript model, load it, and run the `InverseDynamicAnalysis` again:

```
// The study: Operations to be performed on the model
AnyBodyStudy ArmModelStudy = {
  AnyFolder &Model = .ArmModel;
  RecruitmentSolver = MinMaxSimplex;
  RecruitmentLpPenalty = 1.0e+3;
  Gravity = {0.0, -9.81, 0.0};
};
```

We have assigned the rather large value of $1.0e+3$ to `RecruitmentLpPenalty`. Plotting the activities again produces the following results:



This result is much different from the one we had before. The value of $1.0e+3$ completely dominates the criterion, so here we are actually minimizing the sum of muscle activities. This has the effect of recruiting a minimum set of muscles and only those that are best suited at each position. This is known not to be correct because the muscles are not collaborating. So what is RecruitmentLpPenalty good for anyway? Well, the clean min/max criterion with $e1 = 0$ sometimes can cause unrealistic fluctuations of submaximal muscles between time steps. In those cases, small values of RecruitmentLpPenalty, say $1.0e-6$ or $1.0e-5$ can regularize the problem numerically. In this simple case, it makes no difference. If you keep increasing RecruitmentLpPenalty to, say, $1.0e-3$, it will begin to make a difference on the submaximal muscles, and this is a sign that you may have increased it too much.

Quadratic muscle recruitment

As long as the solution algorithm is linear, the value of $e2$ will make no difference. The algorithm is specified by the variable RecruitmentSolver, and the linear options are

- RecruitmentSolver = MinMaxSimplex;
- RecruitmentSolver = MinMaxOOSolSimplex;

These algorithms are very similar in nature and are really just different implementations of the same technology. For very large and complex problems one algorithm may outperform the other, and this is why both are available in the system.

However, there is also a third algorithm available, and it differs radically from the two former:

- RecruitmentSolver = MinMaxOOSolQP;

As the name indicates, this algorithm is quadratic, and it permits inclusion of quadratic terms and thereby

e2 in the criterion. This has two potentials:

1. Small values of e2 may regularize complex problems numerically much like e1 can do.
2. Large values of e2 can change the formulation of the problem into something different just like e1 can do, but unlike e1, it makes physiological sense to use large values of e2.

Initially, try setting up the study like this:

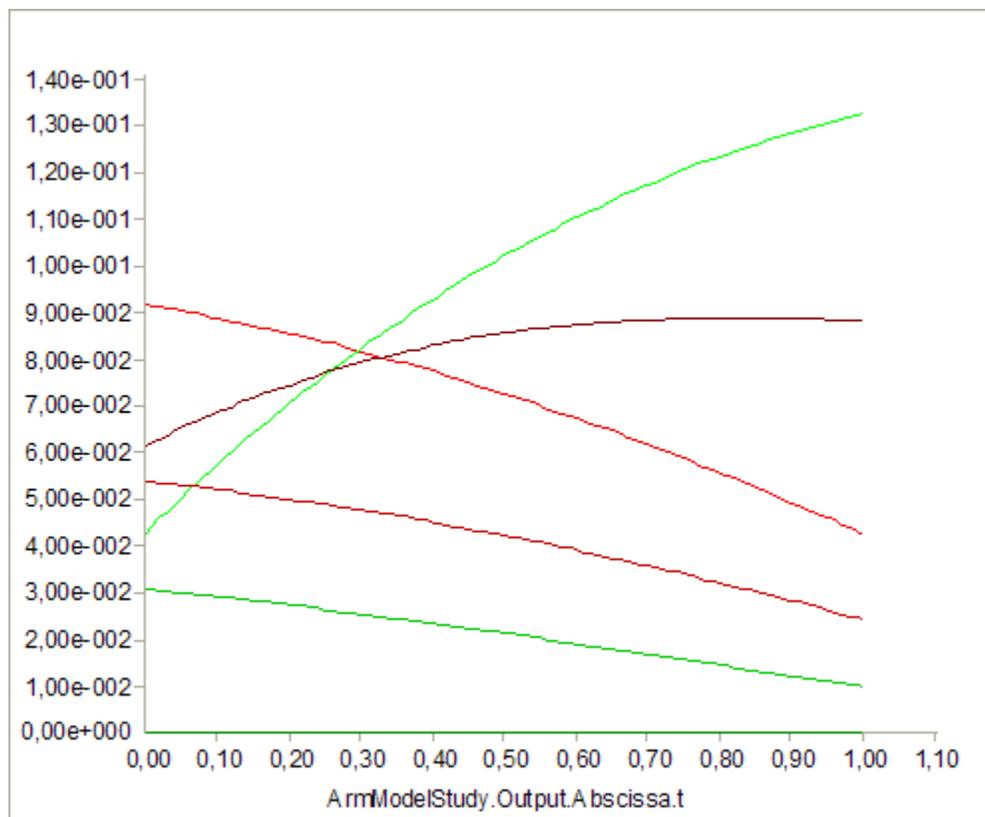
```
// The study: Operations to be performed on the model
AnyBodyStudy ArmModelStudy = {
  AnyFolder &Model = .ArmModel;
  RecruitmentSolver = MinMaxOOSolQP;
  RecruitmentLpPenalty = 0.0;
  RecruitmentQpPenalty = 0.0;
  Gravity = {0.0, -9.81, 0.0};
};
```

As you have probably guessed, the AnyScript name of e2 is RecruitmentQpPenalty. Load and rerun the model again and have a look at the activities. They should be just like before. You have changed the solution algorithm from linear to quadratic but not the formulation of the problem. Since both algorithms solve the same problem, the results are identical.

However, try changing the setting of the variable like this:

```
RecruitmentQpPenalty = 1000.0;
```

This rather high value of e2 will dominate the criterion and leave you with a quadratic solution to the muscle recruitment problem. Some scientists prefer this solution to the min/max formulation, and AnyBody gives you the opportunity to choose min/max, quadratic, or any combination of the two by variation of RecruitmentQpPenalty. The quadratic solution to the problem is the following:



As you can see, the tendencies are much the same as before, but the muscular synergy is less outspoken in the quadratic case, and the maximum muscle activity is therefore higher. Muscles recruited according to the quadratic criterion will tire before muscles recruited according to the min/max criterion, but the difference particularly for the activation envelope is not very dramatic. In any case, the AnyBody Modeling System gives you the opportunity to pick the criterion you believe is the best.

[The final lesson in the study of studies deals with muscle calibration.](#)

Lesson 5: Calibration Studies

One of the challenges in body modeling is that models must be able to change size to reflect individuals of different statures. Even if you are working on a model of a particular individual, you will almost always want to change the dimensions of the model as you are building it. And if you are developing a generic model to represent a range of body proportions, you are likely to want the model to depend on the anthropometrical parameters you define. For instance, the weight of a segment is often represented as some fraction of the full body weight. Such a property you could make parametric by simply defining it as a function of the full body weight by means of a simple formula.

But other dimensions are more subtle and difficult to establish as a direct functional dependency of other parameters. Tendon lengths are perhaps the most prominent example. If you are in doubt of the importance of tendon lengths, just try to bend over and touch your toes with your knees stretched. Some of us have hamstring tendons that are so short that we can hardly reach beyond our knees, so tendon lengths directly limit our ranges of motion. But they also influence the working conditions of our muscles even when the muscle-tendon unit is not stretched to its limit, so it is important that we define the muscle tendon unit so that it fits the body model.

A muscle-tendon unit is attached to at least two segments at its origin and insertion respectively. To make things worse, some muscles span several joints, and most muscles wrap over bones and other tissues with complex geometries on their way from origin to insertion. So, the basic idea behind calibration of tendon

lengths in AnyBody is the assumption that each muscle-tendon unit has its optimal length at some particular position of the joints it spans. We simply define one or several studies that put the body model in these positions and adjust the lengths of the tendons to give the attached muscles their optimal lengths in those positions. When you subsequently run an analysis, the system uses the calibrated tendon lengths regardless of how they are defined in the AnyScript file. (This means that you have to run the calibration(s) every time you have reloaded the model if they are to take effect).

AnyBody has several different types of muscle models. Some are very simple and contain no strength-length relationship, while others do. It goes almost without saying that the former type is not affected by calibration. If you use one of the latter - more advanced - models, however, calibration may be crucial. If the tendon is too long, the muscle will end up working in an unnaturally contracted state where it has very little strength. If the tendon is too short, the muscle will be stretched, and its passive elasticity will affect the force balance in the system. Since the passive elastic force in a muscle-tendon unit typically grows very rapidly with stretching, a too short tendon can cause very large antagonistic muscle actions.

Enough talk! Let's define a muscle and calibrate it. We shall begin with the simple arm model we developed in the "[Getting Started with AnyScript](#)" tutorial. If you have not already saved the model in a file, get it here: [arm2d.any](#).

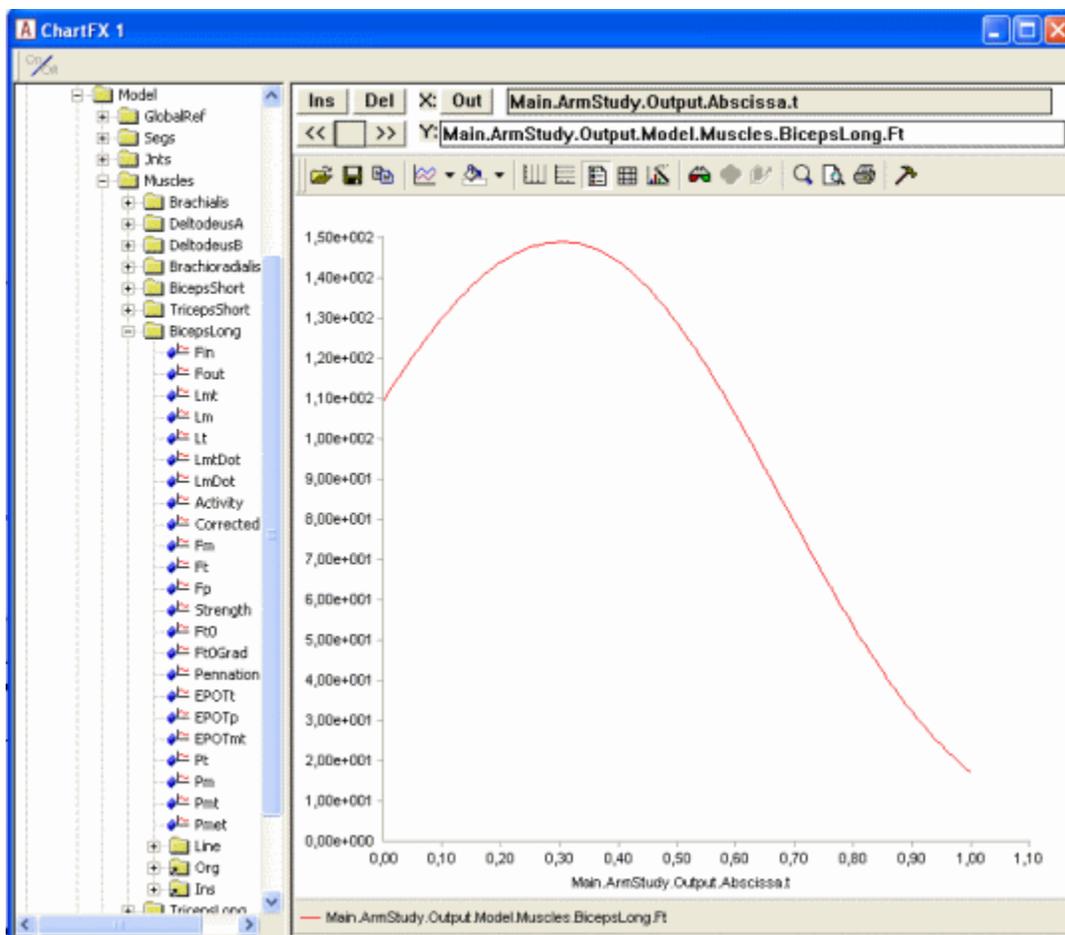
In that simple example, all the muscles were assumed to be of a simple type with constant strength. We shall add another and much more detailed muscle model:

```
// -----
// Muscles
// -----
AnyFolder Muscles = {
  //-----
  // We define one simple muscle model, which we will use
  // for all muscles except biceps long
  AnyMuscleModel MusMdl = {
    F0 = 300;
  };
  AnyMuscleModel3E BicepsLongModel = {
    AnyVar PCSA = 2.66; // Physiological cross sectional area [cm^2]
    F0 = PCSA*30; // Presuming a maximum muscle stress of 30 N/cm^2
    Lfbar = 0.123; //Optimum fiber length [m]
    Lt0 = 0.26; //First guess of tendon slack length [m]
    Gammabar = 0.3*(pi/180); //Pennation angle converted to radians
    Epsilonbar = 0.053; //Tendon strain at F0
    K1 = 10; //Slow twitch factor
    K2 = 0; //Fast twitch factor(zero when no info available)
    Fcfast = 0.4; //Percentage of fast to slow factor
    Jt = 3.0; //Shape parameter for the tendon stiffness
    Jpe = 3.0; //Shape parameter for the parallel stiffness
    PEFactor = 5.0; //Parameter for influence of parallel stiffness
  }; // End of BicepsLongModel
};
```

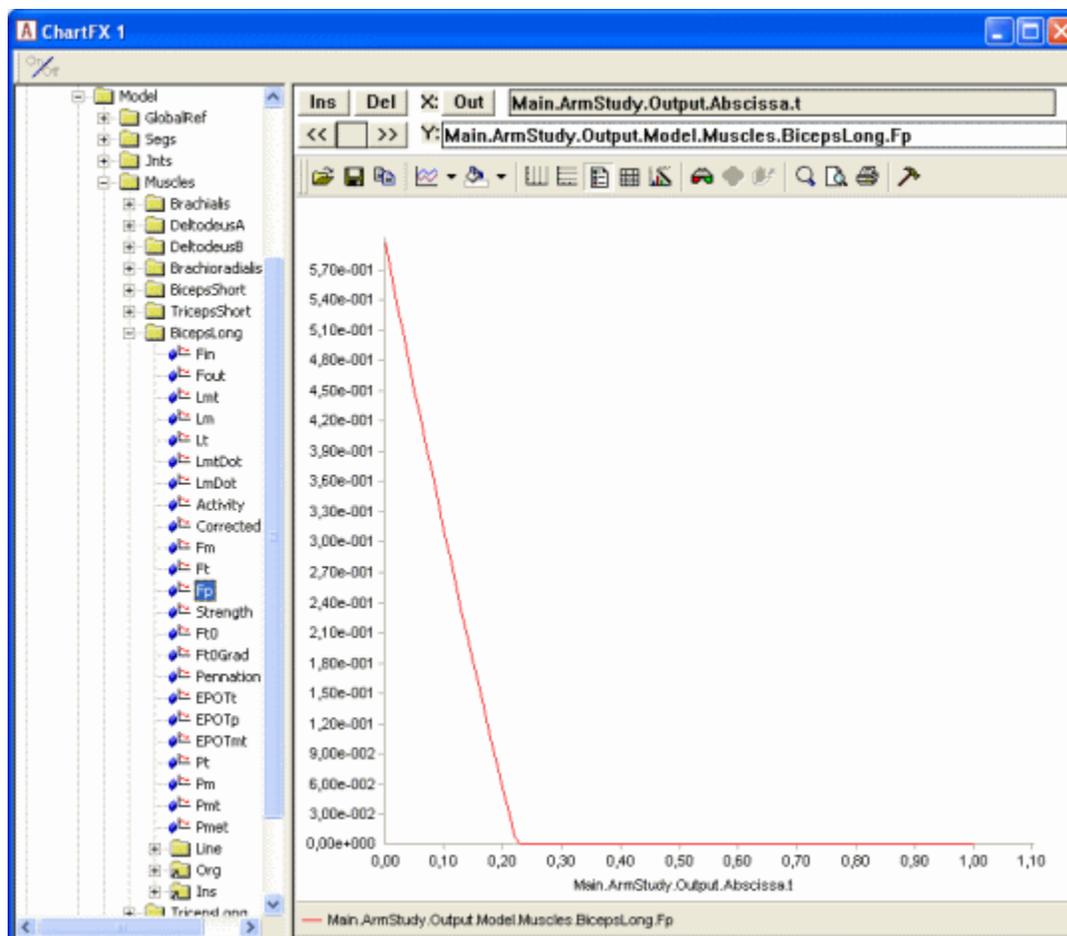
As you can see from the comments, the muscle has many parameters you have to set. The significance of each of these is explained in detail in the [muscle modeling tutorial](#). For this model to take effect, we must assign it to the biceps long muscle. It is a little further down in the file, where the red line must be changed:

```
//-----
AnyViaPointMuscle BicepsLong = {
  AnyMuscleModel &MusMdl = .BicepsLongModel;
  AnyRefNode &Org = Main.ArmModel.GlobalRef.BicepsLong;
  AnyRefNode &Ins = ..Segs.LowerArm.Biceps;
  AnyDrawViaPointMuscle DrwMus = {};
};
```

What we have done here is to give BicepsLong a new and more advanced muscle model. Let's have a look at the consequences. Press the M<-S button or F7 and subsequently run the InverseDynamicAnalysis. Then, open a new ChartFX window to investigate the results.



This graph shows the muscle force or more precisely the force in the tendon. The force in this more complex muscle model is composed of two elements: The active part coming from the contractile element of the muscle, and the passive part due to the stretching of the parallel-elastic part of the muscle. The two parts come together in the tendon force, Ft. The parallel-elastic part of the muscle is represented by Fp in the result tree. If you pick this property, you should get the following graph:



The parallel-elastic force sets in when the muscle is stretched beyond its optimal fiber length. In the movement of this example, the elbow starts at 90 degrees flexion, and as the graph shows, this gives rise to about 10 N of passive force at the beginning of the movement. This indicates that the tendon we have specified is too short. If the movement was extending the elbow instead of flexing it, the passive force would rise sharply. This means that the result of the simulation depends a lot on having the correct length of the tendon. If it is too short, too much of the load will be carried by passive muscle forces. In this example where we have only one muscle with a complex model, it would not be too difficult to adjust the tendon length manually until we get it right, but in models with many muscles, this can be a very tedious task, particularly since it has to be repeated every time the dimensions of the model are changed. Instead, the answer is to let AnyBody calibrate the tendon length automatically.

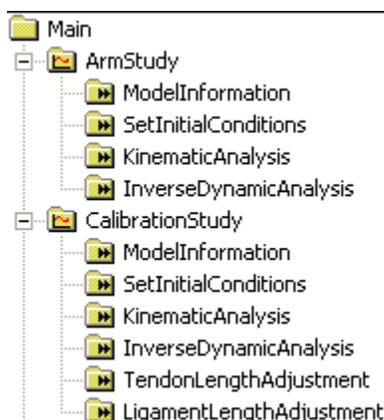
AnyBody's advanced muscle model, the AnyMuscleModel3E, is basically a phenomenological model based on the classical works of Hill. It presumes that each muscle has an optimum contraction in which its fibers have their best force-producing capability. If we knew the set of joint positions corresponding to this optimum fiber length for each muscle, then those joint positions were the ones we would be calibrating the muscle in.

Finding joint positions corresponding to optimum muscle fiber lengths is an active and rather young area of research, and the correct values are only known for a few muscles in the body. However, it is not surprising that we seem to have been built in such a way that our muscles attain their optimum fiber lengths in the joint positions where they do most of their work, and if you are unable to find the information about optimum joint positions you need, then your best choice may be to calibrate the muscle in the joint position where it primarily works.

Calibrating the muscle in a particular position requires a calibration study. It's basic definition is very simple:

```
// =====
// "The body study"
// =====
AnyBodyStudy ArmModelStudy = {
  AnyFolder &Model = Main.ArmModel;
  RecruitmentSolver = MinMaxSimplex;
  Gravity = {0.0, -9.81, 0.0};
};
// A new calibration study
AnyBodyCalibrationStudy CalibrationStudy = {
  AnyFolder &Model = Main.ArmModel;
  nStep = 1;
}; // End of study
```

If you load the model in you can study the structure of the new study:



You can see that it has multiple operations. The interesting ones are the two latter: TendonLengthAdjustment and LigamentLengthAdjustment. As the names indicate they are for tendon and ligament calibration respectively. Notice that the study only has one time step. The model posture in that step should be the position in which you wish to calibrate the tendon. If you run the TendonLengthAdjustment operation you will notice that the model takes the initial posture of the flexion movement it was doing in the InverseDynamicsAnalysis. This is because of the line

```
AnyFolder &Model = Main.ArmModel;
```

The ArmModel contains movement drivers, and when they are included in the study they cause the model to attain the same posture in the calibration study as it does in the inverse dynamic analysis. To be able to calibrate in another posture we must perform a small restructuring of the model and perhaps recommend a organizing things a little differently in general when making models.

We included the movement in the model when we developed it in the "[Getting Started with AnyScript](#)" tutorial because we wanted things to be simple. But think for a moment about how you would typically want to use models. Let's imagine you have developed a model of a leg. One day you might want to simulate squat, another day perhaps gait, and yet another day a football kick. You would want to use the same model but with different sets of drivers. This speaks in favor of having drivers, loads, and other problem-specific properties outside the folder containing the body model.

Calibration is actually an example of using the same model with two different movements, so we have to place the drivers outside the ArmModel folder. In the editor, highlight the entire Drivers folder, cut it out, and paste it in right below the end of the ArmModel folder like this:

```

}; // ArmModel

AnyFolder Drivers = {

    //-----
    AnyKinEqSimpleDriver ShoulderMotion = {
        AnyRevoluteJoint &Jnt = Main.ArmModel.Jnts.Shoulder; // Changed!
        DriverPos = {-100*pi/180};
        DriverVel = {30*pi/180};
        Reaction.Type = {Off};
    }; // Shoulder driver

    //-----
    AnyKinEqSimpleDriver ElbowMotion = {
        AnyRevoluteJoint &Jnt = Main.ArmModel.Jnts.Elbow; // Changed!
        DriverPos = {90*pi/180};
        DriverVel = {45*pi/180};
        Reaction.Type = {Off};
    }; // Elbow driver
}; // Driver folder

```

Notice that after moving the Drivers folder we have changed the references to the joints. We also have to change the study a little bit. This is because the study points at the ArmModel folder, and that no longer contains a movement, so the study would not know how to move the model, unless we add this line:

```

// =====
// "The body study"
// =====
AnyBodyStudy ArmStudy = {
    AnyFolder &Model = .ArmModel;
    AnyFolder &Drivers = .Drivers;
    RecruitmentSolver = MinMaxSimplex;
    Gravity = {0.0, -9.81, 0.0};
};

```

Now we are ready to define a couple of static drivers specifically for calibration of the muscles. We create a CalibrationDrivers folder right below the Drivers folder:

```

// -----
// Calibration Drivers
// -----
AnyFolder CalibrationDrivers = {
    //-----
    AnyKinEqSimpleDriver ShoulderMotion = {
        AnyJoint &Jnt = Main.ArmModel.Jnts.Shoulder;
        DriverPos = {-90*pi/180}; // Vertical upper arm
        DriverVel = {0.0};
        Reaction.Type = {Off};
    };
    //-----
    AnyKinEqSimpleDriver ElbowMotion = {
        AnyJoint &Jnt = Main.ArmModel.Jnts.Elbow;
        DriverPos = {30*pi/180}; // 20 degrees elbow flexion
        DriverVel = {0.0};
        Reaction.Type = {Off};
    };
};

```

These drivers are static because their velocities are zero. They specify a posture with the upper arm vertical and the elbow at 30 degrees flexion. Notice the expressions converting degrees to radians.

The final step is to modify the calibration study to use the calibration drivers:

```
// A new calibration study
// A new calibration study
AnyBodyCalibrationStudy CalibrationStudy = {
    AnyFolder &Model = Main.ArmModel;
    AnyFolder &Drivers = .CalibrationDrivers;
    nStep = 1;
}; // End of study
```

What we have now is a study that uses the model together with two static drivers for calibration of the muscles, and a study that uses the model with the previous set of dynamic drivers. If you run the CalibrationStudy first, the system will adjust the tendon lengths and remember the values for the subsequent run of the AnyBodyStudy. Running this sequence of two studies reveals that there is no more passive force present in the BicepsLong muscle because it has now been calibrated in a more natural position.

The final issue of this tutorial is: How can we handle calibration of different muscles in different positions? For instance, it might be reasonable to believe that the elbow extensors should be calibrated in a different elbow position than the elbow flexors. How can we accomplish that? Well a closer investigation of the calibration study listed above can actually give us a clue. The study contains the following two lines:

```
AnyFolder &Model = Main.ArmModel;
AnyFolder &Drivers = Main.CalibrationDrivers;
```

This tells us that a study manipulates the objects mentioned inside the study folder, in this case the ArmModel and the CalibrationDrivers. Perhaps you remember that we took the drivers out of the ArmModel, so that we could refer separately to them in the study? We did this to be able to not refer to the movement drivers when we run the calibration study and vice versa. Similarly, if we want to calibrate a subset of the muscles, we simply make it possible to just refer to precisely this subset in the study and leave the others out.

Let us create a new muscle model for TricepsLong and calibrate that in another position.

```
}; // End of BicepsLongModel
AnyMuscleModel3E TricepsLongModel = {
    AnyVar PCSA = 15; // Physiological cross sectional area [cm^2]
    F0= PCSA*30; // Presuming a maximum muscle stress of 30 N/cm^2
    Lfbar= 0.194; //Optimum fiber length [m]
    Lt0 = 0.35; //First guess of tendon slack length [m]
    Gammabar = 2.0*(pi/180); //Pennation angle converted to radians
    Epsilonbar = 0.053; //Tendon strain at F0
    K1 = 10.0; //Slow twitch factor
    K2 = 0.0; //Fast twitch factor(zero when no info available)
    Fcfast = 0.4; //Percentage of fast to slow factor
    Jt = 3.0; //Shape parameter for the tendon stiffness
    Jpe = 3.0; //Shape parameter for the parallel stiffness
    PEFactor = 5.0; //Parameter for influence of parallel stiffness
}; // End of TricepsLongModel
```

```
AnyViaPointMuscle TricepsLong = {
    AnyMuscleModel &MusMdl = .TricpesLongModel;
    AnyRefNode &Org = ..GlobalRef.TricepsLong;
    AnyRefNode &Ins = ..Segs.ForeArmArm.Triceps;
    AnyDrawViaPointMuscle DrwMus = {};
};
```

Once again we need two drivers to put the model into the posture for calibration of the TricepsLong muscle:

```
// -----
// Triceps Calibration Drivers
// -----
AnyFolder TricepsCalibrationDrivers = {
  //-----
  AnyKinEqSimpleDriver ShoulderMotion = {
    AnyJoint &Jnt = Main.ArmModel.Jnts.Shoulder;
    DriverPos = {-90*pi/180}; // Vertical upper arm
    DriverVel = {0.0};
    Reaction.Type = {Off};
  };
  //-----
  AnyKinEqSimpleDriver ElbowMotion = {
    AnyJoint &Jnt = Main.ArmModel.Jnts.Elbow;
    DriverPos = {90*pi/180}; // 30 degrees elbow flexion
    DriverVel = {0.0};
    Reaction.Type = {Off};
  };
};
```

As you can see, this differs from the drivers for calibration of BicepsLong only by using 90 degrees elbow flexion rather than 30 degrees.

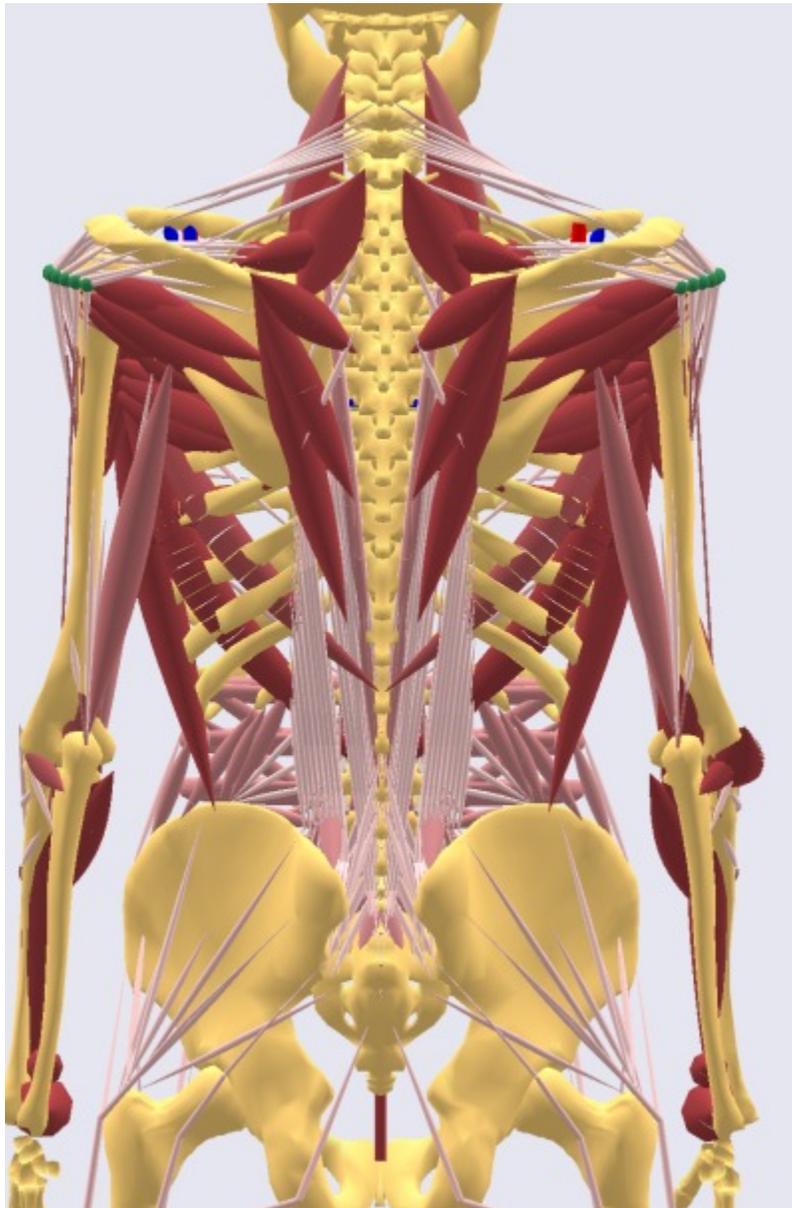
What we could do now is to take the two advanced muscle models out of the ArmModel folder, so that we could refer to them individually in the study; just like we did with the drivers. But let's try something else instead. We'll simply refer directly to the individual elements of the ArmModel in the calibration study rather than the entire ArmModel. This way we are able to leave out the muscles we do not want to include. So we simply make a new study that looks like this:

```
// A calibration study for TricepsLong
AnyBodyCalibrationStudy TricepsCalibrationStudy = {
  AnyFixedRefFrame &GlobalRef = Main.ArmModel.GlobalRef;
  AnyFolder &Segs = Main.ArmModel.Segs;
  AnyFolder &Jnts = Main.ArmModel.Jnts;
  AnyViaPointMuscle &TricepsLong = Main.ArmModel.Muscles.TricepsLong;
  AnyFolder& Drivers = Main.TricepsCalibrationDrivers;
  nStep = 1;
}; // End of study
```

Notice that this study refers to each folder inside the ArmModel individually. This way, we can restrict our references only to the TricepsLong muscle and leave all the other muscles out. This means that the other muscles will not be affected by this calibration. So if you initially calibrate all the muscles by the CalibrationStudy and subsequently run the TricepsCalibrationStudy, then the latter will not overwrite the effect of the former, but only for the muscle mentioned in the study, i.e. the TricepsLong.

Here's a link to the finished [calibration.any](#) example.

Muscle modeling



Muscles are the actuators of living bodies. They are activated by the central nervous system (CNS) by a complicated electro-chemical process. Determining the activation that realizes a desired movement requires an extremely intricate control algorithm. The CNS is superior to any computer man has made in this respect. AnyBody mimics the workings of the CNS by computing backwards from the movement and load specified by the user to the necessary muscle forces in a process known as inverse dynamics. To do so, the system must know the properties of the muscles involved, and this is where muscle modeling comes into the picture.

AnyBody contains three different muscle models ranging from simple to more complicated physiological behavior. The simplest model just assumes a constant strength of the muscle regardless of its working conditions. The more complicated models take such conditions as current length, contraction velocity, fiber

length, pennation angle, tendon elasticity, and stiffness of passive tissues into account. Please refer to the [reference manual](#) for concise information about the available muscle models:

1. AnyMuscleModel - assuming constant strength of the muscle
2. AnyMuscleModel3E - a three element model taking serial and parallel elastic elements into account along with fiber length and contraction velocity
3. AnyMuscleModel2ELin - a bilinear model taking length and contraction velocity into account.

The muscle models can be linked to different types of muscles:

1. AnyViaPointMuscle - a muscle that passes through any number of nodes on segments on its way from origin to insertion
2. AnyShortestPathMuscle - a muscle that can wrap over geometries such as cylinders and ellipsoids and even CAD-defined surfaces. Please beware that this muscle type is very computationally demanding and requires careful adjustment.
3. AnyGeneralMuscle - a more standard actuator-type muscle that can be attached to a kinematic measure.

Please refer to the [reference manual](#) for more information, or proceed to the basics of muscle modeling in [Lesson 1](#).

Lesson 1: The basics of muscle definition

The key to understanding muscles in the AnyBody Modeling System is to realize that they mechanically consist of two separate computational models:

1. The kinematic model, which determines the muscle's path from origin to insertion depending on the posture of the body. This also entails finding the length and contraction velocity of the muscle.
2. The strength model which determines the muscle's strength and possible its passive elastic force depending on the kinematic state of the muscle.

This would be a sad excuse for a tutorial if we did not have an example to work on. So let us quickly construct a very simple example that will enable us to examine the properties of muscles. [Here's an extremely simple one-degree-of-freedom model \(right-click and save to disk\)](#):

```
// This is a very simple model for demonstration of muscle modeling
Main = {

  AnyFolder MyModel = {

    // Global Reference Frame
    AnyFixedRefFrame GlobalRef = {
      AnyDrawRefFrame drw = {
        RGB = {1,0,0};
      };
    }; // Global reference frame

    // Define one simple segment
    AnySeg Arm = {
      r0 = {0.500000, 0.000000, 0.000000};
      Mass = 1.000000;
      Jii = {0.100000, 1.000000, 1.000000}*0.1;
      AnyRefNode Jnt = {
        sRel = {-0.5, 0.0, 0};
      };
      AnyDrawSeg drw = {};
    };

    // Attach the segment to ground by a revolute joint
```

```

AnyRevoluteJoint Jnt = {
  AnyRefFrame &ref1 = .GlobalRef;
  AnyRefFrame &ref2 = .Arm.Jnt;
  Axis = z;
};

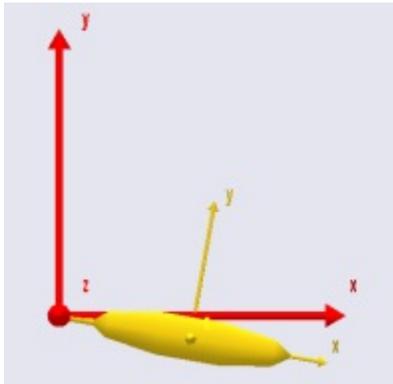
// Drive the revolute joint at constant velocity
AnyKinEqSimpleDriver Drv = {
  DriverPos = {-10*pi/180};
  DriverVel = {40*pi/180};
  AnyRevoluteJoint &Jnt = .Jnt;
  Reaction.Type = {0};
};

}; // MyModel

// The study: Operations to be performed on the model
AnyBodyStudy MyStudy = {
  AnyFolder &Model = .MyModel;
  RecruitmentSolver = MinMaxNRSimplex;
  Gravity = {0.0, -9.81, 0.0};
};
}; // Main

```

When you load the model, open a model view window, and run the SetInitialConditions operation, you should get the following picture:

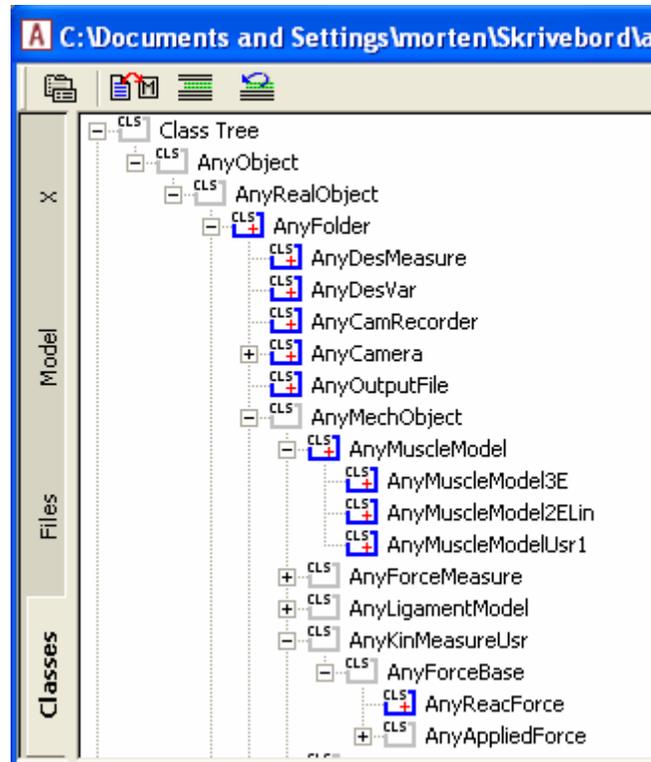


The model has a driver, so you can run the kinematic analysis and see the movement. The arm flexes about the origin of the red reference frame. If you try to run the InverseDynamicAnalysis, you will get an error:

Muscle recruitment analysis failed, simplex solver reports that solution does not satisfy all constraints.

This is because the model does not have any muscles to balance the arm against the downward pull of gravity. Let us define the simplest possible muscle to carry the load. As mentioned above, a muscle has two basic components: a kinematic model, and a strength model. We shall begin with the latter, and for the time being define the simplest possible version.

If you pick the Classes tab in the tree view on the left hand side of the Editor Window, then you will get access to the class tree. Expand the tree as shown in the picture until you get to the AnyMuscleModel.



Notice that this class has three derived classes. These are more advanced muscle models, and we shall get to those later. However for the time being, place the cursor in the Editor View on an empty line just after the end brace of the driver definition, right-click the `AnyMuscleModel` class in the tree, and select "Insert Class Template". This causes an instance of the `AnyMuscleModel` class to be inserted into the model (new code marked with red):

```
// Drive the revolute joint at constant velocity
AnyKinEqSimpleDriver Drv = {
  DriverPos = {-10*pi/180};
  DriverVel = {40*pi/180};
  AnyRevoluteJoint &Jnt = .Jnt;
  Reaction.Type = {0};
};

AnyMuscleModel <ObjectName> = {
  F0 = 0;
};
```

This is the simplest type of muscle model the system provides, and it is simply a specification of strength corresponding to the assumed maximum voluntary contraction of the muscle. A muscle with this type of model does not have any dependency on length or contraction velocity, and it does not take the passive elasticity of the tissue into account. Despite this simplicity, it is used with considerable success for many studies where the movements or postures are within the normal range of the involved joints, and where contraction velocities are small.

Let us perform the necessary modifications to make the model useful to us:

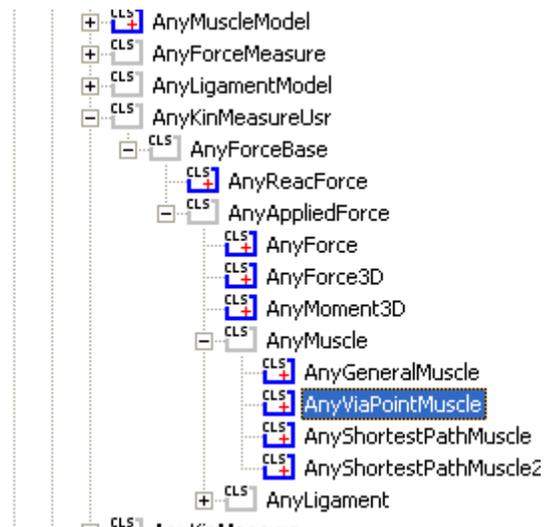
```
AnyMuscleModel SimpleModel = {
  F0 = 100;
};
```

The next step is to define a muscle that can use the model. This is actually the first of the two elements mentioned above: Muscle kinematics.

Again, the AnyBody Modeling System provides a number of choices, and we shall start by picking the simplest one. It is instructive to once again use the tree to insert a template of the muscle object, because the tree reveals the class dependency. A muscle resolves kinematical information in the sense that it has a certain path from origin to insertion, and it also provides force. These two properties are reflected in the way the muscle classes are derived from a kinematic measure as well as force classes.

The simplest type of muscle is the AnyViaPoint muscle. It spans the path between origin and insertion by passing through any number of via points on the way. The via points are fixed to segments or to the global reference frame. It is a simple and convenient way to define many of the simpler muscles of the body, primarily those in the extremities and the spine. You can, in fact, make a pretty decent model of the legs entirely with via point muscles.

Place the cursor right after the end brace of the muscle model, right-click the AnyViaPointMuscle class in the tree, and insert an instance of it:



```
AnyMuscleModel SimpleModel = {
    F0 = 100;
};

AnyViaPointMuscle <ObjectName> = {
    AnyMuscleModel &<Insert name0> = <Insert object reference (or full object
definition)>;
    AnyRefFrame &<Insert name0> = <Insert object reference (or full object definition)>;
    AnyRefFrame &<Insert name1> = <Insert object reference (or full object definition)>;
    //AnyRefFrame &<Insert name2> = <Insert object reference (or full object
definition)>;
};
```

Let us start by filling out what we can and removing what we have no use for:

```
AnyViaPointMuscle Muscle1 = {
    AnyMuscleModel &Model = .SimpleModel;
    AnyRefFrame &<Insert name0> = <Insert object reference (or full object definition)>;
    AnyRefFrame &<Insert name1> = <Insert object reference (or full object definition)>;
};
```

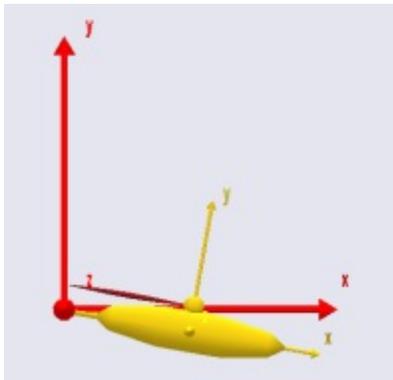
Notice that we have left only two points in the list of via points. This is obviously the minimal requirement and will create a muscle in a single line from origin to insertion. But before we proceed with the definition of the muscle we must define the necessary points on the model to attach the muscle to. We shall define the origin on the global reference frame and the insertion on the segment:

```
// Global Reference Frame
AnyFixedRefFrame GlobalRef = {
  AnyDrawRefFrame drw = {
    RGB = {1,0,0};
  };
  AnyRefNode M1Origin = {
    sRel = {0.0, 0.1, 0};
  };
}; // Global reference frame
// Define one simple segment
AnySeg Arm = {
  r = {0.500000, 0.000000, 0.000000};
  Mass = 1.000000;
  Jii = {0.100000, 1.000000, 1.000000}*0.1;
  AnyRefNode Jnt = {
    sRel = {-0.5, 0.0, 0};
  };
  AnyRefNode M1Insertion = {
    sRel = {0.0, 0.1, 0};
  };
  AnyDrawSeg drw = {};
};
```

With these two points, we can complete the definition of the muscle:

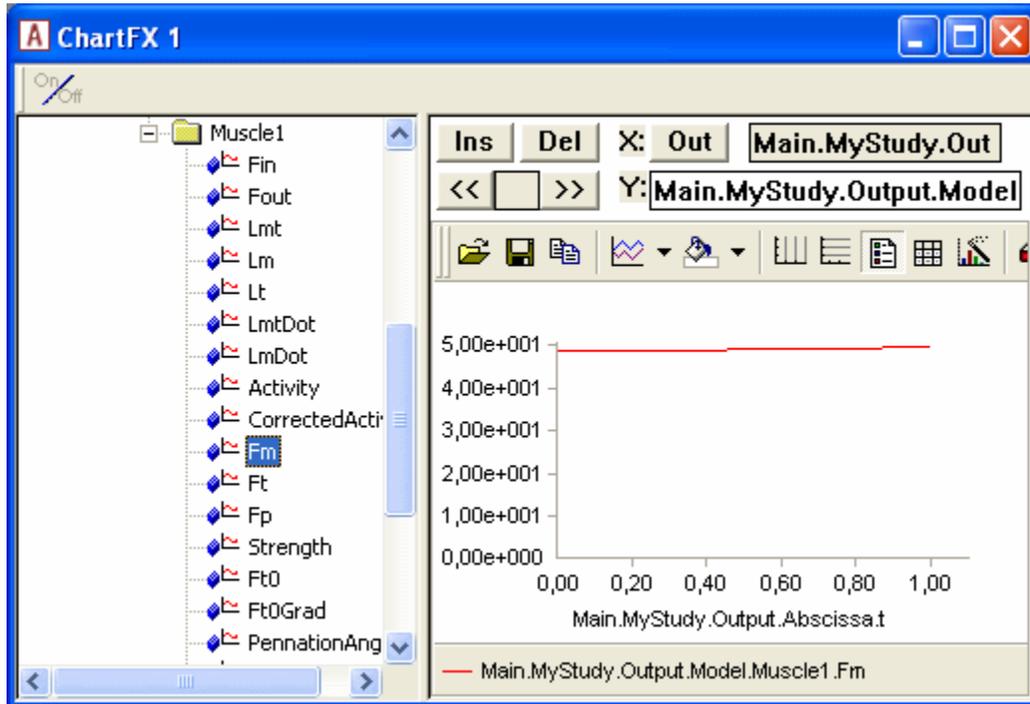
```
AnyViaPointMuscle Musc1e1 = {
  AnyMuscleModel &Model = .SimpleModel;
  AnyRefFrame &Orig = .GlobalRef.M1Origin;
  AnyRefFrame &Ins = .Arm.M1Insertion;
  AnyDrawMuscle drw = {};
};
```

Notice that we have added an AnyDrawMuscle object to the definition. Like other classes in AnyScript, muscles are not drawn in the model view window unless you specifically ask for it. When you load the model and run the SetInitialConditions study you will get the following picture (if your model does not load, and you cannot find the error, [click here to download a model that works](#)):



Notice that the muscle is now able to balance the gravity, and we are able to run the

InverseDynamicAnalysis. If you try it out and subsequently open a chart view, you are able to plot the muscle force:



The muscle force is the item Fm in the list of properties you can plot for a muscle. As you can see, lots of other properties are available, but if you try to plot them you will find that many of them are zero. This is because they are not relevant for this very simple type of muscle. We shall return to the significance of the different properties later in this tutorial.

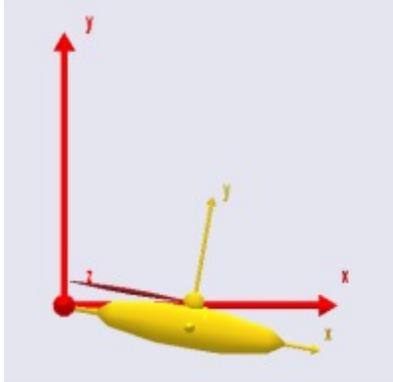
For now, [let's proceed to the next lesson](#) to learn how to control the way a muscle is displayed.

Lesson 2: Controlling muscle drawing

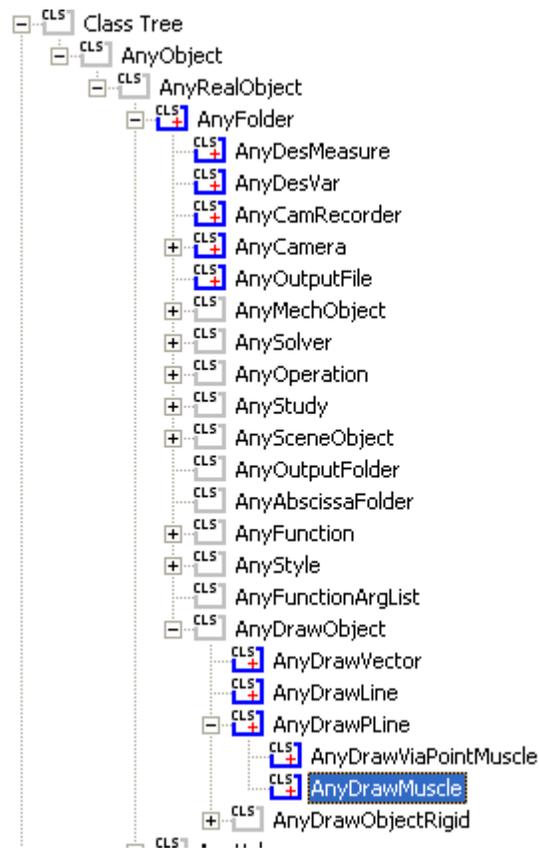
Muscles can be displayed in a variety of fashions depending on the specifications in the AnyDrawMuscle object. Let us take a look at its definition again:

```
AnyDrawMuscle drw = {};
```

It obviously does not contain much, so every setting is at its default value leading to the following display of the muscle:



Let us play around with the settings a bit. An easy way to display all the settings is to discard our manually defined AnyDrawMuscle object and insert a template from the class tree instead:



Erase the previous AnyDrawMuscle, right-click the AnyDrawMuscle in the tree view, and insert an instance:

```
AnyViaPointMuscle Muscle1 = {
  AnyMuscleModel &Model = .SimpleModel;
  AnyRefFrame &Orig = .GlobalRef.M1Origin;
  AnyRefFrame &Ins = .Arm.M1Insertion;
  AnyDrawMuscle drw = {
    //RGB = {0.554688, 0.101563, 0.117188};
```

```

    //Transparency = 1.000000;
    //DrawOnOff = 1.000000;
    //Bulging = 0.000000;
    //ColorScale = 0.000000;
    //RGBColorScale = {0.957031, 0.785156, 0.785156};
    //MaxStress = 250000.000000;
};
};

```

Notice that the <ObjectName> must be manually changed to drw (or any other sensible name). The commented lines (with // in front) are the optional settings. Un-commenting them will not change much because the values they have listed are the default settings. So we need to change some of the values.

The first thing we shall try is to make the muscle bulge. We do this by setting the value of the Bulge variable to 1. What this translates to is to make the muscle bulging proportional to the force in the muscle:

```

AnyDrawMuscle drw = {
    //RGB = {0.554688, 0.101563, 0.117188};
    //Transparency = 1.000000;
    //DrawOnOff = 1.000000;
    Bulging = 1;
    //ColorScale = 0.000000;
    //RGBColorScale = {0.957031, 0.785156, 0.785156};
    //MaxStress = 250000.000000;
};

```

When you try this, you will find that the muscle has become thinner, but you really cannot see it bulge much. The problem is that the thickness of the muscle is scaled by another factor in addition to the force. This enables the system to create nice visualizations for intensive and light exercises alike. The additional factor is the variable MaxStress. The following will increase the muscle thickness:

```

AnyDrawMuscle drw = {
    //RGB = {0.554688, 0.101563, 0.117188};
    //Transparency = 1.000000;
    //DrawOnOff = 1.000000;
    Bulging = 1;
    //ColorScale = 0.000000;
    //RGBColorScale = {0.957031, 0.785156, 0.785156};
    MaxStress = 2500;
};

```

Why does a smaller value of MaxStress lead to a thicker muscle? Well, you can think of the force in a muscle as being the product of a tissue stress and the cross sectional area. So, the smaller the tissue stress, the larger the cross sectional area for a given force. Thus, reducing the value of MaxStress increases the muscle thickness. If you reload and run the inverse dynamic analysis you will see that the muscle now has a significant thickness. Its thickness does not change much over the movement, though. This is because the muscle force is nearly constant over time for the problem we have defined. If we let the joint flex a bit more, then the moment arm of the muscle will become progressively smaller, and we will get a larger muscle force. The easy way to accomplish this is to increase the angular velocity of the joint driver:

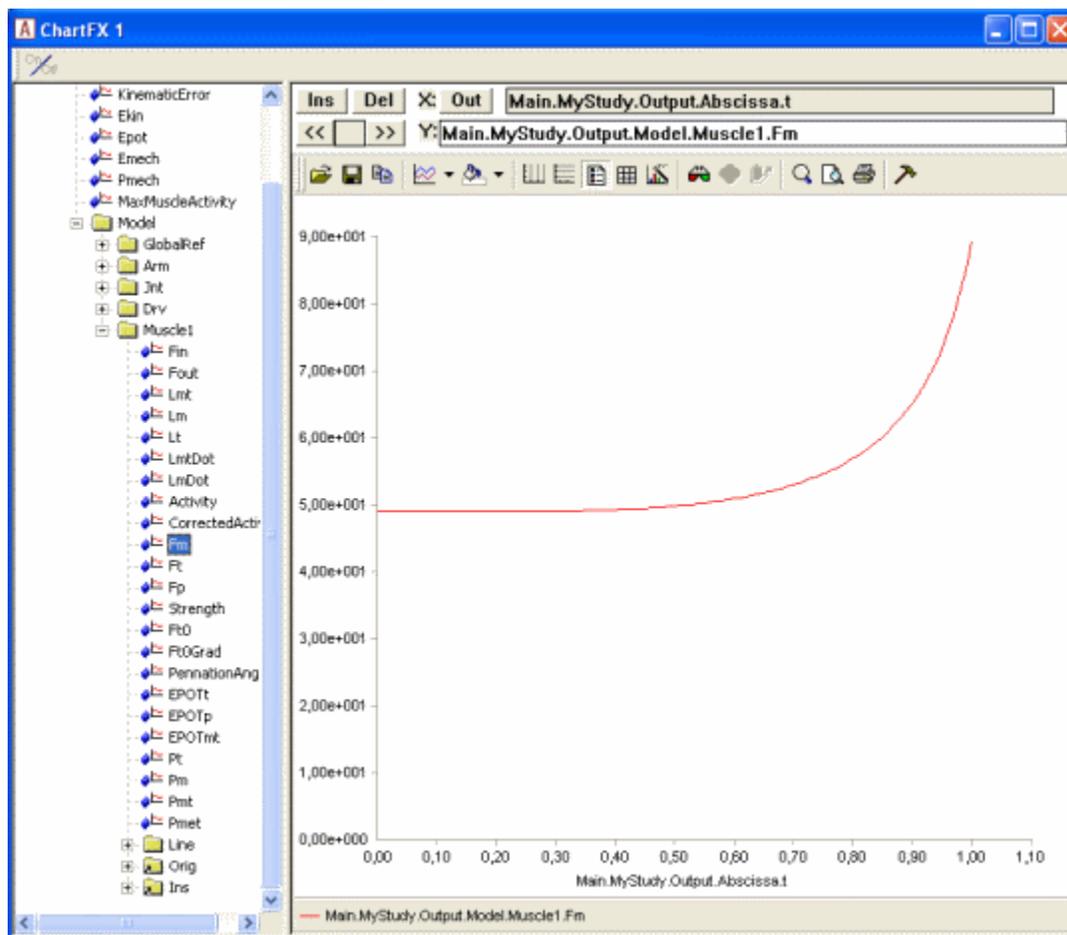
```

// Drive the revolute joint at constant velocity
AnyKinEqSimpleDriver Drv = {
    DriverPos = {-10*pi/180};
    DriverVel = {80*pi/180};
    AnyRevoluteJoint &Jnt = .Jnt;
    Reaction.Type = {0};
};

```

up to an almost vertical position. If you plot the muscle force, F_m , again in a chart view, then you can see how the muscle force goes up drastically with the reduced moment arm:

Consequently the muscle now bulges more towards the end of the movement than it does in the beginning:



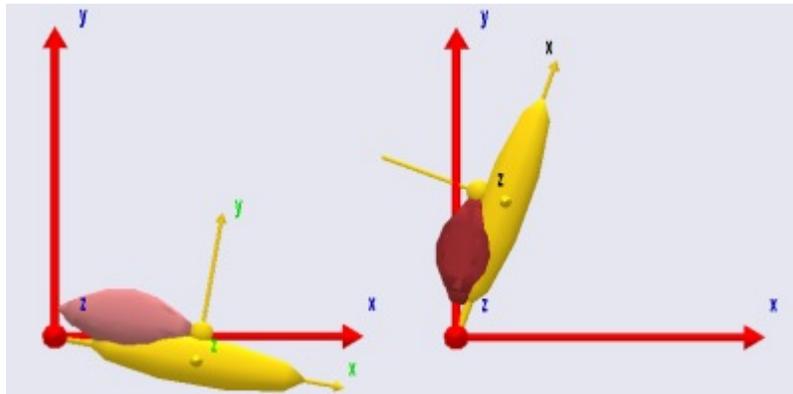
The muscle thickness does not have to reflect force. Choosing other values for the Bulging property will give other results:

Bulging value	Effect	Comment
0	No bulging	This is the default value
1	Muscle force	Thickness is proportional to force
2	Muscle strength	Constant in this case (but relevant for more advanced muscle models)
3	Muscle activity	The ratio between muscle force and muscle strength
4	Constant volume	The muscle gets thicker when it contracts

Muscle state can also be visualized with color. This allows for using bulging to visualize the force, while, for instance, muscle activity can be visualized with color. Try the following:

```
AnyDrawMuscle drw = {
  //RGB = {0.554688, 0.101563, 0.117188};
  //Transparency = 1.000000;
  //DrawOnOff = 1.000000;
  Bulging = 1;
  ColorScale = 1;
  //RGBColorScale = {0.957031, 0.785156, 0.785156};
  MaxStress = 2500;
};
```

When you reload and run the InverseDynamicAnalysis, you will notice that the red shade of the muscle changes as its activity grows:



When the activity is zero, the color defaults to a rather pale red. You can control this "initial" value of the scaled color through the property RGBColorScale. As the activity grows towards 1, the color approaches the default value of the muscle given in the RGB property. For instance, if you want the color interpolated from a cold blue to a warm red as the muscle activity increases, you can use the following settings:

```
AnyDrawMuscle drw = {
  RGB = {1, 0, 0}; //Red
  //Transparency = 1.000000;
  //DrawOnOff = 1.000000;
  Bulging = 1;
  ColorScale = 1;
  RGBColorScale = {0, 0, 1}; //Blue
  MaxStress = 2500;
};
```

Finally, the muscle drawing object has a couple of properties in common with other drawing objects: You can control the transparency of the object through the property of that name. Transparency = 1 means oblique, and with Transparency = 0, the object becomes completely invisible. All values in between causes the object to be semi-transparent. You can also turn of the display of the object entirely off by setting DrawOnOff = 0;

With the drawing of muscles under control, let us proceed to another important issue. [Lesson 3: Via point muscles](#).

Lesson 3: Via point muscles

Although the name of the muscle class we have used to far is AnyViaPointMuscle, the example has only showed the muscle passing in a straight line between two points. Real muscles in the body rarely do so.

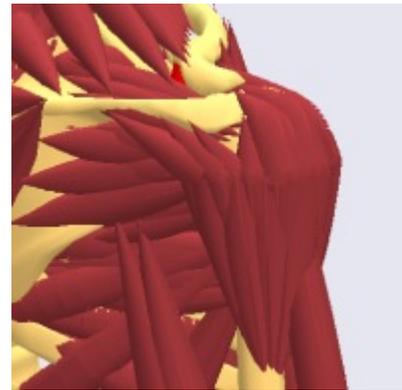
They are usually constrained by various obstacles on their way from origin to insertion, either by connective tissues or by the contact with bone surfaces.

In the former case, the muscle tends to pass as a piecewise straight line between the constrained points, and this is relatively easy to accomplish by means of an `AnyViaPointMuscle`. In the latter case, the muscle may engage and release contact with the bone surfaces it encounters. This wrapping over bones is a problem of contact mechanics and optimization. It requires a different muscle class and it is computationally much more demanding. In this lesson we shall look at `AnyViaPointMuscles` and postpone the discussion of wrapping to the next lesson.

Anatomically, via point muscles are mostly found in the lower extremities and in the spine, while the arms and shoulders almost exclusively have wrapping muscles.



Most muscles in the legs can be modeled reasonably with via point muscles.



The deltoid muscle wraps over the head of the humerus.

Via Point Muscles

Via point muscles pass through a set of at least two points on their way from origin to insertion. Each of the via points must be attached to a segment or the global reference frame of the model. The first and the last of the point sequence are special because the muscle is rigidly fixed to them and hence transfers forces in its local longitudinal direction to them. Conversely, the muscle passes through the interior via points like a thread through the eye of a needle. This means that the muscle transfers only forces to interior via points along a line that bisects the angle formed by the muscle on the two sides of the via point.

Let us modify the model we have been working on to investigate the properties of via point muscles. Initially we reduce the bulging to facilitate study of the muscle path.

```
AnyDrawMuscle drw = {
  //RGB = {0.554688, 0.101563, 0.117188};
  //Transparency = 0.2;
  //DrawOnOff = 1;
  Bulging = 2;
  ColorScale = 1;
  //RGBColorScale = {0.957031, 0.785156, 0.785156};
  MaxStress = 25000;
};
```

We then move the insertion point of the muscle a bit further out and closer to the axis of the Arm segment to make room for a via point:

```
AnySeg Arm = {
  r0 = {0.500000, 0.000000, 0.000000};
  Mass = 1.000000;
  Jii = {0.100000, 1.000000, 1.000000}*0.1;
```

```

AnyRefNode Jnt = {
  sRel = {-0.5, 0.0, 0};
};
AnyRefNode MlInsertion = {
  sRel = {0.3, 0.05, 0};
};
AnyDrawSeg drw = {};
};

```

The next step is to introduce a new point on the Arm segment to function as the via point:

```

AnySeg Arm = {
  r = {0.500000, 0.000000, 0.000000};
  Mass = 1.000000;
  Jii = {0.100000, 1.000000, 1.000000}*0.1;
  AnyRefNode Jnt = {
    sRel = {-0.5, 0.0, 0};
  };
  AnyRefNode MlInsertion = {
    sRel = {0.1, 0.0, 0};
  };
  AnyRefNode ViaPoint = {
    sRel = {0.0, 0.1, 0};
  };
  AnyDrawSeg drw = {};
};

```

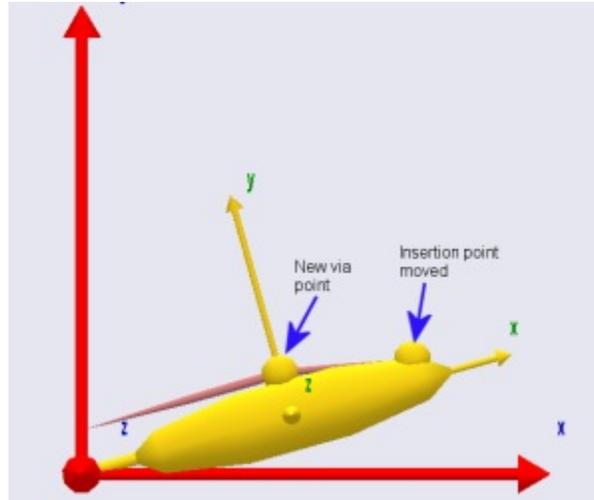
We can then introduce the new point in the sequence of points defining the muscle:

```

AnyViaPointMuscle Muscle1 = {
  AnyMuscleModel &Model = .SimpleModel;
  AnyRefFrame &Orig = .GlobalRef.MlOrigin;
  AnyRefFrame &Via = .Arm.ViaPoint;
  AnyRefFrame &Ins = .Arm.MlInsertion;
  AnyDrawMuscle drw = {
    //RGB = {0.554688, 0.101563, 0.117188};
    //Transparency = 0.2;
    //DrawOnOff = 1;
    Bulging = 2;
    ColorScale = 1;
    //RGBColorScale = {0.957031, 0.785156, 0.785156};
    MaxStress = 250000;
  };
};

```

The figure below shows the result:



A muscle can pass through an unlimited number of via points, and the points can be attached to different segments. This can be used to create rather complex kinematic behaviors of muscles, but it also requires care in the definition to avoid unrealistic muscle paths when the via points move about with the different segments.

From-the-point of view of kinematic robustness, the wrapping muscles are easier to handle than via point muscles, but the price is a much higher computational expense. Wrapping muscles are the subject of [Lesson 4](#).

Lesson 4: Wrapping muscles

Many muscles in the body are wrapped over bones and slide on the bony surfaces when the body moves. This means that the contact forces between the bone and the muscle are always perpendicular to the bone surface, and the muscle may in fact release the contact with the bone and resume the contact later depending on the movement of the body. [Via point muscles](#) are not capable of modeling this type of situation, so the AnyBody Modeling System has a special muscle object for this purpose.

A wrapping muscle is presumed to have an origin and an insertion just like the via point muscle. However, instead of interior via points it passes a set of surfaces. If the surfaces are blocking the way then the muscle finds the shortest geodesic path around the surface. Hence the name of the class: `AnyShortestPathMuscle`. The fact that the muscle always uses the shortest path means that it slides effortlessly on the surfaces, and hence there is no friction between the muscle and the surface.

Enough talk! Let us prepare for addition of a wrapping muscle to our model. If for some reason you do not have a working model from the previous lessons, [you can download one here](#).

A wrapping muscle needs one or several surfaces to wrap on, so the first thing to do is to define a surface. For convenience we shall attach the surface to the global reference frame, but such wrapping surfaces can be attached to any reference frame in the system, including segments. To be able to play around with the position of the surface, we initially define a point on `GlobalRef` for the purpose:

```
// Global Reference Frame
AnyFixedRefFrame GlobalRef = {
  AnyDrawRefFrame drw = {
    RGB = {1,0,0};
  };
  AnyRefNode M1Origin = {
    sRel = {0.0, 0.1, 0};
  };
};
```

```

AnyRefNode CylCenter = {
  sRel = {0, 0, -0.2};
};

}; // Global reference frame

```

Having defined the point, we can proceed to create a surface. The wrapping algorithm in AnyBody will in principle work with any sort of surface including real bone surfaces, but for the time being only parametric surfaces are used. The reason is that the bony surfaces are really a lot of small planar triangles, and the corners and edges of the triangles will cause the muscles to slide discontinuously over the surface, which disturbs the analysis result. The parametric surfaces currently available are cylinders and ellipsoids. Let us try our luck with a cylinder. Go to the class tree, locate the class AnySurfCylinder, and insert an instance into the newly defined node on GlobalRef. Then define the name of the cylinder, add an AnyDrawParamSurf statement, and change the cylinder parameters as shown below:

```

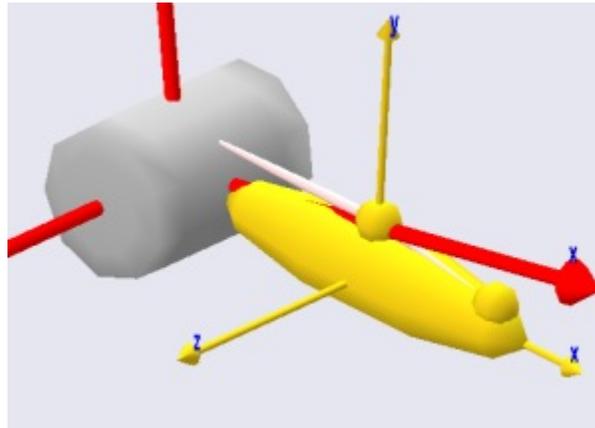
AnyRefNode CylCenter = {
  sRel = {0, 0, -0.2};

  AnySurfCylinder WrapSurf = {
    Radius = 0.15;
    Length = 0.4;
    AnyDrawParamSurf drv = {};
    //CapRatio = 0.100000;
  };
};

}; // Global reference frame

```

Most of this should be self explanatory. However, please notice that the insertion point of the cylinder is at $\{0, 0, 0.2\}$ corresponding exactly to half of the length of the cylinder of 0.4. This causes the cylinder to be inserted symmetrically about the xy plane as illustrated below:



The cylinder direction is always z in the coordinate direction of the object that the cylinder is inserted into. So, if the cylinder does not have the orientation you want, then the key to rotate it correctly is to control the direction of the AnyRefNode that it is inserted into. In fact, let us rotate it just a little bit to make things a bit more interesting:

```

AnyRefNode CylCenter = {
  sRel = {0, 0, -0.2};
  ARel = RotMat(20*pi/180,y);

  AnySurfCylinder WrapSurf = {

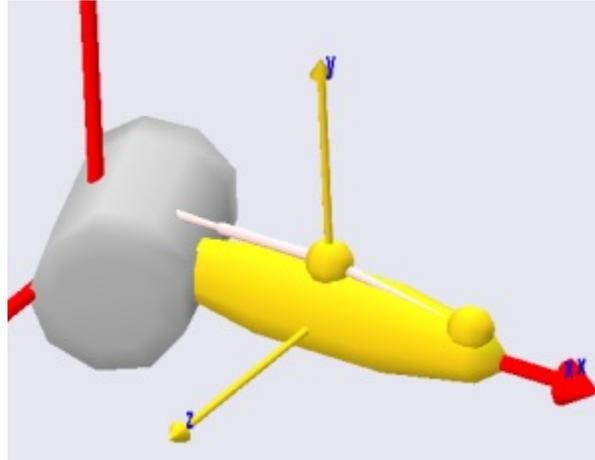
```

```

    Radius = 0.15;
    Length = 0.4;
    AnyDrawParamSurf drv = {};
    //CapRatio = 0.100000;
  };
};

```

Which causes the cylinder to rotate 20 degrees about the y axis.



There are a couple of things to notice about the cylinder: First of all the graphics looks like the cylinder is faceted. This is not really the case. Graphically it is displayed with facets out of consideration of the efficiency of the graphics display, but from the point-of-view of the muscle it is a perfect cylinder. The second thing to notice is that the ends are capped in such a way that the edges are rounded. You can control the curvature of this cap by means of the CapRatio variable that is currently commented out in the cylinder object definition. If you play a bit around with different values of the cap ratio then you will quickly get a feel for the effect of the variable. The caps allow you to let the muscle wrap over the edge of the cylinder if necessary.

The next step is to define a wrapping muscle. We shall create one point on the global reference frame and one point on the arm, and we can then articulate the joint and study the behavior of the wrapping algorithm. The point on the global reference frame is added like this:

```

// Global Reference Frame
AnyFixedRefFrame GlobalRef = {
  AnyDrawRefFrame drv = {
    RGB = {1,0,0};
  };
  AnyRefNode M1Origin = {
    sRel = {0.0, 0.1, 0};
  };

  AnyRefNode M2Origin = {
    sRel = {0.0, 0.15, -0.05};
  };
};

```

Similarly we add a point to the arm:

```

// Define one simple segment
AnySeg Arm = {
  r = {0.500000, 0.000000, 0.000000};
  Mass = 1.000000;
};

```

```

Jii = {0.100000, 1.000000, 1.000000}*0.1;
AnyRefNode Jnt = {
  sRel = {-0.5, 0.0, 0};
};
AnyRefNode M1Insertion = {
  sRel = {0.3, 0.05, 0};
};
AnyRefNode M2Insertion = {
  sRel = {-0.2, 0.05, 0.05};
};

```

Notice that we have given the origin and insertion points a bit of offset in the z direction to make the problem a bit more exciting. The offset will cause the muscles to cross the cylinder in a non-perpendicular path to the cylinder axis such as for instance the pronator muscles of the human forearm do.

It is now possible to define the muscle wrapping over the cylinder. The easiest way to do it is to make a copy of the via point muscle, Muscle1, and then make the necessary changes:

```

AnyViaPointMuscle Muscle1 = {
  AnyMuscleModel &Model = .SimpleModel;
  AnyRefFrame &Orig = .GlobalRef.M1Origin;
  AnyRefFrame &Via = .Arm.ViaPoint;
  AnyRefFrame &Ins = .Arm.M1Insertion;
  AnyDrawMuscle drw = {
    //RGB = {0.554688, 0.101563, 0.117188};
    //Transparency = 0.2;
    //DrawOnOff = 1;
    Bulging = 2;
    ColorScale = 1;
    //RGBColorScale = {0.957031, 0.785156, 0.785156};
    MaxStress = 250000;
  };
};

AnyShortestPathMuscle Muscle2 = {
  AnyMuscleModel &Model = .SimpleModel;
  AnyRefFrame &Orig = .GlobalRef.M2Origin;
  AnySurface &srf = .GlobalRef.CylCenter.WrapSurf;
  AnyRefFrame &Ins = .Arm.M2Insertion;
  SPLine.StringMesh = 20;
  AnyDrawMuscle drw = {
    Bulging = 2;
    ColorScale = 1;
    MaxStress = 250000;
  };
};

```

The two muscles are very similar in their definitions. They both have an origin and an insertion, and they are both displayed on the screen by means of the same type of drawing object. Notice that if you have many muscles in a model and you want to have an easy way of controlling the display of all of them, then you can define the drawing object in an include file, and include that same file in the definition of all the muscles. This way, when you change the display definition in the include file, it influences all the muscles simultaneously.

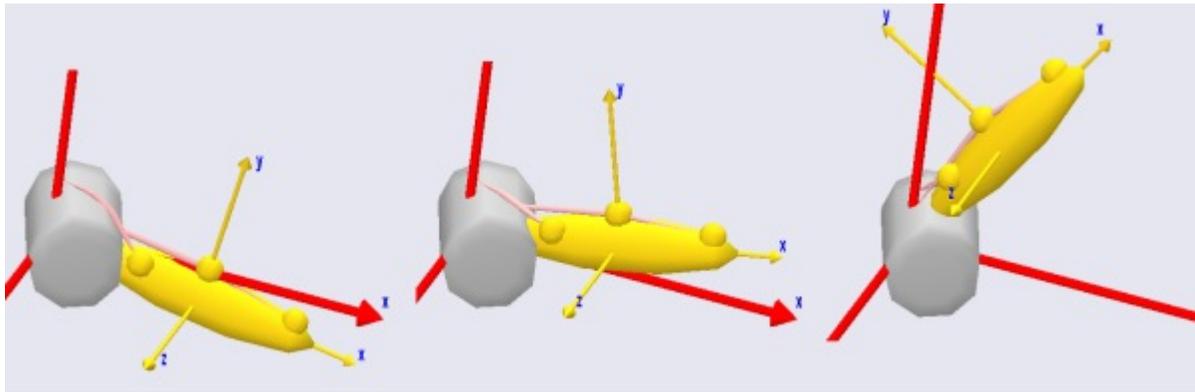
The difference between the two definitions is that the via point of Muscle1 has been replaced by a wrapping surface in Muscle2. Shortest path muscles can have any number of wrapping surfaces specified in sequence just like via point muscles can have any number of via points. In fact, a shortest path muscle can also have via points as we shall see later.

There is one additional specification necessary for a shortest path muscle. The line:

```
SPLine.StringMesh = 20;
```

This line generates a sequence of 20 equidistant points on the shortest path muscle, and these are the points that are actually in contact with the wrapping surface(s). More points will give you a more accurate solution, but they also require more computation time. For shortest path muscles the computation time can be an important issue. Solving the shortest path problem is a matter of contact mechanics, and with many muscles in the model this is easily the more computationally demanding operation of all the stuff that the system does during an analysis. If you have too few points and a complex case of wrapping, the system may sometimes fail to solve the wrapping problem and exit with an error. In that case the solution is to increase the number of points.

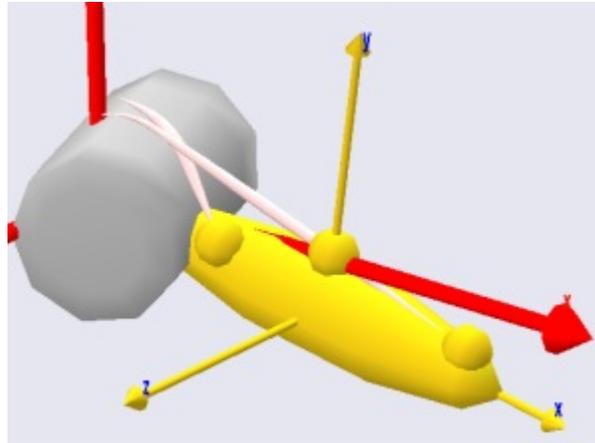
It is time to see what we have done. If you load the model and run the InverseDynamicAnalysis (and have done everything right), you will see the model moving through a sequence of positions like this:



As mentioned above, wrapping muscles can also have via points. In fact, we can easily change the via point muscle, Muscle1, to wrap over the cylinder even though it also has a via point:

```
AnyShortestPathMuscle Muscle1 = {
  AnyMuscleModel &Model = .SimpleModel;
  AnyRefFrame &Orig = .GlobalRef.M1Origin;
  AnyRefFrame &Via = .Arm.ViaPoint;
  AnySurface &srf = .GlobalRef.CylCenter.WrapSurf;
  AnyRefFrame &Ins = .Arm.M1Insertion;
  SPLine.StringMesh = 20;
  AnyDrawMuscle drw = {
    Bulging = 2;
    ColorScale = 1;
    MaxStress = 250000;
  };
};
```

The definition of the two muscle types is very similar, so we only had to change the type from AnyViaPointMuscle to AnyShortestPathMuscle and insert the wrapping surface and the StringMesh specification. This gives us the following result:



As you can see, both muscles are now wrapping over the cylinder, and we can run the InverseDynamicAnalysis. It seems to work, but the system provides the following warning:

WARNING - Via-point 'Main.MyModel.GlobalRef.M1Origin' on 'Main.MyModel.Muscle1.SPLine' is located below the wrapping surface 'Main.MyModel.GlobalRef.CylCenter.WrapSurf'.

This is a warning that you will see rather frequently when working with complex models with wrapping. The warning comes when one of the end points or a via point is located below the surface over which the muscle is supposed to wrap. This means that it is impossible for the muscle to pass through the via point without penetrating the wrapping surface. In this case the system chooses to let the muscle pass through the via point and the back to the wrapping surface as soon as possible. In the present case, the origin point of Muscle1 is only slightly below the cylinder surface, so the problem can be rectified by a small offset on the origin point:

```
AnyRefNode M1Origin = {
  sRel = {0.0, 0.15, 0};
};
```

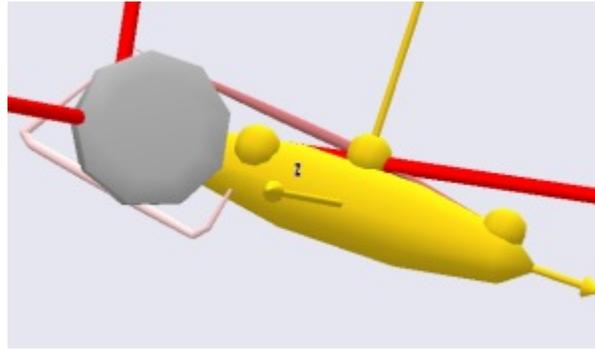
If you are analytically inclined, you may be thinking that the muscles might equally well pass on the other side of the cylinder. And you are quite right. The reason why both muscle pass over the cylinder rather than under is that this is the side that is the closest to the muscles' paths before the wrapping is resolved. This means that we can make a muscle wrap on another side of a wrapping surface by making sure that its initial position is closer to the side we want it to wrap on. The way to do this is to specify one or more so-called initial wrapping vectors. These are really points that the muscle initially should pass through. You can specify as many of these points as you like. In the example below we have used two:

```
AnyShortestPathMuscle Muscle2 = {
  AnyMuscleModel &Model = .SimpleModel;
  AnyRefFrame &Orig = .GlobalRef.M2Origin;
  AnySurface &srf = .GlobalRef.CylCenter.WrapSurf;
  AnyRefFrame &Ins = .Arm.M2Insertion;
  SPLine.StringMesh = 20;
  SPLine.InitWrapPosVectors = {{-0.2, -0.2, 0}, {-0.05, -0.2, 0}};
  AnyDrawMuscle drw = {
    Bulging = 2;
    ColorScale = 1;
    MaxStress = 250000;
  };
};
```

Notice that the InitWrapPosVectors like the StringMesh is part of an object called SPLine. This is an object in

[measure](#) that is really a string that wraps just like a muscle but does nothing else than measure its own length. These objects can be used outside the muscle definition for various purposes in the model, for instance for definition of springs or rubber bands.

After you load the model with the added InitWrapVectors, try using the Step button rather than the run button. This will show you how the system uses the InitWrapVectors to pull the muscle to the other side of the cylinder:



If you keep pressing the step button you will see how the muscle now wraps on the other side of the cylinder.

With the kinematics of muscles well under control, we can proceed to another important and interesting topic, [Lesson 5: Muscle models](#).

Lesson 5: Muscle models

Muscle model is a description of how a muscle behaves under different operating conditions. There are two schools of thought within this area.

- The first school pursues phenomenological models based on the classical work by [A.V. Hill](#). These models are usually based on a description of a muscle as a contractile element in combination with a number of elastic elements. While these models make no attempt to directly model the microscopic mechanisms of muscle contraction, they do reproduce many properties of muscle behavior quite well, and most models of this class can be implemented with great numerical efficiency.
- The second school attempts to directly model the microscopic physical phenomena of cross bridge activity in muscle contraction. The origin of these models is usually attributed to [A.F. Huxley](#), and they lead to differential equations and consequently to much more computationally demanding models.

The AnyBody Modeling System requires muscle models because it must take the strength of different muscles into account when distributing the load over them. A traditional muscle model is one that takes an activation signal and a present muscle state as input and produces a force as output. But inverse dynamics, as it is used in the AnyBody Modeling System, does not work quite like that. Instead of taking an activation signal as input, AnyBody produces the muscle active state as output. This means that typical muscle models from the literature must be mathematically reversed before they can be used in the AnyBody Modeling System. Depending on the complexity of the muscle model, this may be more or less difficult.

AnyBody has three muscle models available differing in complexity and accuracy of their representation of physiological muscles. All of these are phenomenological, i.e. they make no attempt to capture the complexity of cross bridge dynamics. You may ask why we would want three different models? Why don't we just use the better of the three models? The answer is that accurate models are good, but they are never more accurate than the input data, and it is often difficult to find the detailed physiological data that the complex models require. Instead of basing a computation on data of unknown accuracy it is often preferable

to go with a simpler model where the approximations are clear.

In short, AnyBody has the following muscle models available

AnyMuscleModel	<p>This is the simplest conceivable muscle model, and it is the one we have used in the preceding lessons of this tutorial. The only input to the model is the muscle's presumed isometric strength, F_0, i.e. the force that the muscle can exert in a static condition at its optimum length. F_0 is often believed to be proportional to the physiological cross sectional area of the muscle, and it is possible to find that dimension for most significant muscles in the human body from cadaver studies reported in the scientific literature.</p> <p>It is important to stress that the strength of this muscle model is independent of the muscle's current length and contraction velocity. It is known for a fact that muscles do not behave that way, but for models with moderate contraction velocities and small joint angle variations even this simple model will work reasonably well. Such has been shown to be case for bicycling and gait.</p>
AnyMuscleModel2ELin	<p>This model presumes that the muscle strength is proportional to the current length and to the contraction velocity. This means that the muscle gets weaker when its length decreases or the contraction velocity increases. In other words, the muscle strength is bilinear in the length and velocity space. The model also presumes that the tendon is linearly elastic and as such contains two elements: A contractile element (the muscle), and a serial-elastic element (the tendon).</p> <p>The rationale behind this model is that a muscle has a certain passive elasticity built into it. If the muscle is stretched far enough, the passive elasticity will build up force and reduce the necessity for active muscle force. This is in some cases equivalent to an increase of the muscle's strength. Notice, however, that this model has the significant drawback that the force can be switched off even if the muscle is stretched very far, while the true passive elasticity will always provide a force when it is stretched.</p>
AnyMuscleModel3E	<p>This is a full-blown Hill model that takes parallel passive elasticity of the muscle, serial elasticity of the tendon, pennation angle of the fibers, and many other properties into account. However, it also requires several physiological parameters that may be difficult to get or estimate for a particular muscle in a particular individual.</p>

In the remainder of this lesson we shall experiment with the consequences of the different muscle models. The AnyScript model from the previous lesson will suffice very nicely. You can download a functional version of the model here:

[MuscleDemo.5.any](#)

AnyMuscleModel2ELin

Right-click and save the file to your local disk, and subsequently open the model in the AnyBody Modeling System. We have already seen the consequences of using the simple muscle model, so we shall proceed directly to the two-element muscle, the AnyMuscleModel2ELin. Let us define such a muscle model. If you click the Classes tab in the tree view left of the edit window, expand the class tree, right-click the AnyMuscleModel2ELin class, and insert a template, you will obtain the following:

```
AnyMuscleModel SimpleModel = {
    F0 = 100;
};

AnyMuscleModel2ELin <ObjectName> = {
```

```

F0 = 0;
Lfbar = 0;
Lt0 = 0;
Epsilonbar = 0;
V0 = 0;
};

```

Let us briefly review the parameters:

Parameter	Function
F0	In the simple muscle model, F0 is simply the strength of the muscle. In this two-parameter model, F0 is the ideal strength, i.e. the strength of the muscle at neutral fiber length and zero contraction velocity. F0 is measured in force units, i.e. Newton.
Lfbar	The neutral fiber length, i.e. the length of the contractile element at which the muscle has the strength of F0. Lfbar is measured in length units, i.e. meters.
Lt0	The muscle's total length from origin to insertion can be divided into two parts: the length of the muscle's contractile element plus the length of the tendon. The tendon is considered in this model to be linearly elastic, and Lt0 is the slack length of the tendon, i.e. the length when it is taut but carrying no force. Lt0 is measured in length units, i.e. meters.
Epsilonbar	This parameter controls the elasticity of the tendon. The physical interpretation is that it is the tendon's strain when subjected to a force of F0. Prescribing a strain rather than an ordinary spring stiffness is based on the idea that the tendon thickness must be related to the strength of the muscle: strong muscles need strong tendons. Hence, Epsilonbar can be presumed with good accuracy to be the same for a wide variety of very different muscles. Epsilonbar is measured in fractions and is therefore dimensionless.
V0	This model presumes that the muscle's strength depends linearly on its contraction velocity. V0 is measured in absolute velocity, i.e. m/s.

We can study the significance of the parameters in more detail, if we formulate the strength mathematically:

$$Strength = F_0 \left(2 \frac{L_m}{L_f} - 1 \right) \left(1 - \frac{\dot{L}_m}{V_0} \right)$$

You can probably recognize the variable names in the table above from the symbols in the equation. As you can see, this is really a bilinear model, where the variables are L_m and \dot{L}_m . The strength of the muscle vanishes if any of the two parentheses becomes zero. This can happen if either L_m , i.e. the current length of the contractile element, becomes half the length of L_f , or if \dot{L}_m becomes equal to V_0 . Please notice that \dot{L}_m is negative when a muscle is contracting, so meaningful values of V_0 must also be negative. The system automatically truncates negative values of the strength expression to zero.

In a few moments, when we start playing around with the muscle model in AnyBody, you will recognize these properties in the available muscle variables in the Chart View.

Let us assign a name and some reasonable parameters to our two-element muscle model:

```

AnyMuscleModel2ELin Model2 = {
  F0 = 200;
  Lfbar = 0.3;
  Lt0 = 0.5;
  Epsilonbar = 0.05;
  V0 = -8.0;
};

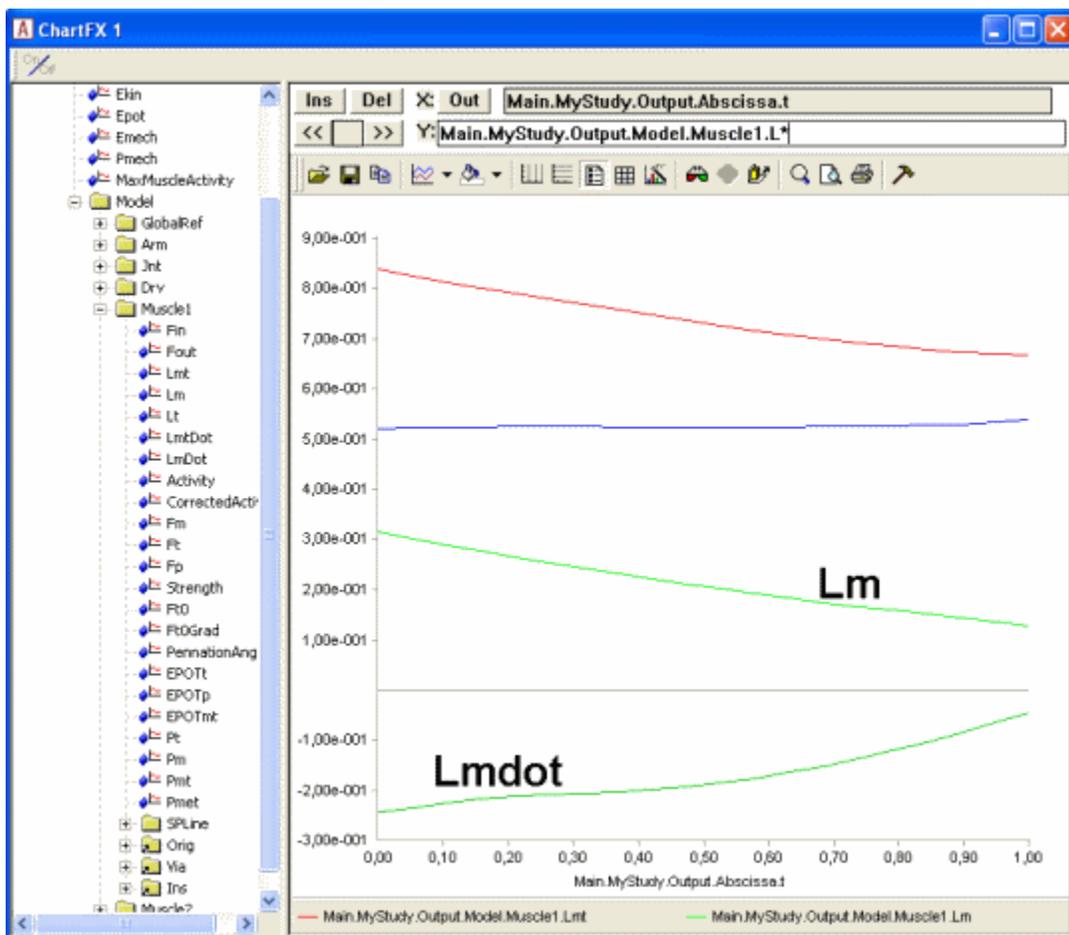
```

```
};
```

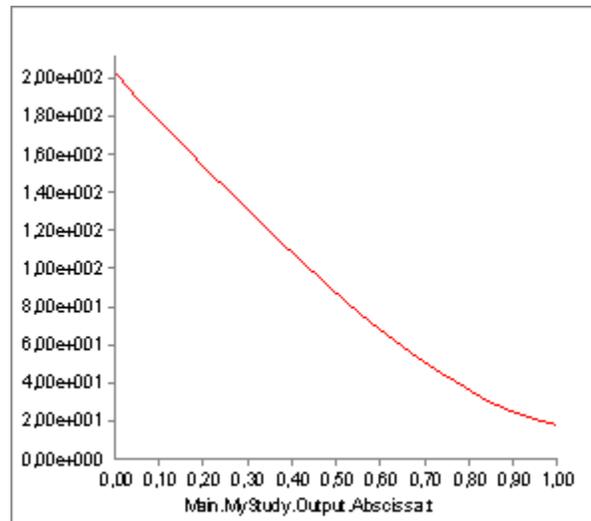
The parameters here are more or less random. In a moment we shall explain the ones that are less random, but first we must assign the new model to Muscle1:

```
AnyShortestPathMuscle Muscle1 = {
  AnyMuscleModel &Model = .Model2;
  AnyRefFrame &Orig = .GlobalRef.M1Origin;
  AnyRefFrame &Via = .Arm.ViaPoint;
  AnySurface &srf = .GlobalRef.CylCenter.WrapSurf;
  AnyRefFrame &Ins = .Arm.M1Insertion;
  Spline.StringMesh = 20;
  AnyDrawMuscle drw = {
    Bulging = 0;
    ColorScale = 1;
    MaxStress = 250000;
  };
};
```

We are ready to run the analysis again and investigate the results. Pick the InverseDynamicAnalysis in the tree of operations and click the Run button. Then open a new Chart View and expand the tree in the Chart View as far down as Muscle1. You will see a whole list of muscle properties that you can chart simply by clicking them. Let us initially see how the properties Lm and Lmdot affecting the strength of the model. You can plot several properties simultaneously in the Chart View by use of an asterisk in the variable specification field at the top of the window like this:

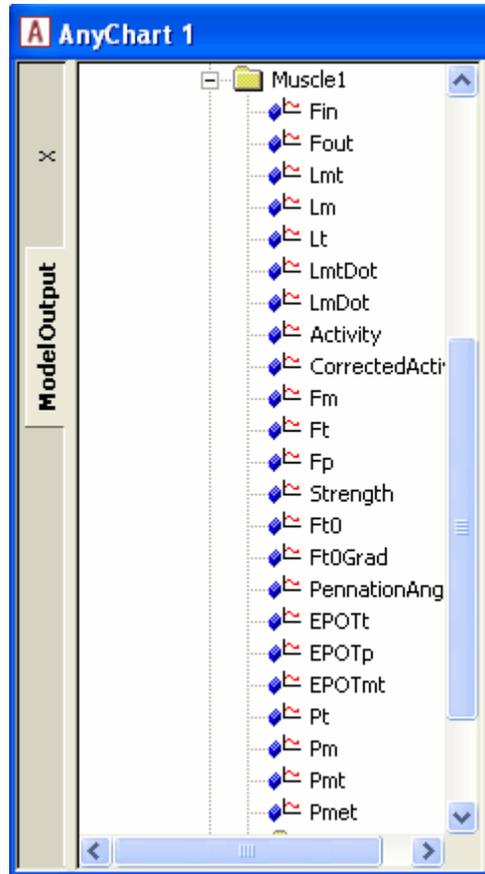


Now we can compare the variation of L_m and $L_{m\dot{}}$ to our settings of $L_{\bar{}}$ and V_0 . L_m seems to vary between approximately 0.31 and 0.15. With an $L_{\bar{}}$ of 0.3 ($= 2 \times 0.15$) this means that the muscle must come close to the minimum length at which it has any strength when we approach the end of the movement. $L_{m\dot{}}$ varies between -0.24 and -0.06, and this is far from its speed limit $V_0 = -8$, so the contraction speed is not expected to have much effect. We can investigate the effect very easily simply by clicking the Strength property of the muscle and obtain the following graph:



The strength does indeed decrease drastically from around 200 N to almost nothing as we expected when the muscle contracts.

Now that we have muscle data available, let us briefly review the parameters presented in the Chart View:



- **Fin** is a force, but it has not physiological significance for a muscle except for internal purposes. The reason why it is included in the output is that it is inherited from the AnyScript classes that a muscle is derived from.
- **Fout** is a force, but it has not physiological significance for a muscle except for internal purposes. The reason why it is included in the output is that it is inherited from the AnyScript classes that a muscle is derived from.
- **Lmt** is the total length of the muscle-tendon unit, i.e. the origin-insertion length.
- **Lm** is the length of the muscle's contractile element.
- **Lt** is the length of the tendon. This is not necessarily the same as Lt0 because the tendon is linearly elastic and therefore stretches slightly with the force.
- **LmtDot** is the rate of change of Lmt, i.e. the length change velocity of the total muscle-tendon unit.
- **LmDot** is the contraction velocity of the contractile element.
- **Activity** is the muscle active state in fractions of maximum voluntary contraction.
- **CorrectedActivity** for this muscle model is the same as Activity.
- **Fm** is the force in the muscle's contractile element. For this muscle type it is equal to the total force in the muscle-tendon unit because the muscle does not have any parallel components.
- **Ft** is the force in the tendon. For this muscle model it is the same as Fm.
- **Fp** is not relevant for this type of muscle model.
- **Strength** is the muscle's strength at each moment of the movement.
- **Ft0** is not relevant for this type of muscle model.
- **Ft0Grad** is the derivative of tendon force with respect to active state. For this muscle model it amounts to exactly the same as the Strength variable, but for muscles with parallel elasticity the two properties will be different.
- **PennationAngle** is not relevant for this muscle model type.
- **EPOTt** is the potential elastic energy in the tendon.
- **EPOTp** is the potential elastic energy in the parallel-elastic element, which is not included in this

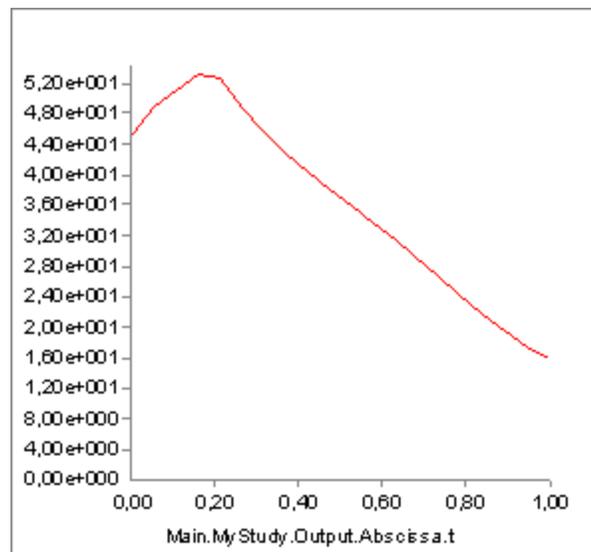
muscle model.

- **EPOTmt** is the total elastic potential energy in the muscle-tendon unit.
- **Pt** is not relevant for this muscle model.
- **Pm** is the mechanical power exerted by the muscle's contractile element.
- **Pmt** is the mechanical power of the muscle-tendon unit on the skeleton.
- **Pmet** is a crude estimate of the metabolic power consumption of the muscle taking different efficiencies for concentric and eccentric work into account.

We have seen how the length of the muscle affects its strength, but what about the velocity? Well, the specified values of -8 m/s is a reasonable estimate for many physiological muscles, but let us try to decrease it and thereby make the muscle more sensitive to contraction velocity:

```
AnyMuscleModel2ELin Model2 = {
  F0 = 200;
  Lfbar = 0.3;
  Lt0 = 0.5;
  Epsilonbar = 0.05;
  V0 = -0.3;
};
```

A value of $V0 = -0.3$ is close to the contraction velocity of the muscle in the beginning of the simulation. This, this decreases the strength of the muscle significantly as we can see by reloading, rerunning and plotting the Strength variable again:



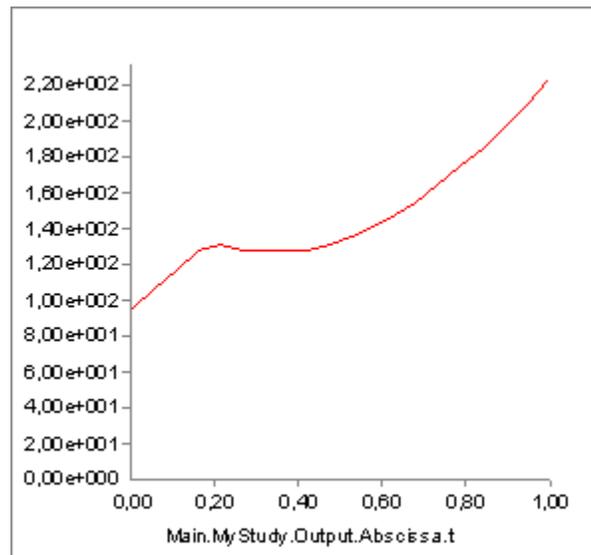
Instead of being monotonically decreasing, the muscle strength now improves slightly in the initial part of the simulation, but it is all through the simulation significantly weaker than before. The initial increase is due to the beneficial effect of the decreasing contraction velocity, so this muscle model in spite of its simplicity is capable of balancing several of the effects of real muscle physiology.

Another of the important input parameters in this example is the nominal tendon length, $Lt0$. This is a parameter that has a very large influence on the muscle's performance. The total origin-insertion length of the muscle-tendon unit depends on the size and posture of the body. The muscle spans this length with the sum of muscle length, Lm , and tendon length, Lt , such that $Lmt = Lm + Lt$. Both Lm and Lt change during the movement of the body. Lt is given by its initial length, $Lt0$, and the elastic deformation. Lm has to take up whatever rest of Lmt that is available after Lt has been subtracted. In some cases, the tendon is significantly longer than the muscle, and this means that a relatively small variation of the tendon length results in a large relative variation of the portion of Lmt that the muscle has to fill. Obviously $Lt0$ plays a significant role for Lt and hence influences the working length of the muscle. Let us investigate this effect by

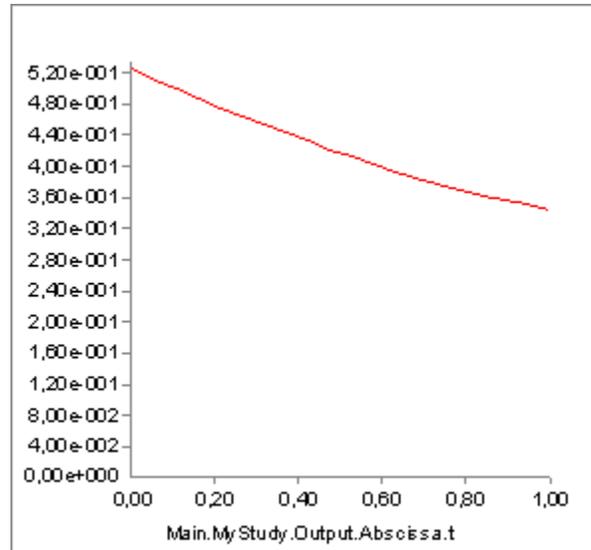
reducing Lt0:

```
AnyMuscleModel2ELin Model2 = {
  F0 = 200;
  Lfbar = 0.3;
  Lt0 = 0.3;
  Epsilonbar = 0.05;
  V0 = -0.3;
};
```

This reduction of the tendon length from 0.5 to 0.3 meters is very significant compared to the nominal muscle fiber length of $L_{fbar} = 0.3$ m. Reducing the length of the tendon increases the length and thereby the strength of the muscle:



The interdependency between the stretch of the tendon, the length of the muscle, and the strength of the muscle is the origin of another approximation in the model: The system computes the changed length of the muscle due to the stretching of the tendon, but this length change is not taken into account in the computation of the muscle strength. Nevertheless, let us investigate how the stretch of the tendon influences the muscle. We shall define an external load on the arm, which causes the tendon to stretch. But before we change anything, let us just notice that the variation of muscle length, L_m , over the movement in the absence of an external load is as shown below:

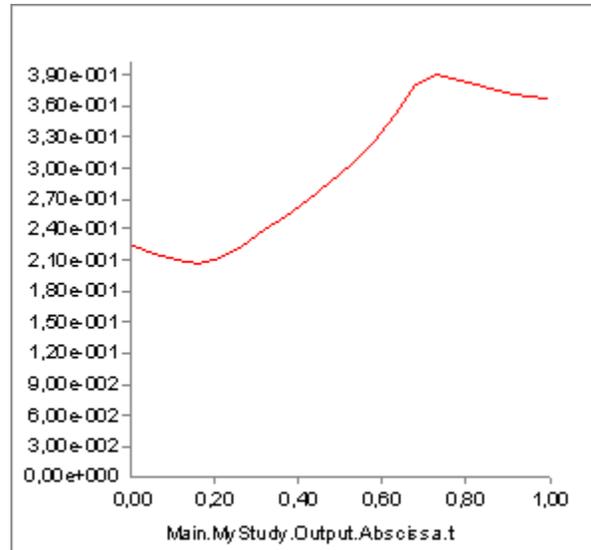


Definition of an external force requires two new elements in the model: The force itself and a new node on the arm, which we shall call hand, to which the load can be applied:

```
// Define one simple segment
AnySeg Arm = {
  r = {0.500000, 0.000000, 0.000000};
  Mass = 1.000000;
  Jii = {0.100000, 1.000000, 1.000000}*0.1;
  AnyRefNode Jnt = {
    sRel = {-0.5, 0.0, 0};
  };
  AnyRefNode M1Insertion = {
    sRel = {0.3, 0.05, 0};
  };
  AnyRefNode M2Insertion = {
    sRel = {-0.2, 0.05, 0.05};
  };
  AnyRefNode ViaPoint = {
    sRel = {0.0, 0.1, 0};
  };
  AnyRefNode Hand = {
    sRel = {0.5, 0.0, 0};
  };
  AnyDrawSeg drw = {};
};

AnyForce3D Load = {
  AnyRefNode &Attachment = .Arm.Hand;
  F = {-100, -100, 0};
};
```

The load is pointing down and backward at a 45 degree angle, so that it changes its moment arm from positive to negative a shortly after the midpoint of the analysis. This causes the muscle length to vary in the following fashion:



The interesting point here is that with the long tendon and the high load, the muscle no longer contracts uniformly. In fact, the muscle extends for much of the movement due to the decreasing load which causes the elastic tendon to contract instead.

While the two-parameter muscle model captures many of the properties of real muscles it also fails to reflect important parts of muscle physiology, so it should be applied with care. In particular it does not model passive elasticity. The following section presents a full-blown Hill-type model, which does not have these shortcomings.

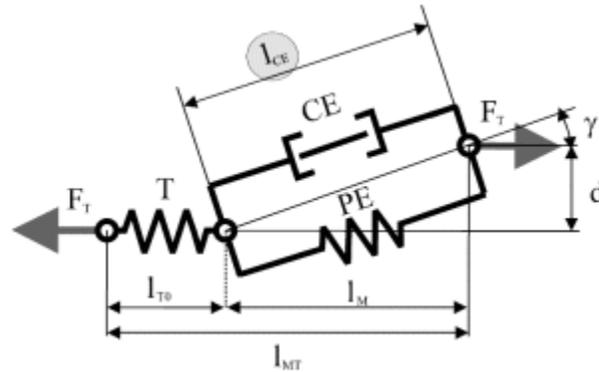
AnyMuscleModel3E

So far we have been focusing our attention on Muscle1 in the demo model and left Muscle2 with the simple muscle model. Let us briefly study what Muscle2 is actually doing (if you need an updated working model, you can download it here: [MuscleDemo.5-2.any](#)). Muscle2 wraps about the cylinder and obviously extends significantly as the arm turns upward. If you run the analysis and plot the length of Muscle2, you will see that it increases 0.7 to 1 meter. For a normal muscle (actually a muscle of this size would probably be found in a giraffe) a stretching of that magnitude would almost certainly lead to some passive force in the muscle.

Passive force is what comes from the structural integrity of the muscle. If we disregard the active properties of the muscle and think of it as simply a piece of material that we can stretch, then the material will provide a passive resistance depending on how far we stretch it. This is the passive component of the muscle force. We can easily find passive muscle force in our own bodies: When we bend forward and try to touch our toes with the straight legs, then most of us will feel the hamstrings getting very taut. This is passive elasticity. The two-element muscle model of the preceding section handles the presence of this elasticity by increasing the strength of the muscle, and this works fine if the muscle is supposed to be active in the sense that the model in such a state would predict a high force with a low muscle activity. But the passive muscle force cannot be switched off, so it will still be present even if it is disadvantageous, and the two-element model will not predict this.

The AnyMuscleModel3E is a full-blown Hill-type muscle model that does not suffer from this deficiency. It is called a three-element model because it has the following components:

1. A contractile element (CE) representing the active properties of the muscle fibers.
2. A serial-elastic (T) element representing the elasticity of the tendon.
3. A parallel-elastic element (PE) representing the passive stiffness of the muscle fibers.



The figure above is a schematic representation of the muscle model. We can get a complete impression of the parameters of the model if we pick the model from the Class List as we have done before and insert a template into our AnyScript model:

```
AnyMuscleModel2Elin Model2 = {
  F0 = 200;
  Lfbar = 0.3;
  Lt0 = 0.3;
  Epsilonbar = 0.05;
  V0 = -0.3;
};

AnyMuscleModel3E <ObjectName> = {
  F0 = 0;
  Lfbar = 0;
  Gammabar = 0;
  Epsilonbar = 0;
  Lt0 = 0;
  Fcfast = 0;
  //Jt = 3;
  //Jpe = 3;
  //K1 = 2;
  //K2 = 8;
  //PEFactor = 5;
};
```

Several of these elements are described already in the two-element model above, but some are new and described in the table below. No excuse we can make is going to soften the fact that muscle modeling at this level of detail is a technical matter, and it is not possible to describe the physiological and mathematical background in detail. Instead please refer to the publications at the end of this lesson for further information:

Gammabar	Gamma is the so-called pennation angle. It reflects that fact that most muscles have the fibers misaligned with the directions of action of the muscle. Gamma changes when the muscle extends or contracts, and Gammabar is the value of Gamma in the muscle's neutral position. It is possible to find values for Gammabar for most major muscles in the human body in the anatomical literature. Gammabar is measured in radians.
Fcfast	Muscle fibers come in two flavors: fast twitch and slow twitch, and the composition of these vary between the muscles as well as between individuals. Fast fibers, as the name indicates, have the ability of fast action at the cost of stamina, and slow fibers have opposite properties. Sprint runners have a high proportion of fast twitch muscles while marathon runners have many slow twitch muscles. Fcfast is the fraction of fast twitch fibers in the muscle. It is a fraction between 0 and 1 and

	hence dimensionless.
Jt and Jpe	<p>Jt and Jpe are elasticity factors for the tendon (serial-elastic) and parallel-elastic elements respectively. The background of these parameters is that the model presumes a nonlinear elasticity of these elements, and the precise shape of the force-deformation characteristics of the element are determined by Jt and Jpe respectively. In essence, Jt and Jpe are material constants and should not vary too much between different muscles or individuals.</p> <p>Recommended values are $Jt = Jpe = 3.0$. These two parameters are dimensionless.</p>
K1 and K2	<p>These two factors are used only to ensure a reasonable relationship between fiber length, fiber composition, and Ffast. As discussed in the preceding section, the strength of a muscle tapers off when its contraction velocity grows. Rather than working with a given maximum contraction speed as the two-element model does, K1 and K2 enable us to link the maximum contraction speed to the physiological properties of the muscle. The idea is that muscles with longer fibers and a larger fraction of fast twitch muscles should have a higher maximum contraction velocity.</p> <p>Preferred values for K1 and K2 differ significantly between authors in the scientific literature, but a good guess would be $K1 = 2$ and $K2 = 8$. K1 and K2 formally have the unit of fractions per time unit, i.e. s^{-1}.</p>
PEFactor	<p>This factor is related to Jpe. Where Jpe controls the shape of the nonlinearity, PEFactor controls the steepness of the force in the parallel-elastic element as it is elongated. If we imagine a completely inactive muscle and load the muscle with a force corresponding to the active strength of the muscle, i.e. F0, then the length of the elongated muscle fibers will be PEFactor x Lfbar. In other words PEFactor is a dimensionless measure of the flexibility of the parallel-elastic element of the muscle.</p> <p>Plausible values for PEFactor would be between 1.5 and 5 where the lower end of the interval requires a very careful tuning of the muscle to the skeleton to avoid unreasonably large passive forces.</p>

Knowing the significance of the different parameters, let us pick reasonable values for Muscle2 and study their influences:

```
AnyMuscleModel3E Model3 = {
    F0 = 100;
    Lfbar = 0.3;
    Gammabar = 30*pi/180;
    Epsilonbar = 0.05;
    Lt0 = 0.5;
    Fcfast = 0.4;
    Jt = 3.0;
    Jpe = 3.0;
    K1 = 2;
    K2 = 8;
    PEFactor = 5;
};
```

Notice that $Lfbar + Lt0 = 0.8$, which is in the range of the Lmt variation of Muscle2. This is important because it gives the muscle a reasonable chance of spanning the origin-insertion length.

We also have to associate Muscle2 with the new muscle model:

```
AnyShortestPathMuscle Muscle2 = {
    AnyMuscleModel &Model = .Model3;
    AnyRefFrame &Orig = .GlobalRef.M2Origin;
    AnySurface &srf = .GlobalRef.CylCenter.WrapSurf;
```

```

AnyRefFrame &Ins = .Arm.M2Insertion;
SPLine.StringMesh = 20;
SPLine.InitWrapPosVectors = {{-0.2, -0.2, 0},{-0.05,-0.2, 0}};
AnyDrawMuscle drw = {
    Bulging = 0;
    ColorScale = 1;
    MaxStress = 250000;
};
};

```

Finally, to have a more clean-cut case, we temporarily remove the external force that we previously added

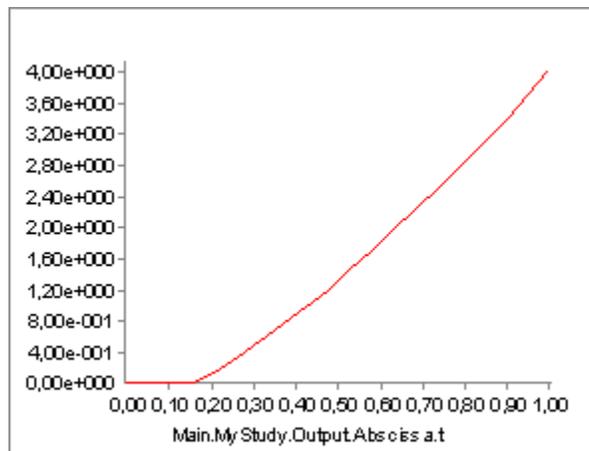
```

/*AnyForce3D Load = {
AnyRefNode &Attachment = .Arm.Hand;
F = {-100, -100, 0};
};
*/

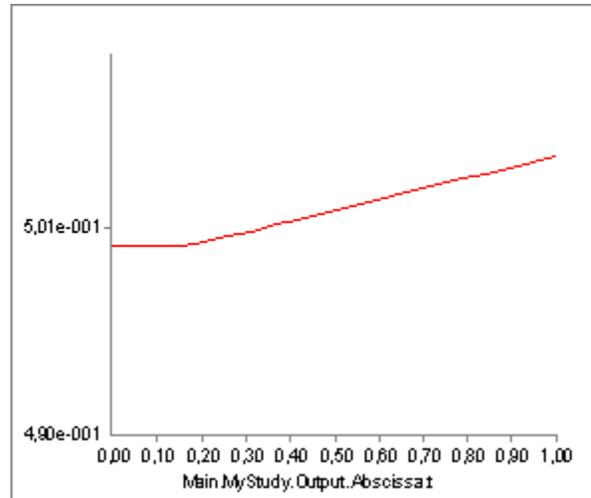
```

We are ready to try running the InverseDynamicAnalysis again. Load the model, pick InverseDynamicAnalysis in the operations tree, and click the Run button. The arm should move as is did in the previous section. Now, using a Chart View we can investigate the behavior of the new muscle. In the Chart View's tree, expand the folders as far as Muscle2, and try charting some of the parameters.

The key to understanding the muscle's behavior is to study the forces in the muscle's different elements. The chart of F_m , which is the force in the muscle's contractile element, is very uninteresting. This muscle does not contribute to carrying the load, and hence the system does not activate it. But the muscle is not without force. The property F_p , which is the force in the parallel-elastic element of the muscle has the following behavior:



In the initial phase of the movement, the parallel-elastic element is slack and adds no force to the muscle. But as the muscle gets extended, the passive muscle force sets in, and it continues to rise as the movement progresses. Notice that this passive force acts against the movement and hence requires Muscle1 to work that much more. But the passive force has another interesting effect, which we can see if we chart the property L_t , i.e. the length of the tendon (Notice that we have changed the scale of the ordinate axis):



From the time the passive force sets in, the tendon starts to elongate a little bit.

The total origin-insertion length of the muscle-tendon unit is the tendon length plus the muscle length, i.e. $L_m + L_t$. When L_t is stretched, the effect is that the muscle fibers stretch that much less, and since the muscle's strength depends on the momentary length of the contractile element, the strain in the tendon can influence the strength of the muscle. The figure above shows that the tendon stretch is rather limited and we might therefore expect that the influence on the muscle strength is also limited. However, some muscles in the human body (for instance m. soleus) have the property of relatively short fibers and a long tendon, and in this case the effect can be significant.

The three-element muscle model attempts to take this into account in the computation of muscle activity, coping with the fact that this is a catch 22 type of problem in inverse dynamics:

- We cannot compute the elongation of the tendon until we know the force in the muscle.
- We do not know the force in the muscle until we have solved the muscle recruitment problem.
- To solve the muscle recruitment we need the momentary strength of each muscle.
- The momentary strength depends on the elongation of the tendon.

We seem to be faced with a circular dependency between the muscle properties. The three-element model copes with this through a one-time correction: It recruits the muscle without taking the tendon elongation into account. Then it computes the tendon elongation. Finally, it computes the influence of the elongation on the muscle's strength and corrects the muscle activity to the level that provides the necessary force with the modified strength. This is only an approximative solution because the change of muscle strength may theoretically alter the distribution of force between the muscles, and this alteration is not done by the system; the correction is local to each muscle.

So much for passive properties. It is more instructive to investigate a muscle model with active force. The easiest way to do so is to enable our hand force again and change it to point directly upward. This causes the previously inactive Muscle2 to become active:

```
// Define one simple segment
AnySeg Arm = {
  r = {0.500000, 0.000000, 0.000000};
  Mass = 1.000000;
  Jii = {0.100000, 1.000000, 1.000000}*0.1;
  AnyRefNode Jnt = {
    sRel = {-0.5, 0.0, 0};
```

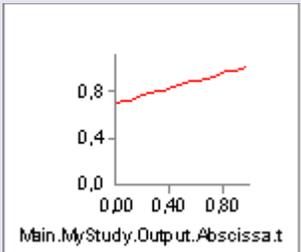
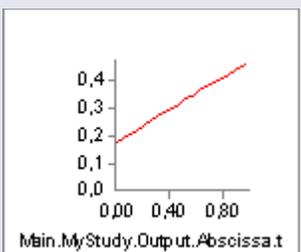
```

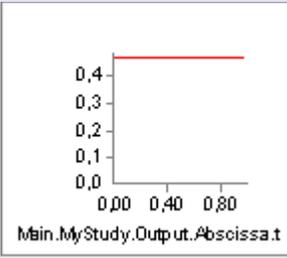
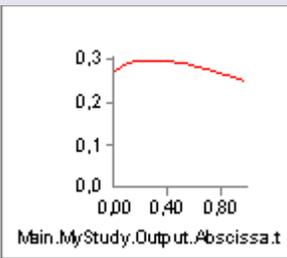
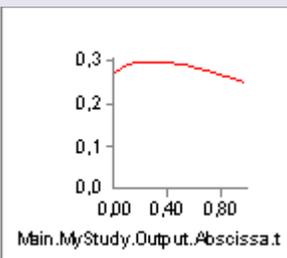
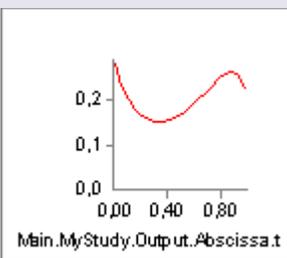
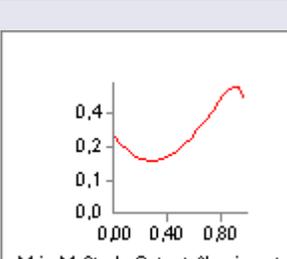
};
AnyRefNode M1Insertion = {
  sRel = {0.3, 0.05, 0};
};
AnyRefNode M2Insertion = {
  sRel = {-0.2, 0.05, 0.05};
};
AnyRefNode ViaPoint = {
  sRel = {0.0, 0.1, 0};
};
AnyRefNode Hand = {
  sRel = {0.5, 0.0, 0};
};
AnyDrawSeg drw = {};
};

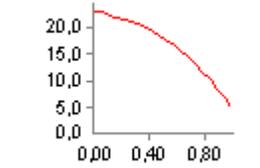
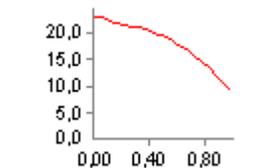
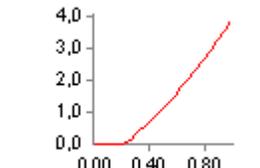
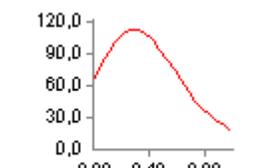
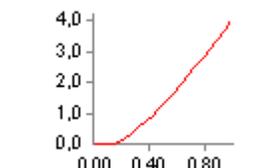
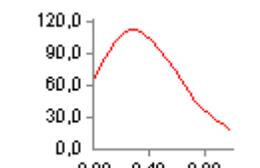
AnyForce3D Load = {
  AnyRefNode &Attachment = .Arm.Hand;
  F = {0, 10, 0};
};

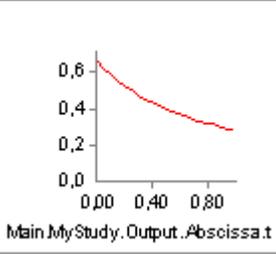
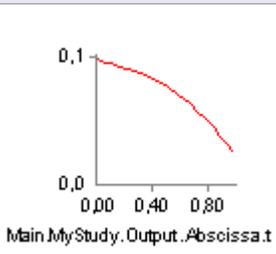
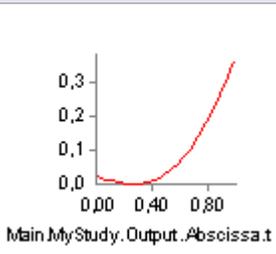
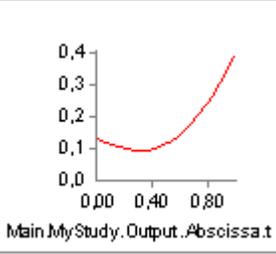
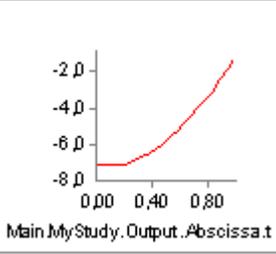
```

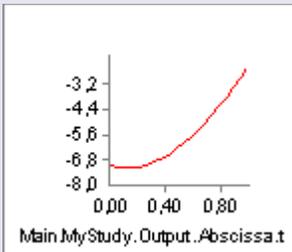
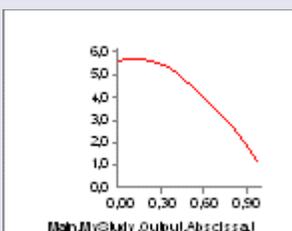
With this we can run the InverseDynamicAnalysis again and get the muscle to do some work. Let us systematically investigate the output:

Fin	This is a force, but it has not physiological significance for a muscle except for internal purposes. The reason why it is included in the output is that it is inherited from the AnyScript classes that a muscle is derived from.	
Fout	This is a force, but it has not physiological significance for a muscle except for internal purposes. The reason why it is included in the output is that it is inherited from the AnyScript classes that a muscle is derived from.	
Lmt	The length of the muscle-tendon unit. If you plot this property you will see that it rises almost linearly as the muscle is extended. Closer investigation, however, will reveal that it is offset slightly by the nonlinearity caused by the elongation of the tendon due to the varying force.	 <p>Main.MyStudy.Output.Abscissa.t</p>
Lm	The length of the contractile element.	 <p>Main.MyStudy.Output.Abscissa.t</p>

Lt	The length of the tendon. This appears to be constant, but the tendon length actually changes slightly over the movement with the changes of muscle force as described above.	 <p>Main.MyStudy.Output.Abcissa.t</p>
LmtDot	The contraction velocity of the muscle-tendon unit. The value is positive because the muscle is getting longer.	 <p>Main.MyStudy.Output.Abcissa.t</p>
LmDot	The contraction velocity of the contractile element of the muscle. The value is positive because the muscle is getting longer.	 <p>Main.MyStudy.Output.Abcissa.t</p>
Activity	This is the muscle activity before correction for the change in muscle length caused by the elastic elongation of the muscle. The complicated variation is caused by the interplay between change of moment arm of the applied force, the passive force in the muscle and the change of muscle strength with the contraction.	 <p>Main.MyStudy.Output.Abcissa.t</p>
Corrected-Activity	This is the muscle activity after correction for the tendon elongation. The difference between this graph and the one above is that the activity toward the end is higher after correction. This can be difficult to understand and illustrates the complexity of muscle modeling. The reason is the following: The force in the muscle reduces towards the end of the movement. When the force is reduced, the tendon contracts, and this means that the muscle must elongate even more. Since the muscle length is already in the interval where further elongation will cause decreased strength, the tendon contraction has the effect of increasing the muscle activity.	 <p>Main.MyStudy.Output.Abcissa.t</p>

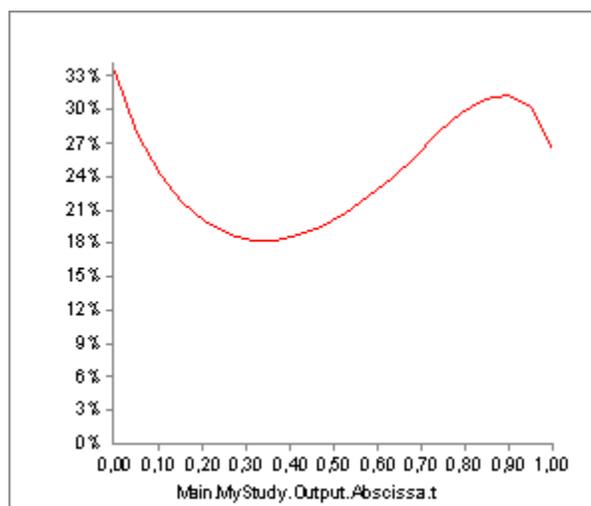
Fm	<p>The force in the contractile element is decreasing throughout the movement because the moment arm of the external force is reducing and also because the passive force in the muscle is contributing more and more to balancing the load.</p>	 <p>Main.MyStudy.Output.Abcissa.t</p>
Ft	<p>The tendon force shows the reduction of the muscle action by virtue of the reduced external force's moment arm alone. A simplified explanation is that $F_t = F_m + F_p$, but this is not entirely true because we also have to account for the pennation angle.</p>	 <p>Main.MyStudy.Output.Abcissa.t</p>
Fp	<p>The passive force in the muscle increases as the muscle is stretched.</p>	 <p>Main.MyStudy.Output.Abcissa.t</p>
Strength	<p>This is the strength of the muscle. It is not corrected for the tendon elongation.</p>	 <p>Main.MyStudy.Output.Abcissa.t</p>
Ft0	<p>The hypothetical force that the tendon would have if the activity of the muscle were zero. The reason why this is slightly different from Fp is that Ft0 acts directly along the action line of the muscle while Fp is diverted by the pennation angle. This property is mostly interesting to scientists involved in detailed modeling of single muscles.</p>	 <p>Main.MyStudy.Output.Abcissa.t</p>
Ft0Grad	<p>The gradient of Ft0 with respect to the muscle activity. For mathematical reasons this is equal to the Strength, and the two graphs are identical. The reason why this property is included under to different names is that the simple muscle model, from which this model is derived, does not have Ft0Grad and hence needs a Strength property.</p>	 <p>Main.MyStudy.Output.Abcissa.t</p>

Pennation-Angle	The pennation angle is the angle between the muscle fiber direction and the muscle line of action. This angle changes when the muscle contracts and elongates, and the model takes this effect into account.	 <p>Main.MyStudy.Output.Abscissa.t</p>
EPOTt	The elastic potential energy stored in the tendon.	 <p>Main.MyStudy.Output.Abscissa.t</p>
EPOTp	The elastic potential energy stored in the parallel-elastic element of the muscle.	 <p>Main.MyStudy.Output.Abscissa.t</p>
EPOTmt	The elastic potential energy stored in the entire muscle-tendon unit. This can have some practical significance for investigation of movement economy and sports activities in general.	 <p>Main.MyStudy.Output.Abscissa.t</p>
Pt	The rate of change of elastic potential energy in the tendon.	
Pm	The mechanical power of the contractile element.	 <p>Main.MyStudy.Output.Abscissa.t</p>

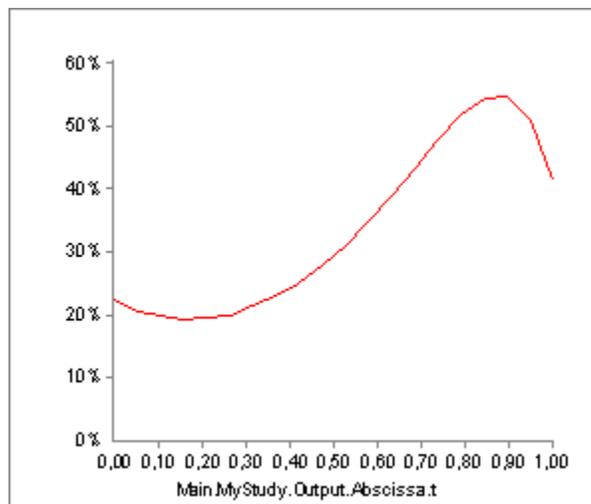
Pmt	The mechanical power of the entire muscle-tendon unit, i.e. the rate of work performed on the skeleton. Notice that the power is negative because the muscle is extending against the force. Muscles behaving like this in the human body are often termed antagonistic muscles.	
Pmet	A crude estimate of the metabolism in the muscle. The estimate is based on presumed efficiencies of the contractile element of 25% for concentric work and -120% for eccentric work. The model does not take the metabolism of isometric force into account.	

Calibration

One of the practical challenges in working with detailed muscle models in complex musculoskeletal systems is the dependency on defined tendon length, Lt_0 . A brief experiment with our model can reveal where the difficulty lies. In the model we have just investigated, the activity of Muscle2 has the following development over the movement:



But what would happen if our guess of tendon length, Lt_0 , in the muscle model definition was just slightly off the correct value? Well if we change the current value from 0.5 m to 0.45 m, i.e. a reduction of 10%, we get the following activity:

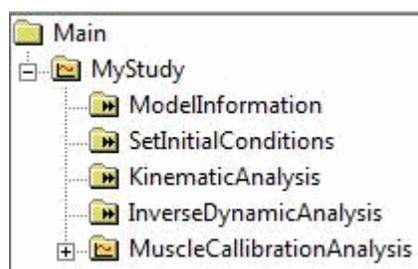


Not only is the shape of the graph different; the maximum activity is also significantly higher. An error of 10% in an anthropometric data value is not uncommon considering the accuracy of measurement methods and variation between individuals, and if the influence on the final result is as strong as this, we would not be able to trust our results. The problem is even more difficult if we desire to scale models up and down in size: Muscles pass along complex paths from origin to insertion, and the lengths of these paths do not scale in a simple fashion with, for instance, overall subject height.

As usual in biomechanical modeling, the solution can be found by relying on nature's ability to make the best of its resources. Nature has not equipped humans with tendons whose lengths are very disadvantageous for our normal activities. We can use this knowledge to calibrate the tendon lengths for an individual of a certain size. Quite simply, we shall presume that the tendon lengths are calibrated by nature to provide the muscles with optimum fiber lengths at certain postures. The AnyBody Modeling System provides two ways to do that: One is cheap and dirty, and the other one requires additional information. Let us take a closer look at them:

Cheap and dirty

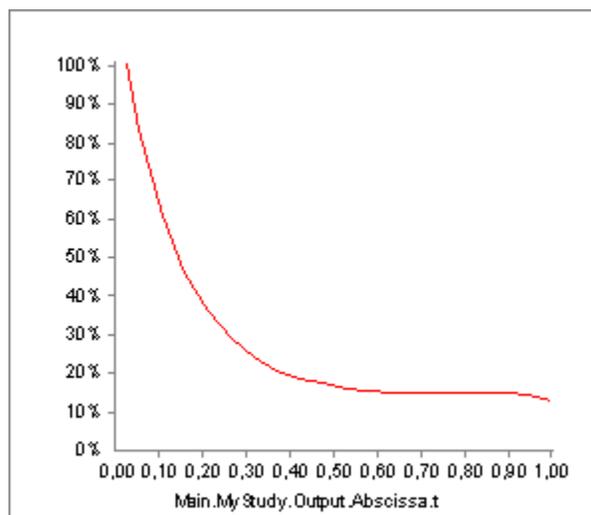
Cheap and dirty is readily available. If you take a closer look at the list of operations in the study tree, you will find one called MuscleCalibrationAnalysis.



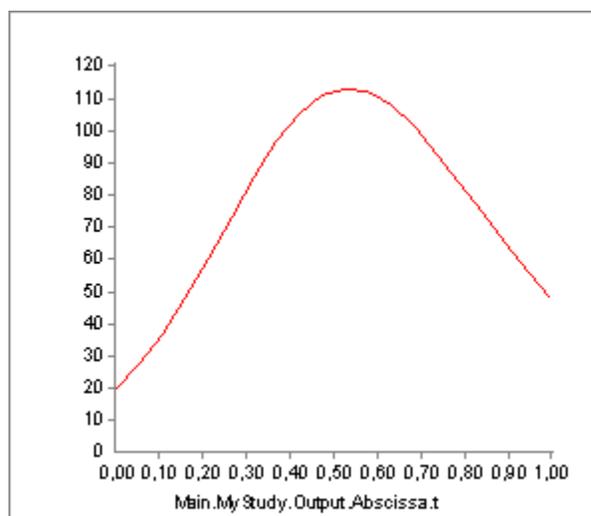
If you run it, you will see the model moving as it does in the InverseDynamicAnalysis. But when the analysis is done, the following message appears in the message window:

```
<address>The tendon length of muscle Main.MyModel.Muscle2 was calibrated. The muscle properties have been updated. </address>
```

Try running the InverseDynamicAnalysis again and plot the Activity of Muscle2. You should see the following:



As you can see, this is again very different from what we have seen before. Plotting the strength will reveal what has happened:



What the MuscleCalibrationAnalysis does is to run through the specified movement and compute the variation of the origin-insertion length of the muscle. It subsequently changes the user-defined value of $Lt0$ such that the length of the contractile element equals the optimum fiber length, $Lm0$, when the origin-insertion length is at its mean value. Notice that this does not necessarily correspond to the length when 50% of the movement has passed.

The rationale behind this method of tendon length calibration is that if you analyze a movement that is representative for what the body is created to do, then the muscles should probably attain their optimum fiber lengths somewhere safely within the interval of movement. Naturally this is not a very accurate way of doing it, and it will not work if you are modeling a movement that is outside the typical posture of the joints in the model.

Please notice that the tendon lengths specified in the AnyScript model are not altered by this method. Every time you reload the model you must run the MuscleCalibrationAnalysis again.

Detailed calibration

There is a more accurate and detailed way of calibrating tendons, but it requires additional information. More precisely it calibrates the tendon lengths at user-defined joint postures. So each muscle is associated with a certain set of joint postures for which the muscle is presumed to be at its neutral position. Please notice that the set of neutral joint postures is in principle different for each muscle in the system. In practice the calibration usually takes place on sets of muscles at a time, where all the muscles in a set is calibrated at the same joint postures. This way, all the muscles in a complicated system can be calibrated with a reasonable number of operations.

Detailed calibration of tendon lengths is covered in the ["Study of studies" tutorial](#). Calibration of ligaments is much the same type of process and is described in detail in the [Ligament tutorial, Lesson 7](#).

But before we come to ligaments we must cover one last aspect of muscle modeling, namely General Muscles. They are the topic of the next lesson, Lesson 6 (coming soon).

References

Hill, A.: The heat of shortening and the dynamics constants of a muscle. Proc. Roy. Soc. B., 126, 136-195, 1938.

Huxley, A.: Muscle structure and theories of contraction, Progr. Biophys. 7, 255-318.

Zajac, F.E.: Muscle and Tendon: Properties, Models, Scaling, and Application to Biomechanics and Motor Control. Critical Reviews in Biomedical Engineering, 17, 359-410, 1989.

Lesson 6: General muscles

Physiological muscles are truly amazing machines, and despite many attempts it has not been possible to make technical actuators that are as light and efficient as natural muscles. As you may have seen in the preceding sections, the mathematical modeling of muscles is not an easy task either. But once it has been done, we can use some of the properties of muscles to our advantage. We would like these "muscles" to be able to have a slightly more general formulation than physiological muscles, which are confined to acting along strings.

The solution is the AnyGeneralMuscle class. This type of muscle is capable of acting on Kinematic Measures. Kinematic measures is an abstract class representing anything you can measure on a model, and there is in fact [an entire tutorial lesson devoted to the subject](#) in the section on [The Mechanical Elements](#). Some examples are:

- A general muscle working on a distance measure between two points becomes simply a linear force provider, or in fact a reaction provider in the sense that the force is not predetermined but will become whatever equilibrium requires.
- A general muscle working on an angular measure, for instance a joint angle, becomes a torque provider.
- A general muscle working on a Center of Mass measure becomes an abstract force working on all segments of the body contributing to the center of mass.

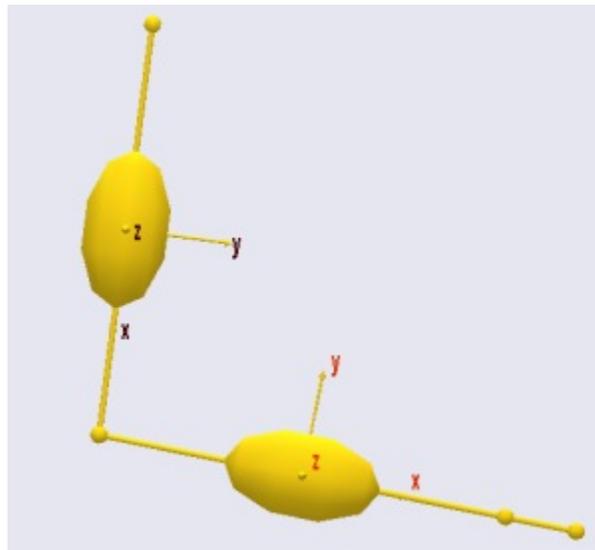
This lesson demonstrates how general muscles can be used for a variety of modeling tasks.

Muscles as joint torque providers

muscles are disregarded and the body is balanced entirely by joint torques. This type of analysis can provide important information about the function of limbs and joints, and it is extremely numerically efficient.

Joint torque inverse dynamics can be accomplished by adding general muscles to the joints to replace the physiological muscles of the body. This way, the "muscle forces" computed in the general muscles will simply be the joint torques.

The example from the preceding lessons is not well suited to play with joint torques, so please download a new example to start on by [clicking here \(right-click and save to disk\)](#). This is in fact a simplified version of the simple arm example from the [Getting Started with AnyScript](#) tutorial, where the muscles have been removed. The model has two segments, an upper arm and a forearm, and is attached to the global reference frame at the shoulder. It has a 100 N vertical load acting downwards at the hand.



The lack of muscles means that the model cannot currently do an inverse dynamics analysis. If you try to run the InverseDynamicAnalysis operation, you will get the following error message:

```
<address>ERROR : C:\Documents and Settings\jr\My
Documents\AnyScripts\demo\MuscleDemo\MuscleDemo.6.any(103) : ArmStudy : Muscle recruitment
analysis failed, simplex solver found that problem was unbounded.</address>
```

which is a mathematical way of stating that the model cannot be balanced in the absence of muscles. In this case we are not going to add real muscles. Instead we shall add general muscles to the revolute joints. The best way to introduce a general muscle is to insert it from the class tree. Place the cursor after the Drivers folder, locate the AnyGeneralMuscle in the class tree, and insert a template:

```
AnyFolder Drivers = {
  //-----
  AnyKinEqSimpleDriver ShoulderMotion = {
    AnyRevoluteJoint &Jnt = ..Jnts.Shoulder;
    DriverPos = {-1.7};
    DriverVel = {0.4};
    Reaction.Type = {0};
  }; // Shoulder driver
  //-----
  AnyKinEqSimpleDriver ElbowMotion = {
    AnyRevoluteJoint &Jnt = ..Jnts.Elbow;
    DriverPos = {1.5};
    DriverVel = {0.7};
  };
}
```

```

    Reaction.Type = {0};
}; // Elbow driver
}; // Driver folder

AnyGeneralMuscle <ObjectName> = {
    //ForceDirection = -1;
    AnyKinMeasure &<Insert name0> = <Insert object reference (or full object
definition)>;
    AnyMuscleModel &<Insert name0> = <Insert object reference (or full object
definition)>;
};

```

Just as normal muscles, general muscles must be associated with a muscle model. Let us insert a simple one:

```

AnyMuscleModel <ObjectName> = {
    F0 = 0;
};

AnyGeneralMuscle <ObjectName> = {
    //ForceDirection = -1.000000;
    AnyKinMeasure &<Insert name0> = <Insert object reference (or full object
definition)>;
    AnyMuscleModel &<Insert name0> = <Insert object reference (or full object
definition)>;
};

```

The empty fields in the muscle model must be filled in:

```

AnyMuscleModel MusModel = {
    F0 = 100.0;
};

```

We shall associate the muscle with the shoulder joint:

```

AnyMuscleModel MusModel = {
    F0 = 100.0;
};

AnyGeneralMuscle ShoulderTorque = {
    //ForceDirection = -1;
    AnyKinMeasure &Angle = .Jnts.Shoulder;
    AnyMuscleModel &Model = .MusModel;
};

```

Providing a torque for the shoulder is not enough. We also need a torque in the elbow:

```

AnyGeneralMuscle ShoulderTorque = {
    //ForceDirection = -1;
    AnyKinMeasure &Angle = .Jnts.Shoulder;
    AnyMuscleModel &Model = .MusModel;
};

AnyGeneralMuscle ElbowTorque = {
    //ForceDirection = -1;
    AnyKinMeasure &Angle = .Jnts.Elbow;
    AnyMuscleModel &Model = .MusModel;
};

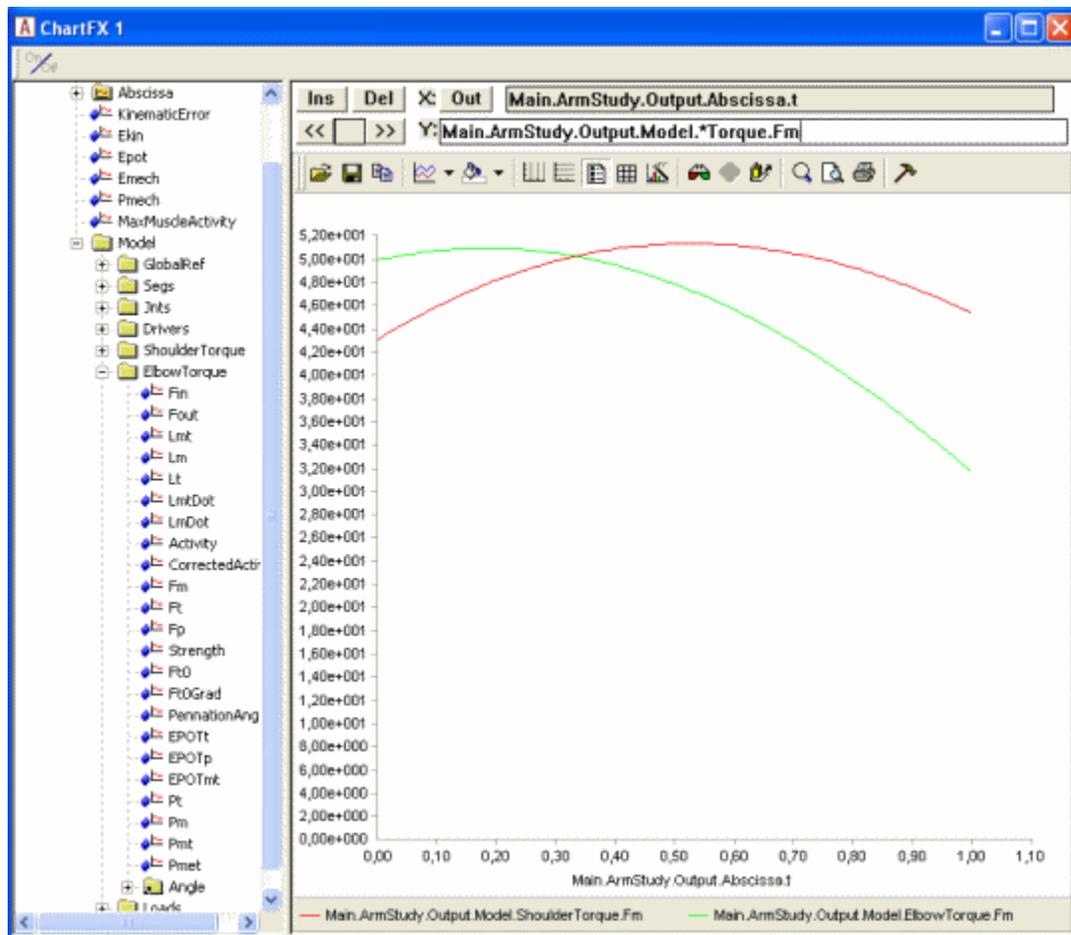
```

Having provided torques for the shoulder and elbow it should be possible to run the inverse dynamic analysis. However, attempting to do so will provide the same depressing error message as before. The reason is that general muscles share the ability to be unilateral with normal muscles. The direction of action is controlled by the variable ForceDirection. If the muscle acts in the positive direction of the joint angle, then its direction should be set = 1, and if it is in the negative joint angle direction it should be -1. In the present case the external load tends to work in the negative angle direction for the shoulder as well as the elbow, and hence the muscles should counteract in the positive direction:

```
AnyGeneralMuscle ShoulderTorque = {
  ForceDirection = 1;
  AnyKinMeasure &Angle = .Jnts.Shoulder;
  AnyMuscleModel &Model = .MusModel;
};
```

```
AnyGeneralMuscle ElbowTorque = {
  ForceDirection = 1;
  AnyKinMeasure &Angle = .Jnts.Elbow;
  AnyMuscleModel &Model = .MusModel;
};
```

Now the InverseDynamicAnalysis can be performed. Having done so, we can open a new Chart View and look up the two joint torques as the Fm property of the general muscles. We can plot both of them simultaneously using an asterisk as shown below:



Notice that in this case we have used the same strength (muscle model) for both joints. However, the maximum joint torque in physiological joints varies a lot. The knee extension strength, for instance is significantly larger than the elbow extension strength. If you perform this type of modeling you can define joint torque muscles with strengths comparable to the available joint torque and the system can give you an estimate of how many percent of each joint's strength is used in a given situation. You can also define different strengths of extension and flexion muscles in a given joint and thereby take for instance the difference in strength in the knee in these two directions into account.

Another useful property of the general muscles used at joint torque providers is that you can handle closed loops and other statically indeterminate situations, which are not treatable by traditional inverse dynamics because the equilibrium equations do not have a unique solution. The muscle recruitment algorithm will then distribute the load between joints according to their individual strengths, and it is therefore important to have reasonable estimates of joint strengths for this type of situation.

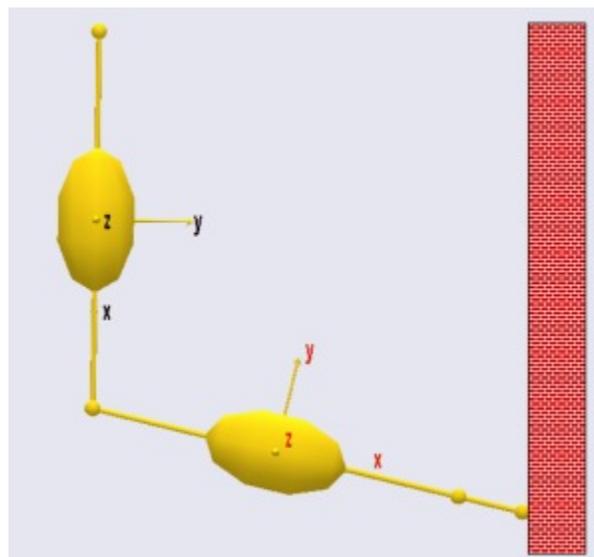
Contact and other boundary conditions

One of the characteristics of muscles is that they are unilateral, i.e. they can only exert force in one direction. Mathematically this behavior creates a significant amount of problems, but many mechanical phenomena have the same characteristics, namely any kind of contact phenomenon. Biomechanics is full of contact problems:

- The contact between a foot and the floor
- The contact between the upper thighs and the seat of a chair
- The contact between two articulating surfaces in a joint.

There is another less appreciated similarity between muscle forces and contact forces: neither is without limit. Muscle forces are obviously limited by the strength of the muscle. Contact forces to the environment may seem like they are only limited by the strength of whatever is supporting the body, but it can also be limited by friction and by the pressure on the contacting tissues; if you have a stone in one shoe you will very likely put less weight on that foot than on the other.

So the muscles of the body in addition to creating equilibrium are constrained by the available contact forces to the environment, and these often have different limits in different directions, typically a high limit in compression perpendicularly against the supporting surface, a smaller limit for friction tangentially to the surface, and no reaction available in tension. Mathematically and mechanically this is very much how muscles work, and the conditions therefore affect the mechanics of the entire system much like muscles do and can be mimicked by means of general muscles.



We are going to make a couple of changes to the simple arm model to investigate contact in more detail. We shall imagine that the hand of the model has a vertical wall to support against. We have to change the kinematics to make the arm slide along the wall. It would be really difficult to figure out which joint angle variations are needed to make the hand move vertically, so we drive the hand directly instead.

```
AnyFolder Jnts = {
    //-----
    AnyRevoluteJoint Shoulder = {
        Axis = z;
        AnyRefNode &GroundNode = ..GlobalRef.Shoulder;
        AnyRefNode &UpperArmNode = ..Segs.UpperArm.ShoulderNode;
    }; // Shoulder joint

    AnyRevoluteJoint Elbow = {
        Axis = z;
        AnyRefNode &UpperArmNode = ..Segs.UpperArm.ElbowNode;
        AnyRefNode &LowerArmNode = ..Segs.LowerArm.ElbowNode;
    }; // Elbow joint

}; // Jnts folder

AnyKinLinear HandPos = {
    AnyRefFrame &ref1 = ..GlobalRef.Shoulder;
    AnyRefFrame &ref2 = ..Segs.LowerArm.PalmNode;
};

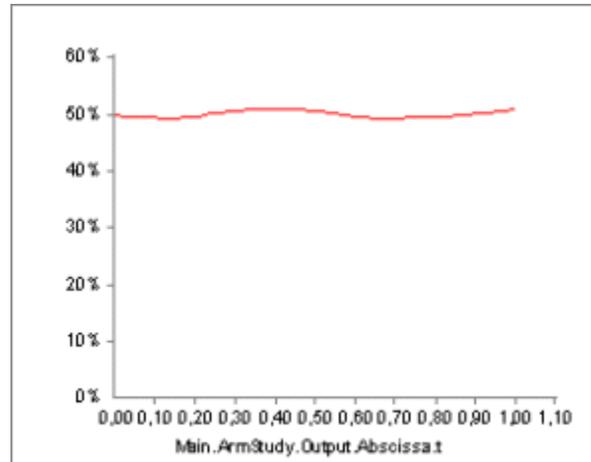
AnyFolder Drivers = {
    AnyKinEqSimpleDriver HandDriver = {
        AnyKinLinear &Measure = ..HandPos;
        MeasureOrganizer = {0,1};
        DriverPos = {0.45, -0.6};
        DriverVel = {0, 0.5};
        Reaction.Type = {0, 0};
    };
    /* //-----
    AnyKinEqSimpleDriver ShoulderMotion = {
        AnyRevoluteJoint &Jnt = ..Jnts.Shoulder;
        DriverPos = {-1.7};
        DriverVel = {0.4};
        Reaction.Type = {0};
    }; // Shoulder driver

    //-----
    AnyKinEqSimpleDriver ElbowMotion = {
        AnyRevoluteJoint &Jnt = ..Jnts.Elbow;
        DriverPos = {1.5};
        DriverVel = {0.7};
        Reaction.Type = {0};
    }; // Elbow driver
    */}; // Driver folder
```

Notice that the previous two joint angle drivers have been disabled. Otherwise the system would become kinematically over-determinate. Notice also that the new driver drives two degrees of freedom corresponding exactly to the two drivers we have disabled. Finally, please notice the line

```
Reaction.Type = {0, 0};
```

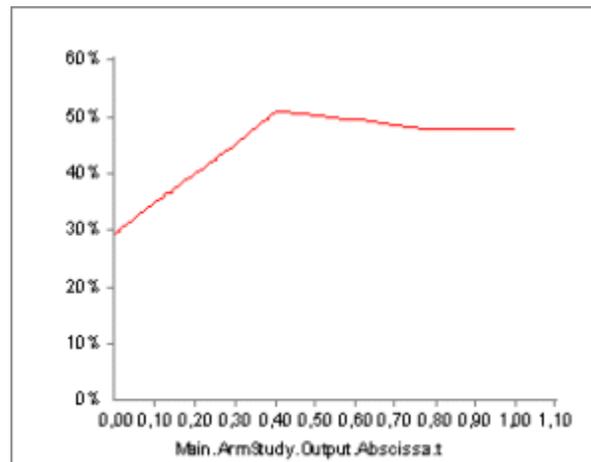
This means that the wall presently provides no reaction forces to the arm. Plotting the MaxMuscleActivity provides the following result:



The muscle activity is rather constant which is the natural consequence of the moment arms being rather constant. The gravity as well as the applied load of 100 N are vertical, so one might be tempted to think that a horizontal support would not make much of a difference. We can do a quick test by simply switching on the horizontal support of the driver:

```
Reaction.Type = {1, 0};
```

This produces immediate proof that mechanics is usually more complicated than expected; even this very simple mechanical system behaves differently from what we might expect:



Notice that the muscle activity is much smaller in the beginning of the movement with the reaction switched on and much the same towards the end of the movement. It seems like the muscles are able to use the horizontal reaction force to their advantage depending on the posture of the mechanism.

Walls in general do not work like that; they can only provide reaction pressure but no tension. This we can mimic with general a muscle. We first switch the reaction off again:

```
Reaction.Type = {0, 0};
```

Subsequently we define a general muscle:

```
AnyMuscleModel MusModel = {
```

```

    F0 = 100.0;
};
AnyMuscleModel ReacModel = {
    F0 = 10000.0;
};

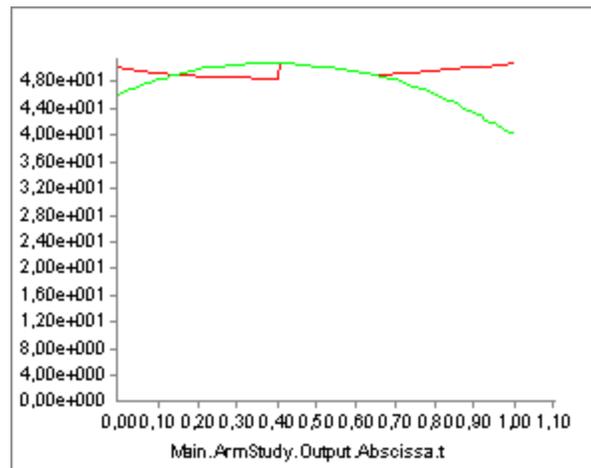
AnyGeneralMuscle WallReaction = {
    ForceDirection = -1;
    AnyKinMeasureOrg Org = {
        AnyKinMeasure &wall = ..HandPos;
        MeasureOrganizer = {0};
    };
    AnyMuscleModel &Model = .ReacModel;
};

```

There are two things to notice here

1. The muscle model for the reaction, ReacModel, is much stronger than the joint muscles. This is because the wall is presumed to be very strong.
2. The ForceDirection property equals -1. This means that the force is working in the opposite direction of the Kinematic measure, i.e. in the negative global x direction, just like a contact force with the wall would do.

Running the InverseDynamicAnalysis again and plotting the two joint torques provides the following graph (notice they can be plotted simultaneously with the specification line Main.ArmStudy.Output.Model.*Torque.Fm):



The red curve is the shoulder joint torque, and the green curve is the elbow torque. Notice that the envelope of these two curves is in fact identical to the MaxMuscleActivity curve we plotted above for the case of no support. You would think that the support would be beneficial in the final stages of the movement where the arm could rest a bit against the wall. Actually, it is beneficial for the elbow, but the reaction force also increases the torque about the shoulder, and since the shoulder (red curve) has the higher load of the two, this limits the benefit of the support. Let us see what happens if we turn the reaction force the other way like if the hand could pull against the far side of the wall:

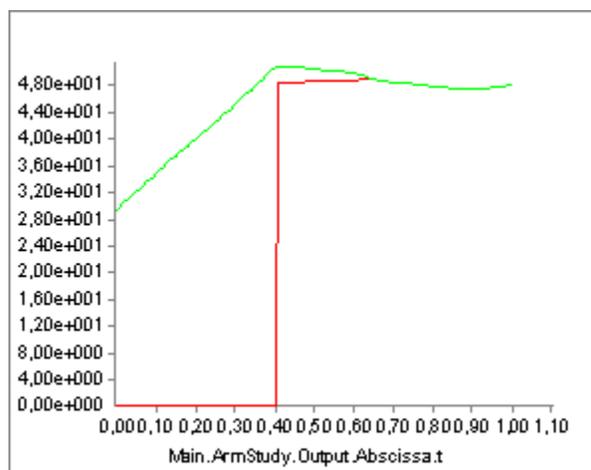
```

AnyGeneralMuscle WallReaction = {
    ForceDirection = 1;
    AnyKinMeasureOrg Org = {
        AnyKinMeasure &wall = ..HandPos;
        MeasureOrganizer = {0};
    };
    AnyMuscleModel &Model = .ReacModel;
};

```

```
};
```

If you run the model again and plot the same graphs, you will see this:



The wall is obviously useful in the initial stages of the movement where the torque generated by the reaction force is in the beneficial direction for both the joints. In the later stages of the movement the presence of the wall decreases the envelope of the muscle forces slightly, but it has increased the torque in the elbow. The explanation is that the elbow can increase its action beyond what is necessary to carry the load and generate an additional pressure against the wall, which then decreases the torque in the shoulder.

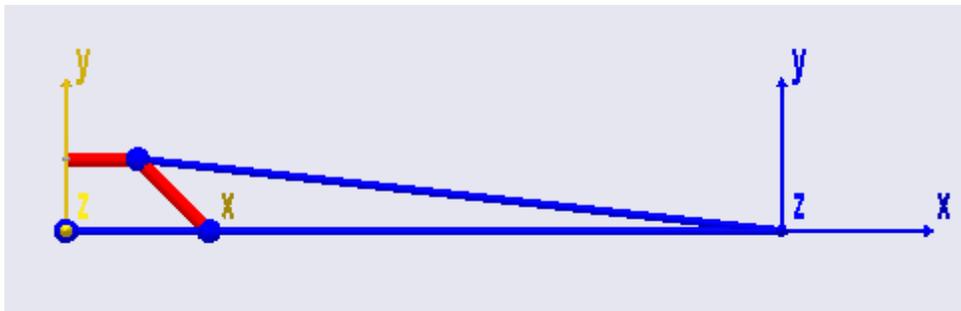
This example shows how complicated the mechanics of the body is: Even this very simplified case would have different solutions if the parameters of the model were different. For instance if the shoulder were much stronger compared to the elbow, then the elbow would not have been able to help the shoulder in the latter case because the elbow would have the higher load compared to its strength. On the contrary, the shoulder would have been able to help the elbow in the former case by generating an additional force pushing against the wall.

This completes the part of this tutorial dealing with muscles. But we are not completely finished yet. The [next lesson](#) deals with the important topic of ligament modeling.

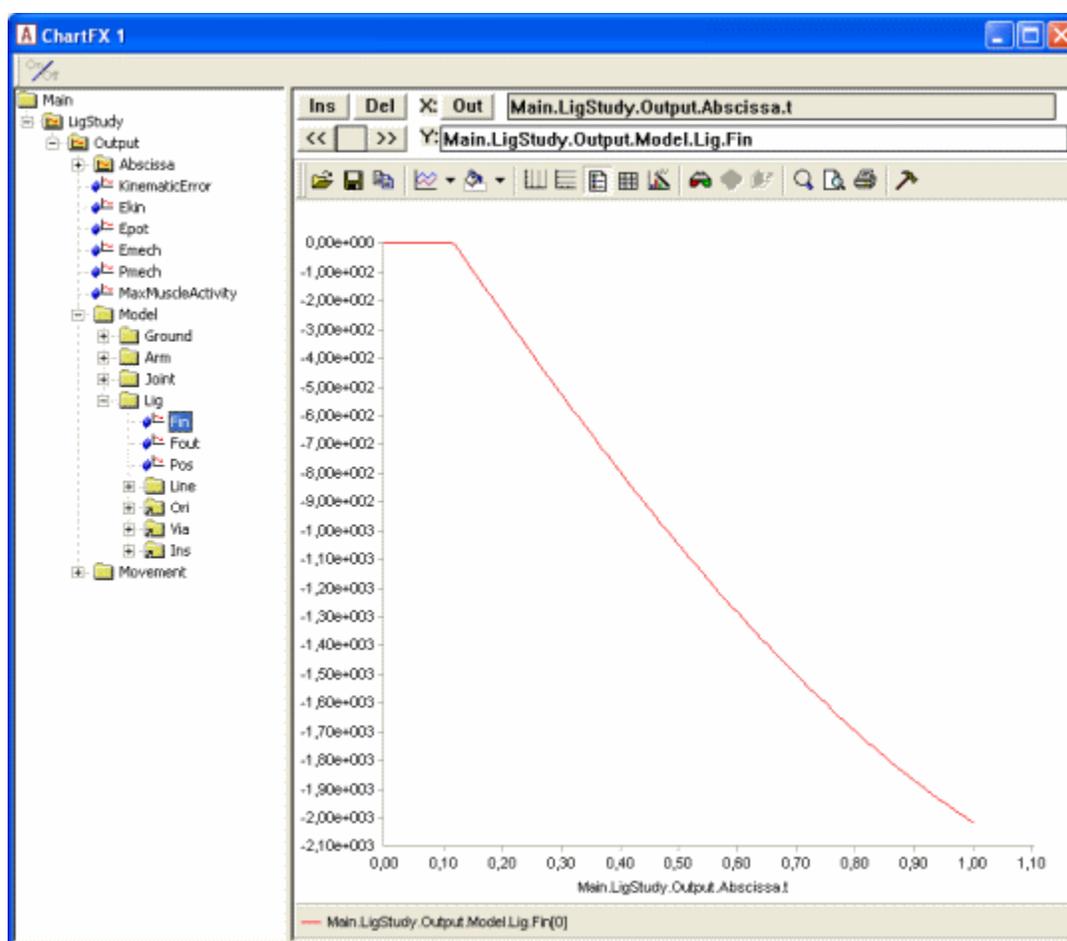
Lesson 7: Ligaments

Ligaments are passive structures that connect articulating bones and keep joints assembled. Mechanically they are much like muscles but with no active contractile element. Ligaments only provide forces when they are stretched by the relative movement of the bones they connect.

This tutorial demonstrates how to define, control, and calibrate ligaments. We need a model to work on. Please download and save the model [Demo.Ligament.any](#). Once you have stored it on your hard disk, load it into the AnyBody Modeling System and run the SetInitialConditions operation.



As you can see, the model is very simple. The blue structure is an "arm" that extends from the center of the yellow Ground reference frame. It is hinged at the Ground's origin, and a driver bends it downwards. With the movement, the red ligament is stretched, and a force builds up in it. Try running the InverseDynamicAnalysis operation. You will see the arm move, and you can subsequently open a Chart View to investigate the results:

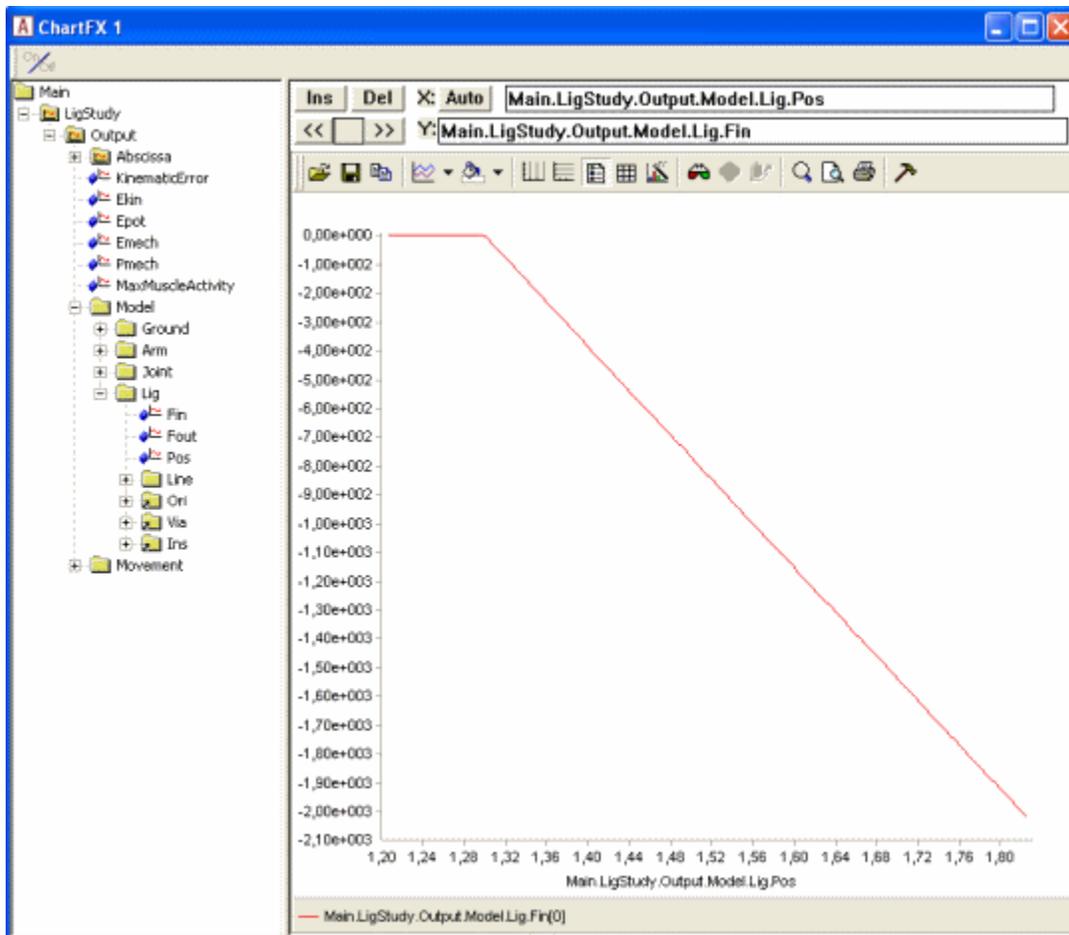


As you can see, the ligament force builds up from nothing to about -2000 N as it is stretched. The value is negative by convention because it works in the opposite direction of the stretching. Notice that the graph has an initial horizontal part. This is because force does not build up until the ligament is stretched beyond its slack length, L_0 .

Basic mathematical behavior

It looks like the force development is slightly nonlinear. This would make sense because ligament elasticity is generally nonlinear, but in this case it just shows that the abscissa is not the ligament length but rather an artificial "time" that is proportional to the joint angle.

In the Chart View you can plot any output data against each other. Let's select instead of time the ligament length. Click the "Out" button, and the field containing the abscissa becomes white. You can now type "Main.LigStudy.Output.Model.Lig.Pos" in the abscissa field:



That's better. Now the elasticity of the ligament is completely linear over the slack length. Let us take a look at the definition of the ligament model:

```
AnyLigamentModelPol LigModel = {
    L0 = 1.30; // Slack length
    eps1 = 0.2; // Strain where F1 is valid
    F1 = 1000; // Force in the ligament at strain eps1
};
```

As you can see, we have only defined three properties. L0 is the slack length. The ligament is not stretched until its length goes beyond L0, so its strain is zero at L0. When the ligament is stretched, it also builds up a force. The rate of force development with stretching can be thought of as the stiffness of the ligament, and

work with strain here rather than absolute length change? The reason is that ligaments are rather stiff structures, so small length changes can cause large forces, and it is therefore necessary that the slack length fits the model precisely. This length will usually have to be tuned to size changes of the body model. When we work with strain, the stiffness becomes a more generic property of the ligament and is independent of the length it gets calibrated to.

The three parameters we have defined leave room for no more than a linearly elastic behavior with a slack length. Ligament elasticity is generally not linear, so we need something extra to be able to specify nonlinear behavior. The mathematical background for the `AnyLigamentModelPol` is that it takes the form:

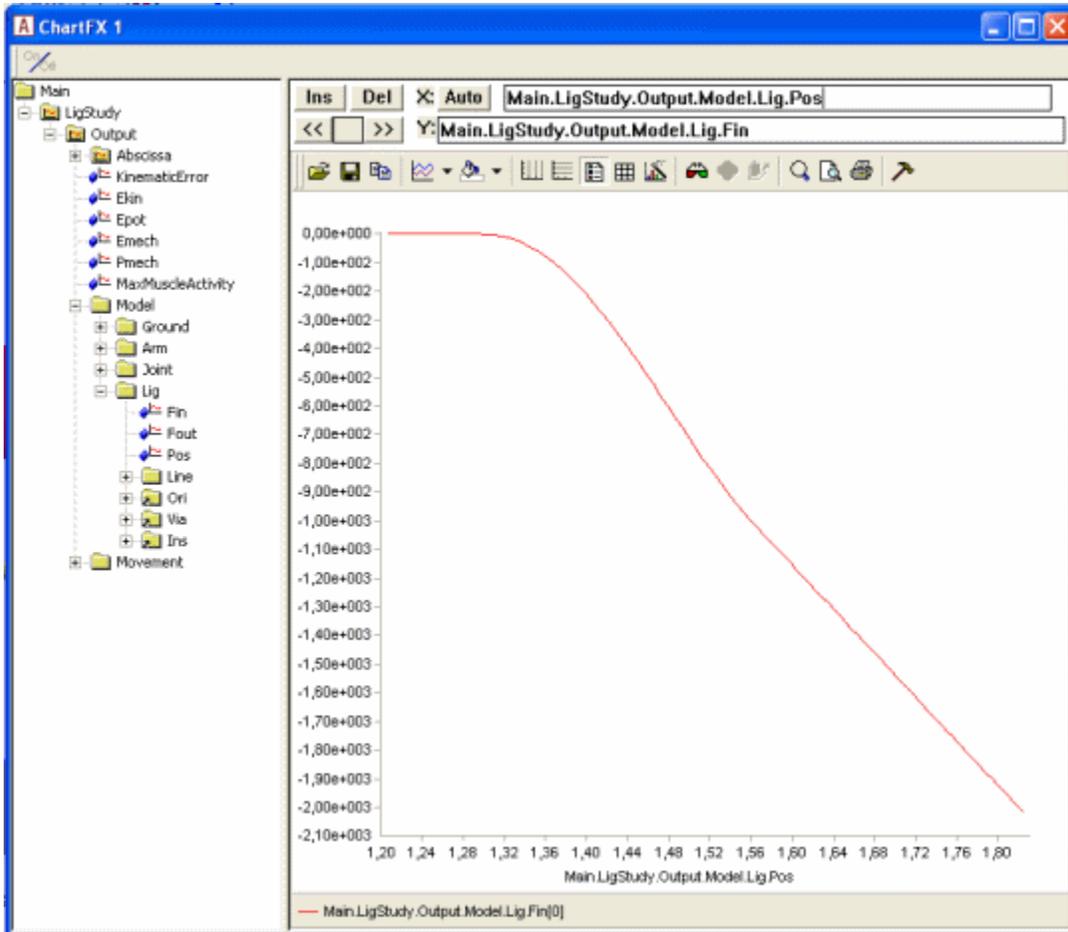
$$F = C_0 + C_1\varepsilon + C_2\varepsilon^2 + C_4\varepsilon^4$$

As you can see, it is a fourth order polynomial with the third order term missing. The 0'th order coefficient accounts for the slack length, and the first order coefficient accounts for the slope when the model is linear and the second and fourth order terms are missing. But in the presence of the nonlinear terms it becomes very difficult to interpret the significance of each term. For this reason, the nonlinearity in the model is defined by two parameters with an easier interpretation than the above-mentioned C_2 and C_4 .

The two parameters are called a_0 and a_1 respectively. The first parameter, a_0 , defines the slope of the curve at slack length. If you study the curve above, you can see that it has a sharp kink at the slack length. It changes abruptly from zero slope to the nominal slope given by $(\text{eps1}, F1)$. The default value of a_0 is 1, and this corresponds to the slope right after the kink being defined entirely by $(\text{eps1}, F1)$. In other words, the curve is pointing directly at the point $(\text{eps1}, F1)$. In fact, the significance of the a_0 is that it interpolates the slope between zero (for $a_0 = 0$) and the linear slope you see in the curve above for $a_0 = 1$. Try inserting the following:

```
AnyLigamentModelPol LigModel = {
  L0 = 1.30; // Slack length
  eps1 = 0.2; // Strain where F1 is valid
  F1 = 1000; // Force in the ligament at strain eps1
  a0 = 0.0;
};
```

Subsequently reload the model, run the `InverseDynamicAnalysis`, and plot the ligament force again. You will see the following:

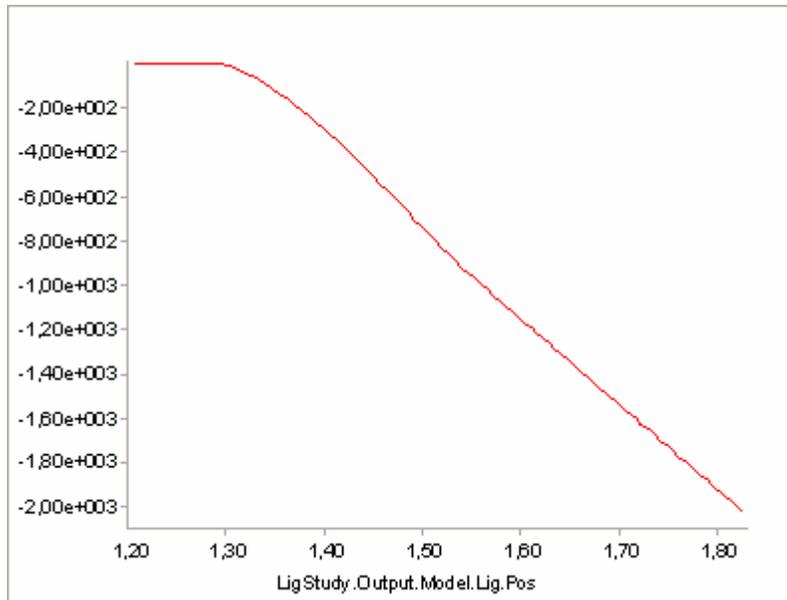


The specification has created a continuous slope of 0 where the curve previously had a kink. Notice that the curve converges back to the "nominal" slope given by the two points (L0,0) and (eps1,F1)

If you try the following:

```
AnyLigamentModelPol LigModel = {
  L0 = 1.30; // Slack length
  eps1 = 0.2; // Strain where F1 is valid
  F1 = 1000; // Force in the ligament at strain eps1
  a0 = 0.5;
};
```

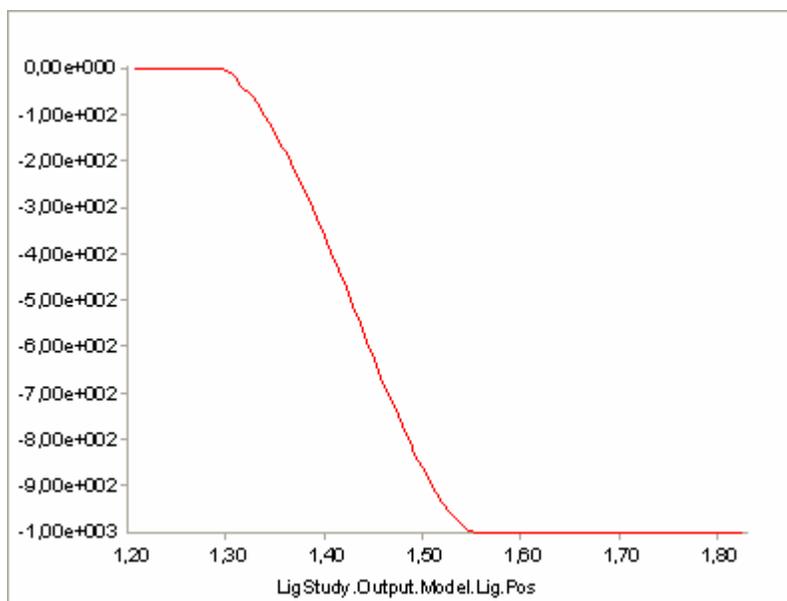
- then you get something in between:



The significance of a_1 is much the same, except it has its effect at the point (ϵ_{s1}, F_1) . Rather than at $(L_0, 0)$. If, for instance you insert this:

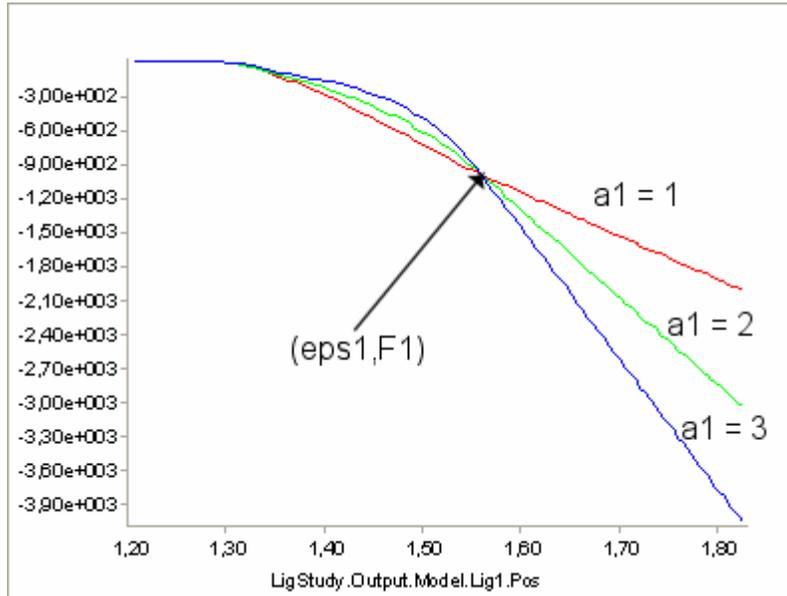
```
AnyLigamentModelPol LigModel = {
  L0 = 1.30; // Slack length
  eps1 = 0.2; // Strain where F1 is valid
  F1 = 1000; // Force in the ligament at strain eps1
  a0 = 0.5;
  a1 = 0.0;
};
```

- then you will get a curve that attains zero slope at (ϵ_{s1}, F_1) :



So, $a_1 = 0.0$ corresponds to zero slope, and the default value of $a_1 = 1.0$ corresponds to the slope given by

the values of L_0 , eps1 , and F_1 . You can similarly increase the slopes by increasing a_1 :

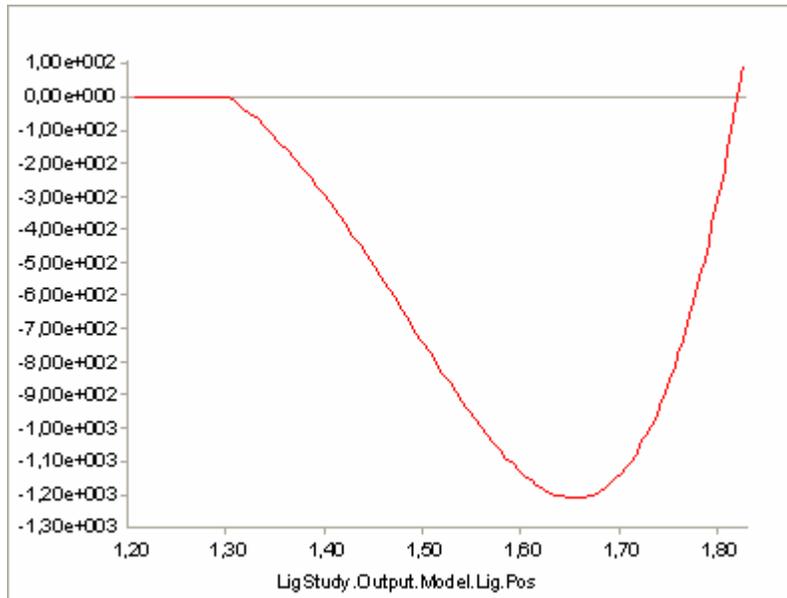


Unlike normal fourth order polynomials, these curves will continue predictably with no oscillation for as long as desired after $(\text{eps1}, F_1)$. The reason for this behavior is the default setting of the parameter

```
LinRegionOnOff = On
```

which causes the curve to continue a linear behavior after $(\text{eps1}, F_1)$. You can, however, obtain the clean fourth order polynomial behavior if you like by switching this setting off:

```
AnyLigamentModelPol LigModel = {
  L0 = 1.30; // Slack length
  eps1 = 0.2; // Strain where F1 is valid
  F1 = 1000; // Force in the ligament at strain eps1
  a0 = 0.5;
  a1 = 1.0;
  LinRegionOnOff = Off;
};
```



Clearly, this causes the curve to diverge after (eps1,F1), which is typical for higher order polynomials. Unless you have some special reason for wanting the pure fourth-order behavior, we recommend that you leave `LinRegionOnOff = On`.

Calibration

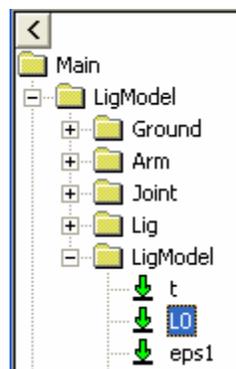
Most ligaments in the body are rather stiff structures in which the force builds up quickly when they are stretched beyond the slack length. This means that a small error in slack length specification could lead to a large error in computed ligament force. It therefore becomes crucial that the ligaments fit the other parts of the model exactly.

The easiest way to determine ligament slack lengths is by means of joint angles. For most joints where ligaments play an important role, it is obvious in which position of the joint the ligament becomes taut. Therefore, ligaments are calibrated just like muscles by positioning the joints in question and letting the system automatically change LO of each ligament to the length in that position.

Let's try to calibrate our ligament. The first thing we must do is to create a Calibration Study:

```
AnyBodyCalibrationStudy LigCali = {
  AnyFolder &Model = .LigModel;
  nStep = 1;
  // This driver puts the joint into the calibration position
  AnyKinEqSimpleDriver Position = {
    DriverPos = {-pi/4};
    DriverVel = {0.0};
    AnyRevoluteJoint &Jnt = Main.LigModel.Joint;
  };
};
```

Notice the driver in the study. It positions the joint at the angle of $-\pi/4$. This becomes the position in which the ligament has its slack length. Try loading the model and then browse your way through the tree to the LO property of the ligament model:



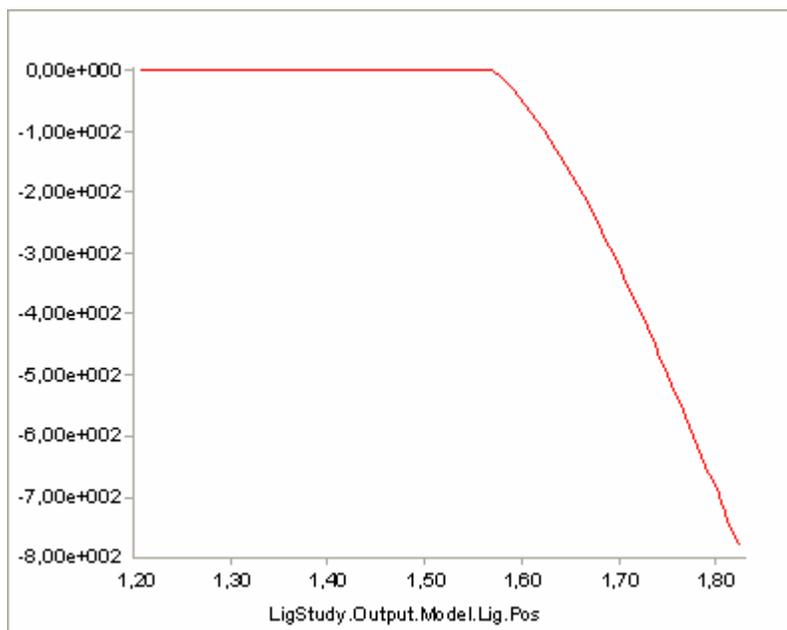
Double-click it, and its value is shown in the Object Description Window. You should find a value of

Main.LigModel.LigModel.LO = 1.300000;

This is the slack length of the ligament at load time as defined in the ligament model. Now, run the LigCali.LigamentLengthAdjustment operation, and subsequently double-click the LO property again. Now you will see a value of

Main.LigModel.LigModel.LO = 1.573132;

The system has extended the ligament length a bit to fit the joint angle of $-\pi/4$. Run the InverseDynamicAnalysis study again, and see the influence of the increased slack length:



You can find the final version of the ligament demo file [here](#).

The mechanical elements

Musculoskeletal modeling is really just an advanced application of the laws of mechanics described by one of the greatest scientists of all times, Sir Isaac Newton, more than 300 years ago. So the elements of the models you are working on in the AnyBody Modeling system are mostly mechanical in nature, and to use

them you must have sound understanding of the laws of mechanics in general and of Newton's three laws of motion in particular.

The mechanical elements of an AnyBody model are

- **Segments**
used to represent bones and other rigid elements of models
- **Joints**
used to connect segments and allow them to articulate with respect to each other
- **Drivers**
used to specify the movement the model should perform and optionally provide power input as motors
- **Kinematic measures**
abstraction representation of kinematical constraints
- **Forces**
forces applied to the model

This tutorial also contains a short introduction to inverse dynamics and how it differs from forward dynamics.

This tutorial consists of the following lessons:

- [Lesson 1: Segments](#)
- [Lesson 2: Joints](#)
- [Lesson 3: Drivers](#)
- [Lesson 4: Kinematic Measures](#)
- [Lesson 5: Forces](#)

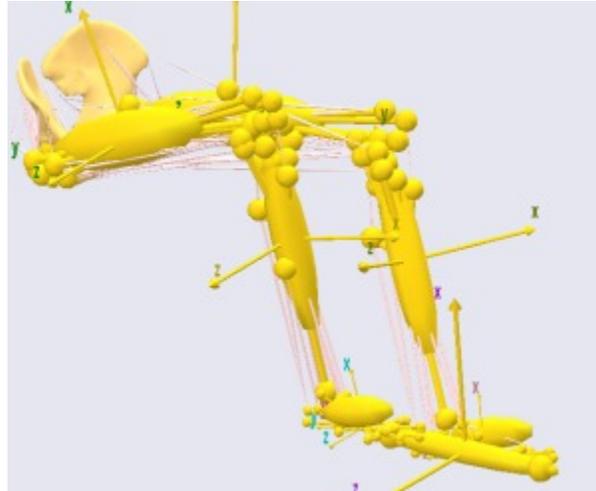
Let's head for [Lesson 1: Segments](#).

Lesson 1: Segments

Segments are defined by the AnySeg keyword in AnyScript. They are the rigid bodies on which the system bases its analysis. In a body model, segments are usually bones, but since an AnyBody model often comprises various equipment and other items, segments are also used to model cranks, pedals, handles, tools, sports equipment, tables, chairs, and all the other environmental objects a body may be connected to.

In fact, An AnyBody model does not have to entail a living body. You can easily create an AnyBody model of a machine in which no biological elements take part.

Segments in AnyBody are basically a set of mass properties as you can see below.



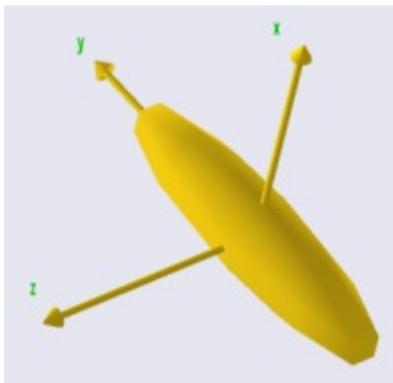
Segments do not have any particular shape associated with them. By default a segment is originated in its Center of Mass (CoM), but it is possible to move the CoM away from the origin of the segment's reference frame. The mass properties are defined by means of a mass and an inertia tensor. The segments in the picture above visualize their mass properties by ellipsoids.

Another important property of a segment is that it can have nodes, so-called AnyRefNodes, assigned to it. The connections between the segment and the AnyRefNodes are rigid, so the nodes move with the segment. The nodes are visualized by the heads of the pins sticking out from the ellipsoids.

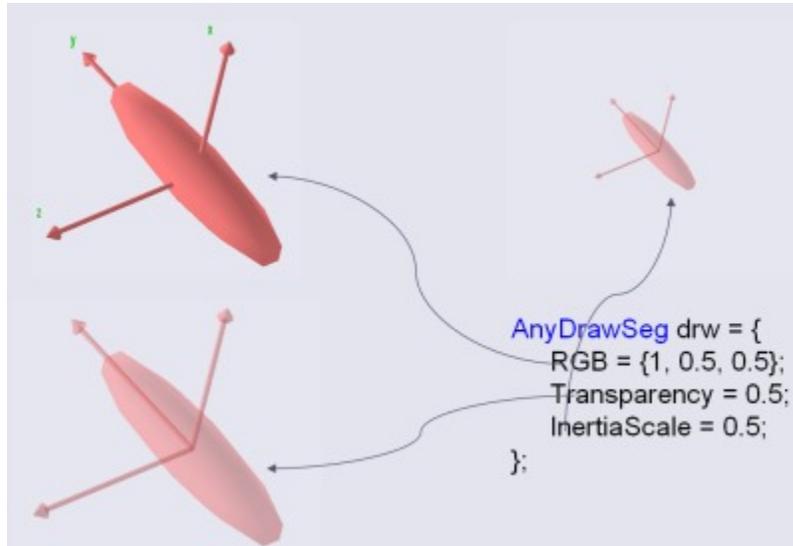
A basic definition of a segment could go like this:

```
AnySeg Potato = {
  Mass = 1;
  Jii = {0.01, 0.001, 0.01};
  AnyDrawSeg drw = {};
};
```

Notice that the AnyDrawSeg is just an empty pair of braces signifying that we are using the standard settings. This will produce the following image:



The AnyDrawSeg always represents segments as ellipsoids with axis ratios corresponding to the inertia properties. But the AnyDrawSeg class has multiple settings that can be used to control the appearance of the segment:



Please refer to the reference manual for further explanation. The [Getting Started with AnyScript](#) tutorial provides examples of segment definitions.

Next up is [Lesson 2: Joints](#).

Lesson 2: Joints

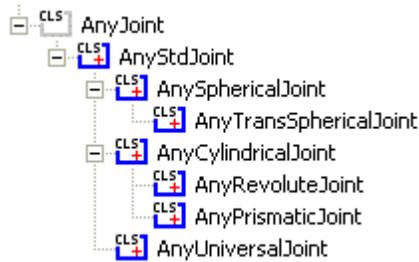
You normally think of a joint as something that provides the body with its movement capability. We interpret joints that way because we would not be able to move if our joints were rigid. But there is also an opposite perception of a joint: as a constraint. If we did not have joints, then our bodies would disconnect into a heap of bones.

The latter perception is how joints really work in AnyBody. Imagine you have two segments with no joints at all. They each have 6 degrees of freedom in space: 3 translations and 3 rotations. So two disjoint segments give us 12 degrees of freedom. If we connect them by a ball and socket joint, then we eliminate 3 degrees of freedom because they can no longer translate freely with respect to each other, and we are left with a mechanism with $12 - 3 = 9$ degrees of freedom. AnyBody will keep track of all this for you, but it makes things much easier to understand if you get used to thinking of joints as constraints.

As a final word about perceiving joints as constraints, it might be worth mentioning that these constraints are not taken into account at the moment when you load a model into AnyBody. By that time, the segments are simply positioned in space where you located them in their definition. In principle, the segments may be in one big, disorganized heap.

The joint constraints are not imposed until you perform some sort of analysis. Each study has the `SetInitialConditions` operation for the particular purpose of resolving the constraints and connecting things. The mathematics of that is a nonlinear system of equations. Such a system may have multiple solutions or no solutions at all. Even if it has a unique solution, it may be impossible to find. This means that if the segments are too disorganized from their final positions when they are defined, then the system might not be able to resolve the constraints and put them in their correct positions. The remedy is to define the segments so that their initial positions are not too far away from the configuration they will have when the constraints are resolved. You can read much more about this subject in the tutorial [A study of Studies](#).

AnyBody provides you with a variety of ways you can connect segments by joints. The class tree reveals the following joint class structure:



The different types are described in detail in the [reference manual](#). For examples on how to use joints, please download and study the following two examples:

- [Slider crank in 2D](#)
- [Slider crank in 3D](#)

The next chapter is [Lesson 3: Drivers](#).

Lesson 3: Drivers

Drivers create movement in a model. They are really functions of time determining the position of a joint or the distance between two points or some other kinematic measure at any given time through the simulation period.

There are various drivers available to create different types of time dependency. For a demonstration of the different types, please [download and study the Driver demo](#).

Next up is [Lesson 4: Kinematic Measures](#).

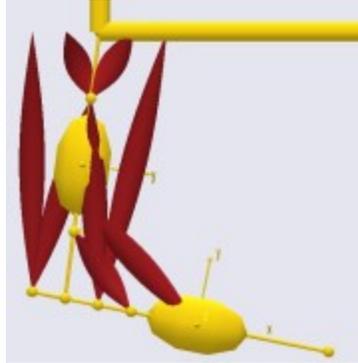
Lesson 4: Kinematic Measures

You are not likely to have any sort of idea what a kinematic measure is. Don't worry - you're not supposed to know about it. The concept was invented by AnyBody Technology as a way of describing dimensions in a kinematic model that you might want to get information about or control with drivers. A joint angle or a distance between two points are examples of kinematic measures. The position of the center of gravity of the entire model or a subset of its segments are other examples.

If you define a kinematic measure in your model, then you can study its development. But more importantly you can control it. You can add a driver to a kinematic measure, and that way control the movement of the mechanism. Such a driver can be added even when the measure is a less tangible quantity like the collective center of gravity that is not attached to a particular segment.

Joints can be understood as kinematic measures equipped with drivers. For instance, a spherical joint is a distance between two points on two different segments that is driven to be zero. This means that, using kinematic measures, you can define types of joints that are not available as predefined objects in AnyScript.

Do you remember the simple arm example of the "[Getting Started with AnyScript](#)" tutorial? That was a 2-D model of an arm where we produced the movement by driving the angles of the shoulder and elbow joints directly.



But let us imagine that we wanted the hand to reach out and grab something at a specific position. It would probably be difficult to figure out precisely how to drive the two joint angles to put the hand in the position we wanted it to attain. Instead, we would want to be able to put the hand (actually the wrist since this simple model has no hand) directly at the desired position in space and have the elbow and shoulder joints follow implicitly. This is where the kinematic measures come into play. Let's start off with the model just about where we left in the "Getting Started with AnyScript" tutorial. Please [click here to download the necessary file](#), and save it in some working directory on your own hard disk.

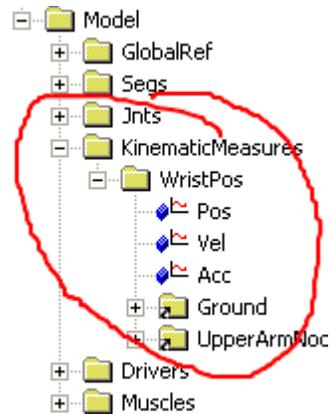
Let us try initially to create a kinematic measure that will allow us to track the movement of the wrist. To honor the folder structure of the model we shall create a new folder for the kinematic measure. Let's place it just below the Jnts folder to reflect the kinship between kinematic measures and joints:

```
}; // Jnts folder
AnyFolder KinematicMeasures = {
  AnyKinLinear WristPos = {
    // These are the nodes that the measure refers to
    AnyFixedRefFrame &Ground = Main.ArmModel.GlobalRef;
    AnyRefNode &UpperArmNode = Main.ArmModel.Segs.LowerArm.HandNode;
    Ref = 0;
  };
}; // KinematicMeasures
```

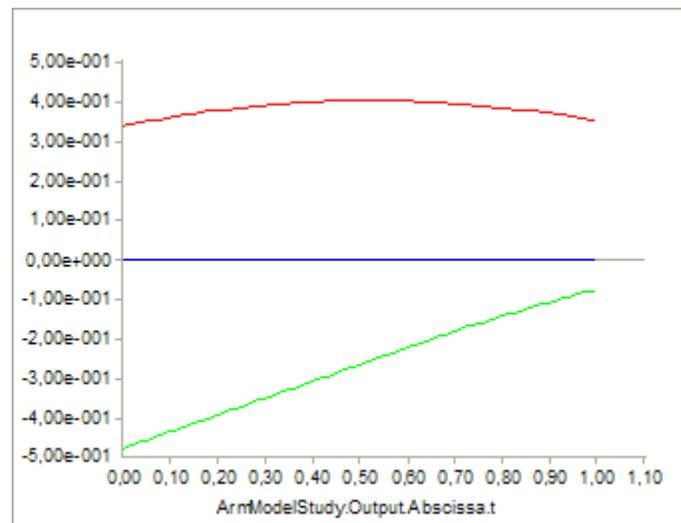
An AnyKinLinear is a kinematic measure that gauges the spatial vector between two points. The line Ref = 0 means that the coordinates of this linear distance are measured in the coordinate system first of the measure's end points which in this case happens to be the global reference frame. For other options, please refer to the [Reference Manual](#).

So far, we have just added a measure that allows us to track the movement of the hand, but it is still driven by the joint drivers as before. Let's investigate what we have. Load the model and run a KinematicAnalysis or an InverseDynamicAnalysis, and subsequently open a ChartFX view.

Expanding the tree though Main.ArmModelStudy.Output.Model.KinematicMeasures.WristPos will give you the options shown to the below.



Click Pos, and you will get three graphs tracking the x, y, and z components of the WristPos kinematic measure.



The z component (blue curve) of the measure remains zero throughout the movement because the model is two-dimensional. The top curve (red) is the x component, and the bottom curve (green) is the y component.

Now comes the beauty of kinematic measures: Rather than just observing them, you can actually drive them!

We shall replace the existing drivers on the shoulder and elbow joints by drivers on the x and y components of the WristPos kinematic measure.

We need to remove the existing elbow and shoulder drivers to avoid kinematic redundancy. You can enclose the drivers in comment characters `/* */`, or you can simply erase them, leaving you with an empty drivers folder:

```
AnyFolder Drivers = {
}; // Drivers folder
```

The next step is to fill drivers for the WristPos measure into the Drivers folder. We initially make an empty skeleton. Notice that we are using an AnyKinSimpleDriver here. If you had measured the hand position by a

interpolation driver instead.

```
AnyFolder Drivers = {
    AnyKinEqSimpleDriver HandMotionXY = {
    };
}; // Drivers folder
```

We can now fill contents into the HandMotionXY driver that will guide the hand through space:

```
AnyFolder Drivers = {
    AnyKinEqSimpleDriver HandMotionXY = {
        AnyKinLinear &Jnt = ..KinematicMeasures.WristPos;
        MeasureOrganizer = {0,1};
        DriverPos = {0.4,-0.5};
        DriverVel = {0.2,0.5};
        DriverAcc = {0.0,0.0};
        Reaction.Type = {Off,Off}; // The muscles must do the work
    };
}; // Drivers folder
```

The first of the red lines above refers to the WristPos kinematic measure. It simply specifies that this is the measure we want to drive. Notice, however that this measure has three components, namely the x, y and z coordinates. But we only want to drive two of them. The MeasureOrganizer handles that problem. It lines up the coordinates of the measure in a row for driving. MeasureOrganizer = {0,1} means that the vectors of driver specifications, such as DriverPos and DriverVel, refer to the x (number 0) and y (number 1) coordinates of the measure.

The values we suggest for DriverPos and DriverVel have been found by inspection of the graphs depicted above showing the development of the measure coordinates when we used the shoulder and elbow drivers. This is good practice because it is so easy to specify wrist positions that the arm cannot reach and thereby provoke a kinematic incompatibility that may be difficult to find in more complex cases.

To conclude, the special feature about kinematic measures is that you can drive them. In AnyBody, you can drive anything that you can measure, and this is really a unique facility. If something went wrong for you along the way, you can [download a commented version of the final result here](#).

Driving models by motion capture marker trajectories

One very common use of kinematic measures is to impose a measured movement on a model. The measurement can for instance be in terms of optical marker trajectories or joint angles measured by goniometers. In this tutorial we shall focus on optical markers.

Marker trajectories are recorded by a motion capture (MOCAP) system. It comprises multiple synchronized video cameras observing a set of spherical markers attached to a moving body and software to compute the marker coordinates in space by triangulation of the simultaneous pictures recorded by the cameras. Different types of MOCAP systems produce output on different formats. AnyBody needs to read the marker trajectories from text files on the following format:

Time	x	y	z
0.000000000000	0.84147098599	-0.54030230550	0.000000000000
0.00100100100	0.84142823805	-0.54036887714	0.000000000000
0.00200200200	0.84129997953	-0.54056856433	0.000000000000
0.00300300300	0.84108613608	-0.54090127577	0.000000000000
0.00400400400	0.84078658373	-0.54136685730	0.000000000000
0.00500500500	0.84040114917	-0.54196509307	0.000000000000
0.00600600600	0.83992961007	-0.54269570542	0.000000000000
0.00700700700	0.83937169543	-0.54355835492	0.000000000000
0.00800800800	0.83872708599	-0.54455264021	0.000000000000

```

0.00900900900 0.83799541478 -0.54567809793 0.00000000000
0.01001001000 0.83717626771 -0.54693420265 0.00000000000
0.01101101100 0.83626918423 -0.54832036673 0.00000000000
0.01201201200 0.83527365810 -0.54983594020 0.00000000000
0.01301301300 0.83418913820 -0.55148021065 0.00000000000
0.01401401400 0.83301408734 -0.55325177839 0.00000000000
0.01501501500 0.83174961018 -0.55515095782 0.00000000000
0.01601601600 0.83039421700 -0.55717631355 0.00000000000
0.01701701700 0.82894718724 -0.55932688186 0.00000000000
0.01801801800 0.82740776078 -0.56160163587 0.00000000000
0.01901901900 0.82577513921 -0.56399948535 0.00000000000
0.02002002000 0.82404848719 -0.56651927660 0.00000000000

```

The first column is time, and the subsequent columns are values of a kinematic measure. In general you can have any number of columns, but in the case of marker trajectories the number of columns will be three, corresponding to the x, y and z coordinates of the marker through space. The columns are separated by spaces or tabs. The first line in the file is ignored if it does not contain numbers, so it can be used for a header as is shown here.

Driving a pendulum

We need a model to work on. Please download and save the file [mocap.any](#) in a working directory. Load the model into AnyBody and open a new model view. You should see a vertical segment with a point in each end. It is in fact a pendulum model linked to the global reference frame by a revolute joint at its upper end point. We use this example because it is very simple and has a remote similarity with a human limb.

The pendulum only has one single degree of freedom. Let us presume that we have conducted a MOCAP experiment that has tracked the movement of the end point of the pendulum and that we have saved the marker trajectories on the file [p1.txt](#). Please download the file and save it in the same directory as mocap.any.

The mocap.any model that you have downloaded cannot analyze because it is lacking a movement driver. We are going to use the MOCAP trajectory saved in p1.txt to drive the model. The straightforward way to do this would be to define a linear kinematic measure between the laboratory origin and the end point of the pendulum and subsequently drive this measure by the measured trajectory. Let us do precisely that. Place the cursor in the mocap.any file just below the Joint definition, click the Classes tab in the tree view on the left hand side of the editor window, locate the AnyKinLinear class, right-click it, and insert a class template:

```

AnyRevoluteJoint Joint = {
  AnyRefFrame &Ground = .GlobalRef;
  AnyRefFrame &Pendulum = .Pendulum.Origin;
};

AnyKinLinear <ObjectName>
{
  //Ref = -1;
  AnyRefFrame &<Insert name0> = <Insert object reference (or full object definition)>;
  //AnyRefFrame &<Insert name1> = <Insert object reference (or full object
definition)>;
};
}; // MyModel

```

Next we fill in the necessary information to point to the correct elements in the model:

```

AnyKinLinear P1Lin = {
  //Ref = -1;
  AnyRefFrame &LabOrigin = .GlobalRef;
  AnyRefFrame &P1 = .Pendulum.P1;
};

```

We now have a linear measure that is in fact a three-dimensional vector from the origin of the global reference frame to the end point of the pendulum. But so far we are only measuring the vector. The next step is to actually drive it by the measured trajectory. We do so by introducing an interpolation driver. Place the cursor right below the linear measure, go to the class tree, locate the AnyKinEqInterPolDriver class, and insert a class template in the model:

```
AnyKinLinear PlLin = {
  //Ref = -1;
  AnyRefFrame &LabOrigin = .GlobalRef;
  AnyRefFrame &P1 = .Pendulum.P1;
};

AnyKinEqInterPolDriver <ObjectName>
{
  //MeasureOrganizer = ;
  Type = ;
  //BsplineOrder = 4;
  //T = ;
  //Data = ;
  //FileName = "";
  //AnyKinMeasure &<Insert name0> = <Insert object reference
  (or full object definition)>; You can make any number of these objects!
};
```

The interpolation driver allows you to either type the vector of interpolated values directly into the AnyScript file, or to read the data off an external file. It would be very messy to have all the MOCAP'ed data directly in the AnyScript model, so we opt for reading them directly from the P1.any file. This is done by the following changes:

```
AnyKinEqInterPolDriver PlDriver = {
  Type = Bspline;
  BsplineOrder = 4;
  FileName = "P1.txt";
  //AnyKinMeasure &<Insert name0> = <Insert object reference
  (or full object definition)>; You can make any number of these objects!
};
```

Notice that we have selected a Bspline interpolation and that the order is set to 4. A Bspline is a smooth approximation of the data points, so AnyBody is converting the discrete measured values to a continuous interpolation function. The advantage of this is that you do not have to perform the analysis precisely at the sampled times in the MOCAP experiment. You can do more or less time steps exactly as you like.

The final step is to specify what the driver should drive, i.e. point at the linear measure we defined before:

```
AnyKinEqInterPolDriver PlDriver = {
  Type = Bspline;
  BsplineOrder = 4;
  FileName = "P1.txt";
  AnyKinMeasure &Lin = .PlLin;
};
```

The model now loads, but it also produces the following warning:

The model may be statically indeterminate. There are 8 reactions and only 6 rigid body degrees of freedom.

The message warns you that there are too many elements in the model that can provide reaction forces. In general, we MOCAP markers are just registering the positions in space. They do not provide any sort of

forces to realize this movement. So we need to switch the reaction forces of the new driver off like this:

```
AnyKinEqInterPolDriver P1Driver = {
  Type = Bspline;
  BsplineOrder = 4;
  FileName = "P1.txt";
  AnyKinMeasure &Lin = .P1Lin;
  Reaction.Type = {Off, Off, Off};
};
```

Try loading the model again and run the Kinematic Analysis (In this tutorial we do not use the inverse dynamic analysis). Most likely it will not work. You will get the following error message:

```
Model is kinematically over-constrained : Position analysis failed :
1 unsolvable constraint(s) found
```

The reason will be obvious if you instead run the ModelInformation operation. It produces a whole lot of output in the message window among which you find:

```
1) List of segments:
0: Main.MyModel.Pendulum
Total number of rigid-body d.o.f.: 6
-----
2) List of joints and kinematic constraints:
Joints:
0: Main.MyModel.Joint (5constr., 1coords.)
Total number of joint coordinates: 1
Drivers:
0: Main.MyModel.P1Driver (3constr.)
Other:
- none!
Total number of constraints:
Joints: 5
Drivers: 3
Other: 0
Total: 8
```

The model appears to have six degrees of freedom (one segment in space has six degrees of freedom) but eight kinematic constraints. Therefore, it is over-determinate. The reason for this problem is that the pendulum only has one degree of freedom when the constraints of the hinge have been subtracted, but we have added three drivers to it by means of the three coordinates of the linear measure. To solve this problem we need to select one of the three coordinates for driving and leave the other two coordinates to their own devices. This way we avoid driving more degrees of freedom than the model actually has. So, which one should we choose? Does it matter or is it enough that we have one driver for the one degree of freedom? Unfortunately it does indeed matter. The coordinate we choose to drive should be as descriptive as possible for the movement of the mechanism. Let us look at the first few lines of the P1.any file:

Time	x	y	z
0.00000000000	0.84147098599	-0.54030230550	0.00000000000
0.00100100100	0.84142823805	-0.54036887714	0.00000000000
0.00200200200	0.84129997953	-0.54056856433	0.00000000000

The movement is basically in two dimensions, so the z coordinate is constantly zero. This coordinate does not provide any information about the oscillating movement of the pendulum, so it cannot be used. The x and y directions will work ? perhaps ? but the x coordinate seems to be the better choice given the pendulum?s typical oscillating movement.

There are at least two ways to only drive the pendulum by the x coordinate. One is obvious and the other is smart. We shall begin with the obvious way for instructional purposes and switch to the smart way

afterwards. To directly drive just one coordinate we need a driver file with just one column of data in addition to the time column. Please download this version: [p1x.txt](#) and save it in the same directory as the other files of the model. Then make the following changes:

```
AnyKinEqInterPolDriver P1Driver = {
  Type = Bspline;
  BsplineOrder = 4;
  FileName = "P1x.txt";
  AnyKinMeasure &Lin = .P1Lin;
  MeasureOrganizer = {0};
  Reaction.Type = {Off};
};
```

The interpolation driver now uses the new file with just the x coordinates. The MeasureOrganizer is a property you can use to select the pertinent components of the kinematic measure you are driving. The measure returns an {x,y,z} vector, and MeasureOrganizer = {0} means that we are picking only the first component (number 0 because all numbers begin with zero in AnyBody) to drive. Finally, since we are only driving one coordinate, the Reaction.Type vector should now only have one component.

Load the model again, and run the kinematic analysis. You should now see it moving from side to side as you would expect a pendulum to do. So far so good!

Let us briefly review what we have learned so far:

- Models can be driven by MOCAP data
- You need to drive as many degrees of freedom as the model has ? no more and no less.
- You must choose the coordinates to drive carefully.

There are in fact more issues to consider and smarter ways to create the drivers, and these are the subjects of the next section.

Local and global coordinates

Before we begin, here's a link to a functioning model in case you had trouble with the preceding section: [mocap2.any](#).

We begin this section with a question: Will this also work if the oscillations are larger? We can try it very easily. Please download and save this file: [p2x.txt](#). Then make the following change:

```
AnyKinEqInterPolDriver P1Driver = {
  Type = Bspline;
  BsplineOrder = 4;
  FileName = "P2x.txt";
  AnyKinMeasure &Lin = .P1Lin;
  MeasureOrganizer = {0};
  Reaction.Type = {Off};
};
```

Run the kinematic analysis again. You will see the pendulum moving in a non-pendulum-like fashion. More precisely the pendulum makes an additional cycle at each end of its primary movement. This was not the movement that was motion captured, so the analysis is in fact wrong.

The reason for the problem is that the global x direction does not determine the movement very well when the pendulum is close to horizontal. Here, driving in the y direction would be much better.

The elegant solution to the problem is to change coordinate system of the driver. If the driver works in the pendulum coordinate system rather than the global coordinate system, then the x direction will be tangential

to the path of the pendulum regardless of which direction the pendulum has. But before we can make that shift, we shall implement the smart way of picking a degree of freedom to drive that we promised in the preceding section. The idea is based on definition of a new segment representing the MOCAP marker:

```
AnyKinEqInterPolDriver P1Driver = {
  Type = Bspline;
  BsplineOrder = 4;
  FileName = "P2x.txt";
  AnyKinMeasure &Lin = .P1Lin;
  MeasureOrganizer = {0};
  Reaction.Type = {Off};
};
AnySeg M1 = {
  Mass = 0;
  Jii = {0, 0, 0}/10;
};
```

The new segment has no mass and no rotational inertia. The first thing to do is to lock its rotation, and the most compact way of doing it is this:

```
AnySeg M1 = {
  Mass = 0;
  Jii = {0, 0, 0}/10;
};
AnyKinEq RotLock = {
  AnyKinRotational rot = {
    Type = RotAxesAngles;
    AnyRefFrame &ground = ..GlobalRef;
    AnyRefFrame &Marker = ..M1;
  };
};
```

Now the marker can only translate, and we shall drive it in all three translations by means of the original MOCAP'ed data:

```
AnyKinLinear M1Lin = {
  //Ref = -1;
  AnyRefFrame &LabOrigin = .GlobalRef;
  AnyRefFrame &M1 = .M1;
};
AnyKinEqInterPolDriver M1Driver = {
  Type = Bspline;
  BsplineOrder = 4;
  FileName = "P1.txt";
  AnyKinMeasure &Lin = .M1Lin;
  // MeasureOrganizer = {0};
  Reaction.Type = {On, On, On};
};
```

There are several things to notice here: We have created a new linear measure between the laboratory and the marker segment, M1. Then we have modified the interpolation driver pretty much back to what it was when we first defined it with the exception that it now drives M1 instead of the pendulum, and it does so using all three coordinates. Notice also that the reactions are on. This is because when we start making kinetic analysis, we cannot have a segment floating freely in the air with nothing to keep it in place.

Now all that is missing is to create a link between M1 and the pendulum:

```
AnyKinEqInterPolDriver M1Driver = {
```

```

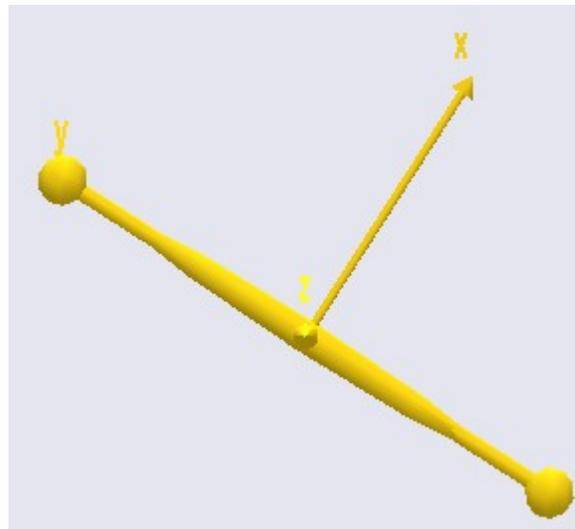
Type = Bspline;
BsplineOrder = 4;
FileName = "P1.txt";
AnyKinMeasure &Lin = .M1Lin;
//     MeasureOrganizer = {0};
Reaction.Type = {On, On, On};
};
AnyKinEq MarkerBodyConstraint = {
  AnyKinLinear lin = {
    AnyRefFrame &Marker = ..M1;
    AnyRefFrame &Body = ..Pendulum.P1;
  };
  MeasureOrganizer = {0};
};

```

This brings us exactly back to where we started. If you have done everything right, you now have a model that oscillates like it did at the end of the preceding section. So, why did we go to all that trouble for nothing? Well, the new approach has two advantages:

1. You do not have to edit columns out of the marker trajectory file if you only want to drive one degree of freedom. The degrees of freedom to drive are controlled by the link between the marker and the corresponding point on the body.
2. It allows you to drive the body using local instead of global coordinates.

The second advantage is what will justify the trouble of setting the system up; it is going to allow us to drive the pendulum correctly also for larger displacements. As the picture indicates, the pendulum has its own local reference frame that moves with it. As you can see in the figure, this reference frame has its x axis perpendicular to the length axis of the pendulum and therefore directed along the movement, no matter which position the pendulum has. So, even when the pendulum has large oscillations, the local x direction remains a good direction for driving the pendulum.



Let us try to do precisely that. Please download and save this file in the same directory as the model: [P2.txt](#). Then make the following change:

```

AnyKinEqInterPolDriver M1Driver = {
  Type = Bspline;
  BsplineOrder = 4;
  FileName = "P2.txt";
  AnyKinMeasure &Lin = .M1Lin;

```

```
//      MeasureOrganizer = {0};
Reaction.Type = {On, On, On};
};
```

The model now uses the new P2.txt file containing all three coordinates to drive the movement. If you reload the model by pressing F7 and re-run the kinematic analysis, then you should see the same erroneous pendulum movement as before. So, here comes the trick: We are going to switch the constraint between the marker and the pendulum to work in the pendulum's local coordinate system:

```
AnyKinEq MarkerBodyConstraint = {
  AnyKinLinear lin = {
    AnyRefFrame &Marker = ..M1;
    AnyRefFrame &Body = ..Pendulum.P1;
    Ref = 1;
  };
  MeasureOrganizer = {0};
};
```

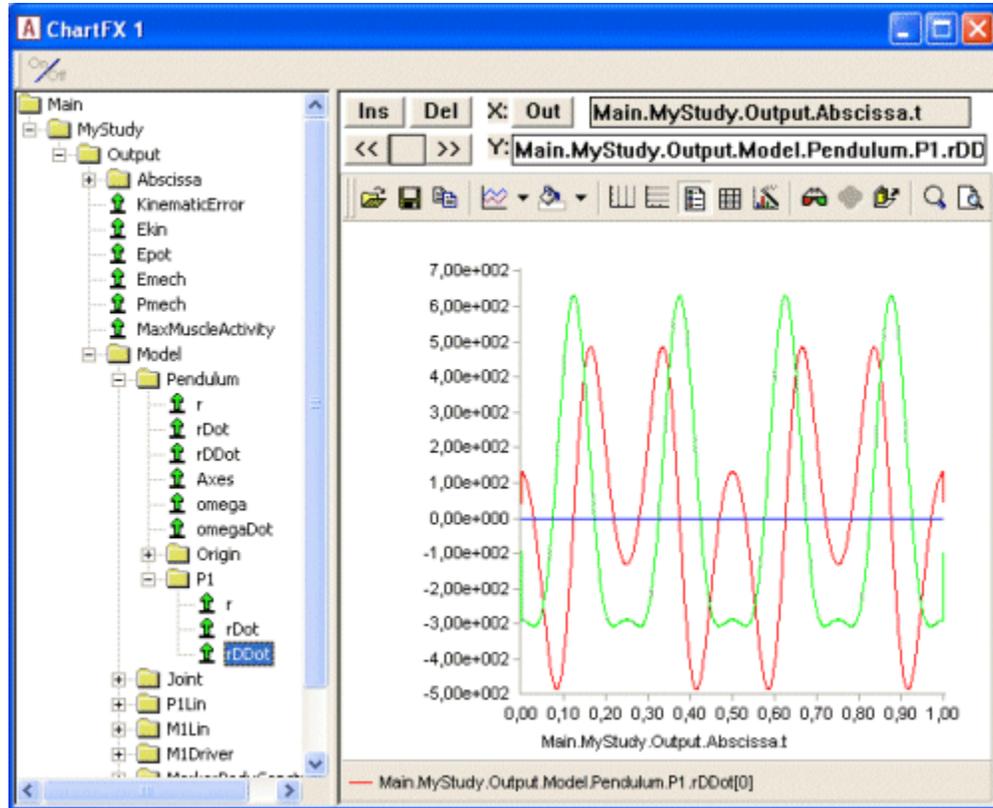
This is a very simple little trick. The line `Ref = 1` simply states that the linear measure between the marker and the pendulum point should be measured in the local coordinate system of the pendulum. Every linear measure has a `Ref` specification. If you do not set it explicitly, the system initiates `Ref` to -1, which means the global reference frame. After the global reference frame, the reference frames of the measure components are listed in numerical order starting from zero. Since `M1` is the first measure component, its reference frame would be numbered zero. So `Ref = 0` would refer the linear measure to the marker coordinate system. `Pendulum.P1` is the second component and is therefore numbered 1. Please load the model again (F7) and re-run the kinematic analysis (F5). The movement should now be correct. Please notice that even though we are driving in the local pendulum coordinate system we did not have to make any manual conversion of the MOCAP marker data. The MOCAP marker is still driven in the global laboratory coordinate system. It is only the measure between the marker and the body that has been converted to local coordinates, and this is handled automatically by `AnyBody` when you make the switch of reference, `Ref = 1`, to the local system.

The extremities of living creatures work much like the pendulum we have studied here in the sense that they twist and turn in the global reference frame making it tricky to drive the segments in global coordinates. Therefore it is usually a major advantage to drive models with MOCAP data using local reference frames.

If you have trouble getting the model to work, then you can download a workable copy here: [mocap3.any](#). The topic of the next lesson is noise and accuracy, which is a major pitfall of driving models by MOCAP data.

Noise and accuracy

Nothing man-made is completely perfect and this also goes for experimental data. Motion capture data is infested with a range of different errors such as soft tissue artifacts, marker placement inaccuracy and random noise. The data we have used so far is very accurate because it has been manufactured artificially and stored with 10 decimals in the marker trajectory files we have used. So if we plot the accelerations of the pendulum marker point, we get the following nice set of curves:

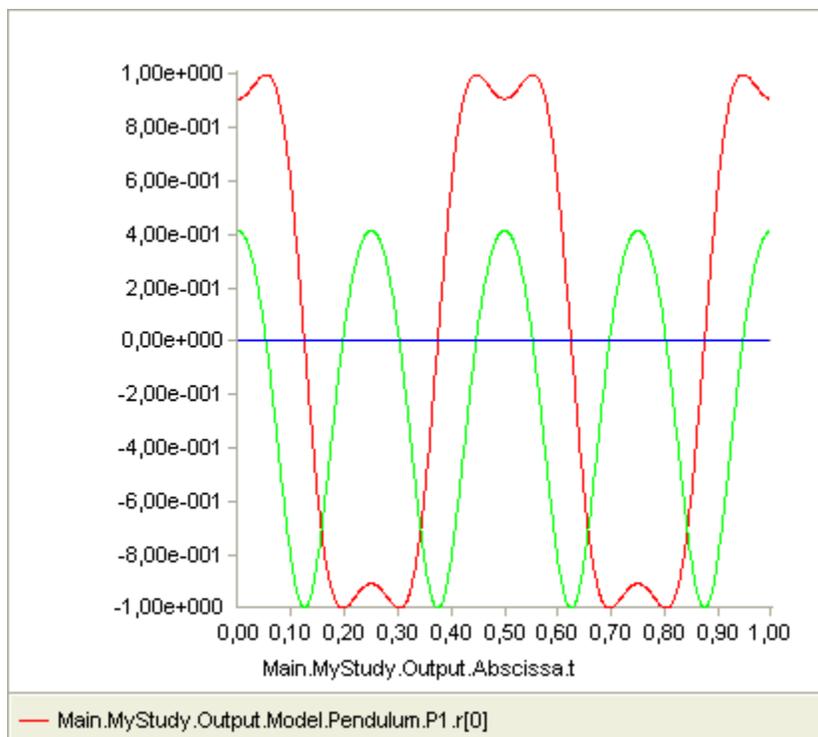


Notice that the accelerations are between approximately -500 and 600.

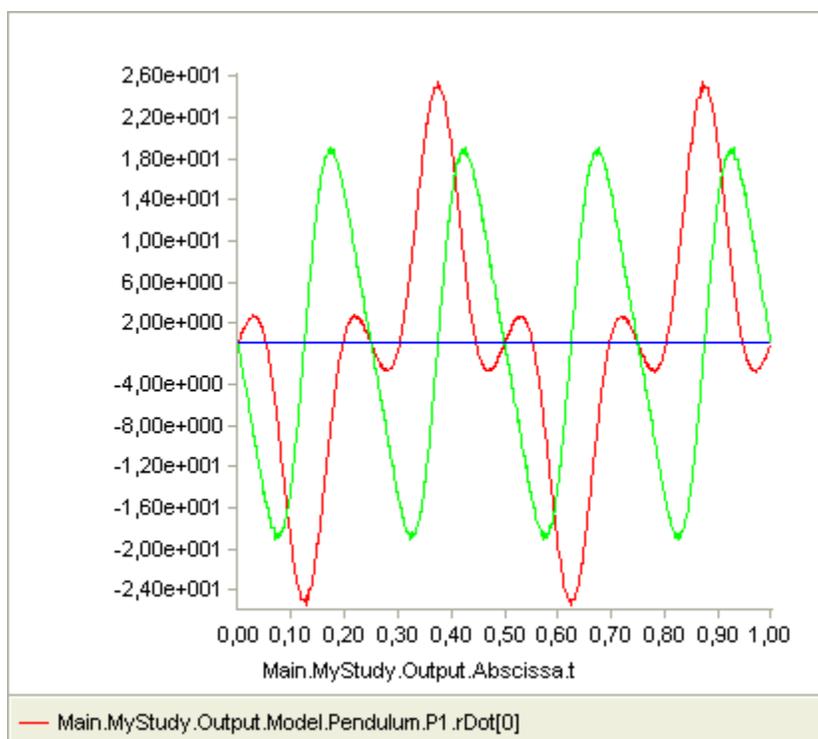
Now, let us introduce some random noise. An easy way to do so is to simply truncate the decimals off the columns in the marker trajectory file. Please download this file, where the numbers only have three decimals: [P2trunc.txt](#). Then make the following change in the model:

```
AnyKinEqInterPolDriver M1Driver = {
  Type = Bspline;
  BsplineOrder = 4;
  FileName = "P2trunc.txt";
  AnyKinMeasure &Lin = .M1Lin;
  // MeasureOrganizer = {0};
  Reaction.Type = {On, On, On};
};
```

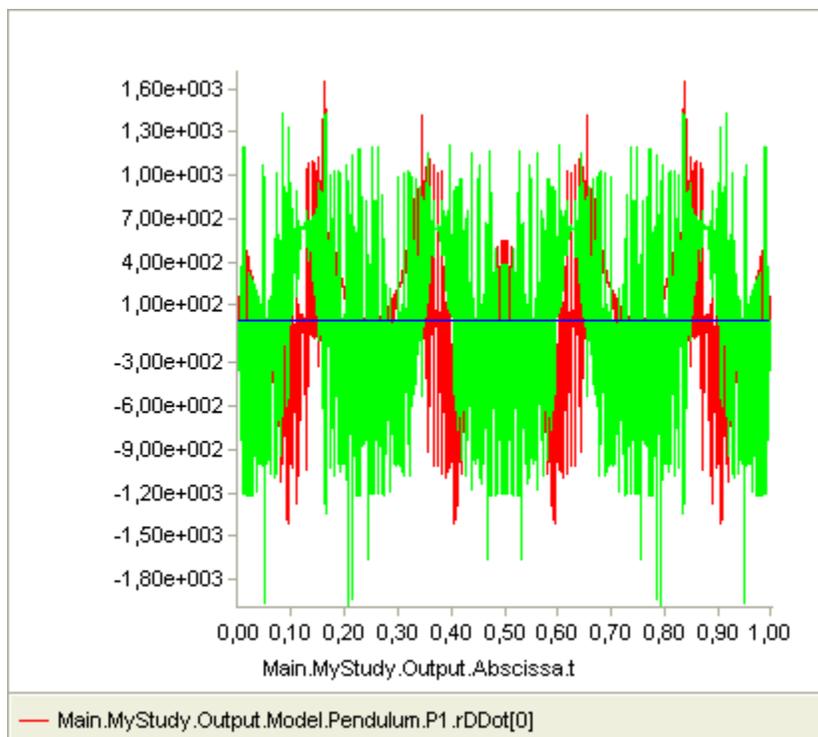
Please reload (F7) the model and re-run (F5) the kinematic analysis. The pendulum appears to move as it did before. If we investigate the positions of the driven point, then we get the following:



This appears to work very nicely. Plotting velocities produces this nice result:



Still, there is not much indication that anything might be wrong with the result, except perhaps a tiny hint of visible noise near the turning points of the graphs. Finally, let us study the accelerations:



Oops, something appears to have gone completely wrong here. The accelerations are noisy and several times larger than before. What could be the problem? The problem is actually, that the tiny amount of random noise we introduced by truncating some of the decimals from the marker trajectory gets amplified by an order of magnitude for each differentiation. The noise is indistinguishable on the position, hardly detectable on the velocities, but very large on the accelerations. This is a significant problem because the inertia forces in a mechanical system depend on the accelerations, so the noise will completely dominate the computation of forces in the system.

AnyBody interpolates the data by a smooth spline interpolation, and it is actually possible to dampen the noise somewhat by increasing the order of the spline interpolation and/or downsampling the data. Especially the latter is a good choice because most MOCAP systems sample at a much higher frequency than necessary for most movements. However, the best way to solve the problem is to low pass filter the data before sending them to AnyBody and making sure that the data is stored in the text file with as many decimals as possible. This will get rid of most of the high frequency noise in the MOCAP data. Furthermore, whenever a model is driven by MCOAP data it is advisable to check that accelerations are not oscillating more than expected and that accelerations of body parts are not higher than expected. Distal body parts are likely to sustain more acceleration than proximal parts.

The last lesson in the tutorial on mechanical elements is [Lesson 5: Forces](#).

Lesson 5: Forces

There are several types of forces in an AnyBody model; forces in joints, forces in muscles, and gravity forces working on the segments. This section, however, deals only with the application of external forces. The following two examples illustrate many of the feature.

1. [Demo.Forces.any](#)
2. [Demo.AnyForce.any](#)

The first example is a rather basic application of time-varying forces to the well-known 2-D arm model. The example shows forces defined directly as a mathematical function of time and forces interpolated between a set of measured values.

The second example illustrates the difference between locally and globally defined forces and how forces acting on a segment can be summed up.

Advanced script features

AnyScript is a powerful programming language designed particularly to make life easy for body modelers. Generality and versatility, however, often come at the cost of complexity, and there are some advanced topics you must grasp to fully realize the potential of the language. This section presents some of those topics.

This tutorial consists of the following lessons:

- [Lesson 1: Using References](#)
- [Lesson 2: Using Include Files](#)
- [Lesson 3: Mathematical Expressions](#)

We shall begin with [Lesson 1: Using references](#).

Lesson 1: Using References

AnyScript is really a programming language, and just like any other programming language you can define variables and assign values to them. For instance, you may write

```
AnyVar a = 10.0;
AnyVar b = a;
```

Folders are also variables, and a folder definition can go like this:

```
AnyFolder MyFolder = {
  // A whole lot of stuff inside
};
```

However, folders cannot be assigned like a and b above, so the following is illegal:

```
AnyFolder MyFolderCopy = MyFolder;
```

In general, you can only do direct assignment of value variables, i.e. variables containing numbers or collection of numbers. This assignment is allowed:

```
AnyVector aa = {1,2,3};
AnyVector bb = aa;
```

But folder assignments are not allowed. So how can you refer to large portions of the model in just one assignment operation? The answer is that you can refer by reference, and just about any assignment between variables of compatible type will work:

```
AnyFolder &MyFolderCopy = MyFolder;
```

The ampersand, '&', in front of the variable name specifies that this is a reference. What it means that MyFolderCopy will just point to MyFolder, so whatever you do to MyFolderCopy will happen to MyFolder. It is as simple as that. A pointer variable takes up very little space in the computer because it does not copy the data it is pointing to.

This demo example illustrates some of the important uses of pointer variables:
[creatingandreferringtoobjects.any](#)

Now, let's continue to [Lesson 2: Using Include Files](#).

Lesson 2: Using Include Files

If you have any sort of experience with C or C++ programming, then the concept of include files will be very familiar to you. The idea behind include files is very simple: You divide one long file into several smaller ones. This is primarily useful, if the division into smaller files is based on some logical principle. Simple as it may be, it enables some pretty neat model structures that can really help your work.

Usually, the structure of files in a model is such that one file is the main file (containing the Main folder), and the main file contains statements to include other files. An include file can include other files and so on.

Consider, for instance, the case of one very large AnyScript model. If you have the model in a single .any file, then it may be difficult to locate a particular muscle or another element that you are looking for. Instead, you could choose to put all the muscle definitions into a separate file. At the position in the main file where you removed the muscle information, you simply add a statement to include the new muscle file called muscles.any. The statement could look like this:

```
#include "muscles.any"
```

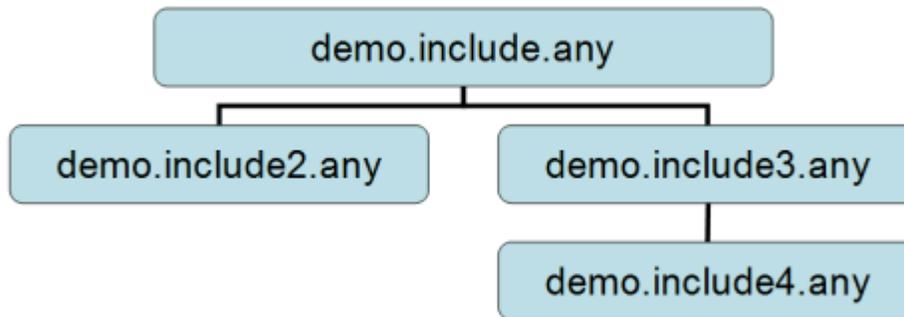
Notice the leading # symbol. It signifies that this is a macro statement, and it is the only type of statement in AnyScript that does not require a semicolon in the end. This is because the statement is not formally a part of the AnyScript language. It is something that is processed before the actual model is parsed.

When the system loads the model and reaches the include statement, it simply reads the include file, and subsequently continues reading the main file. It is a very simple principle, but it does have some interesting implications:

- You can divide large models into smaller and more manageable chunks
- You can create blocks of data that are easy to re-use in your model. Simply put the data in a file and include that same file several times at different positions in your the main file. For instance, if you have modeled two arms, you might want to use the same set of muscles for both of them. In that case, create one file containing the muscles and include it twice.
- You can create libraries of files containing elements you often use in your modeling tasks, and when you build a new model much of the work is accomplished simply by including the files you have made previously. It is much like constructing models from larger building blocks.

The principle of include files is demonstrated in the following four interconnected files:

- [demo.include.any](#) (the main file)
- [demo.include2.any](#)
- [demo.include3.any](#)
- [demo.include4.any](#)



Right-click the files and save them in a directory of your choice. Then start AnyBody and load the main file, demo.include.any.

Next up is [Lesson 3: Mathematical Expressions](#).

Lesson 3: Mathematical Expressions

One of the definite advantages of a modeling language like AnyScript is that mathematical expressions become a natural element in model construction. By means of mathematical expressions in models you can make the model parametric, enable scaling in various ways, and create dependencies between elements.

In AnyScript you can in principle write a mathematical expression involving variables and references to other objects and to time anywhere in an object definition where you would otherwise use a number. Furthermore, AnyScript handles scalar numbers, vectors, matrices, and in fact tensors of arbitrary dimensions.

Unlike most programming languages, definition sequence does not have any significance in an AnyScript model. This means that variables can refer to other variables that are created further down in the model like this:

```
AnyVar b = a;
AnyVar a = 10;
```

Instead of the sequence of **definition**, AnyScript variables depend on the sequence of **evaluation**. Some expressions can be evaluated when the model is loaded, while others have to wait for certain operations to complete. For instance, a muscle force is not known until an InverseDynamicAnalysis operation is performed. The system keeps track of when everything is evaluated and will complain if you try to use a variable prematurely.

For instance, kinematic analysis is the first step of an inverse dynamic analysis, so you can make an external force or a muscle strength depend on a position. This is because forces and muscles strengths are not used until after the kinematic analysis when the positions have been evaluated. However, you cannot make a position depend on a muscle force because muscle forces are always computed after positions.

Much of the capability of the mathematical expressions is demonstrated in the example [Demo.MathExpressions.any](#).

Building block tutorial

Developing accurate models of the human body is an enormous task, and it is not something each user can do from scratch. We all have to rely on models other people have made, and if we keep improving and

exchanging them, we shall end up with a very good supply of models that fit most purposes. [The AnyBody Model Repository](#) is an attempt to provide such a library.

These are some of the tasks you will want to accomplish with predefined models:

- To change the model pieces to fit your own purposes - preferably without tampering with the interior workings of the parts you are using.
- To be able to combine existing body parts to larger models.
- To be able to attach the parts you can find to model bits you construct yourself.

All this can be done very elegantly in the AnyScript language provided you keep it in mind when you construct your models. The AnyBody Model Repository is constructed that way, and it contains numerous examples of the technique. In short, it uses the following elements of the language to make it happen:

1. Include files
2. Parameters
3. Equipping parts with their own interfaces

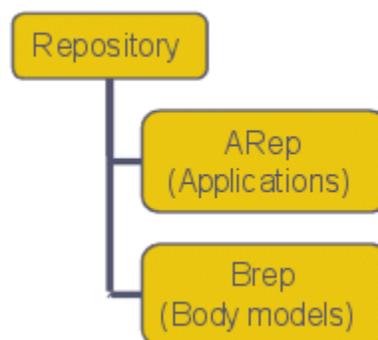
While there are many different ways models could be constructed to obtain the modularity we are looking for, the AnyScript Model Repository represents one very well-structured solution, and AnyBody Technology strongly recommends following the structure of this library when new models are developed.

The Repository Model Structure

The model repository is really not a part of the AnyBody Modeling System. It is a library of models that scientists and other advanced users have developed and made available in the public domain. The AnyBody Modeling System does not require you to structure your models in any particular way. But it is much easier to manage large models if you divide them into logical parts, and if you follow the structure of the Repository, then you can use the body parts in the Repository for your own models.

So this tutorial is an introduction to the Model Repository structure as well as a case in point of how models can be organized and interfaced with each other in general.

The Repository has its files structured into two main groups:



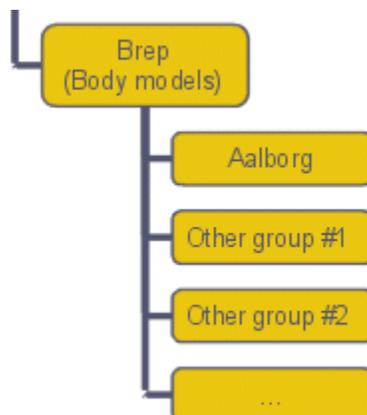
ARep stands for "Application Repository", and it contains the various devices, environments and working situations you may want to hook the body up to. An application could be a model lifting a box, walking, or riding a bicycle. This means that the ARep branch is where you can find the main files of models you can analyze, i.e. the files you actually load into the AnyBody Modeling System. You will know them because they have "Main" in their names: <application name>.Main.any.

BRep is short for "Body Repository", and it contains AnyScript models of the body with no attachments and no specification of movement, forces, or supports. The entire body model contains many hundred muscles

and it is rather heavy computationally. For this reason the BRep directory is structured to enable the user to link applications to subsets of the body model such as the lower extremities or the shoulder model.

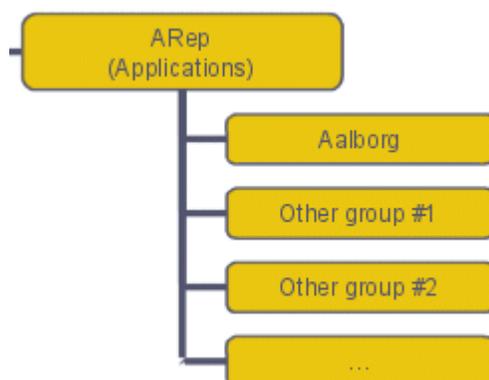
The idea behind the division into ARep and BRep is that each user wants to model the human body in a special situation. This can take place in the ARep branch with references to the BRep branch but without tampering with the more delicate BRep parts at all.

Let us stay with the BRep branch for just a moment. The initial models were created by the [AnyBody Research Group](#) from Aalborg, Denmark, but from a rather early stage in the development, other groups of model developers chipped in. So the BRep branch is divided into separate parts where each group of developers can keep their own models:

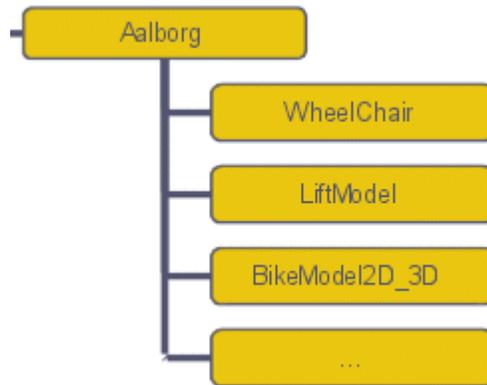


When you develop an application you can choose to link to whatever body model is your favorite or even choose to generate your own. You may also copy the models of another group into a separate directory and introduce the changes you favor into it.

Body modeling is challenging because so much data is involved, so most users will - at least initially - prefer to link to the body models that are already in the BRep branch. This means that the user will create an application in the ARep directory that links to a number of model parts in the BRep directory. The ARep directory is structured pretty much like the BRep branch:



Within each of the subdirectories in ARep you will find the different applications that each group has developed, for instance:



You can find more information on the structuring of the individual body part files in the [Structure lesson](#).

In the rest of this tutorial we shall consider the situation where a new application is to be built using body parts from the Aalborg branch of the BRep. We shall do so using three different strategies of increasing complexity:

1. When an existing application is similar enough to what you want to do to form the basis of the new application.
2. When a new application is constructed using a set of conveniently organized body parts called body collections.
3. When no existing application is similar to the new application and the new application requires a non-typical collection of body parts.

This tutorial is based on version 6.1 of the AnyScript model repository. Please notice that the repository models are subject to frequent updates and that a newer, better, and possibly slightly incompatible version may be available from the homepage of the [AnyBody Research Project](#). Also the demo models provided in the AnyBody Modeling System may be updated compared to the version used here. To make sure that you have a compatible version for this tutorial, please begin by downloading a repository here: [Repository.6.1.BlockTutorial.zip](#) (15 MB). As the name indicates, it is a zip file which must be unpacked preserving its directory structure to some working directory of your local hard disk.

With that done, [please proceed to lesson 1: Modification of an existing application](#).

Lesson 1: Modification of an existing application



The ARep branch of the repository contains a large amount of applications where different collections of body parts are hooked up to more or less complicated environments. Some of these environments may be extremely simple, such as a floor to stand on, while others may be mechanisms in their own right such as wheel chairs or bicycles with complicated crank mechanisms. In the vast majority of cases, the easiest way to develop a new application is to find a similar existing application, copy it, and modify it to suit your purpose. This is what we shall do in this initial lesson of the building block tutorial.

The standing model

The Aalborg branch of the ARep part of the repository contains a number of versions of standing models. These models are useful as starting points for many applications comprising the entire body. In the following we shall perform two modifications of a static standing model that will transform it to a dynamic model operating a hand-driven pump.

The first step is to go to ARep/Aalborg and locate the directory called StandingModel. Make a copy of the directory and rename the copy to HandPump (or HandPumpTutorial. If you are working on the full version of the repository, there might be a HandPump model already. This model originates from the from this tutorial). Then go into the new HandPump directory, locate the file named StandingModel.Main.any and rename it to HandPump.Main.any. Then double-click the HandPump.main.any file to open it in the AnyBody Modeling System, and we are ready to go.

Before starting to modify the model, time may be invested well in familiarization with its basic structure. The standing model was originally created as an AnyBody-parallel to so-called digital manikins. It is a model whose posture is controlled by a set of anatomical joint angles specified in the file mannequin.any. If you browse down a little bit into the main file you will come to the following section:

```

//This file contains joint angles which are used at load time
// for setting the initial positions
#include "Mannequin.any"

// This file contains the exact same joint variables as the mannequin
// file but their values are obtained from the model
// once the kinematic analysis has been done
#include "MannequinValuesFromModel.any"

AnyFolder ModelEnvironmentConnection = {
  #include "JointsAndDrivers.any"
  //This file will read values in the "Mannequin.any" file and calculate the Axes
  //matrices for the segments in the model
  #include "InitialPositions.any"
};

```

Double-clicking the line with "Mannequin.any" will open up the mannequin file. The first part looks like this:

```

AnyFolder Mannequin = {

  AnyFolder Posture = {
    //This controls the position of the pelvi wrt. to the global reference frame
    AnyVar PelvisPosX=0.046;
    AnyVar PelvisPosY=1.16;
    AnyVar PelvisPosZ=0;
    //This controls the rotation of the pelvis wrt. to the global reference frame
    AnyVar PelvisRotX=0;
    AnyVar PelvisRotY=0;
    AnyVar PelvisRotZ=0;

    // These variables control the rotation of the thorax wrt the
    // pelvis
    AnyVar PelvisThoraxFlexion=0;
    AnyVar PelvisThoraxLateralBending=0;
    AnyVar PelvisThoraxRotation=0;

    AnyVar NeckExtension=0;

    AnyFolder Right = {
      //Arm
      AnyVar SternoClavicularProtraction=-23; //This value is not used for initial
position
      AnyVar SternoClavicularElevation=11.5; //This value is not used for initial
position
      AnyVar SternoClavicularAxialRotation=-20; //This value is not used for initial
position

      AnyVar GlenohumeralFlexion =-0;
      AnyVar GlenohumeralAbduction = 30;
      AnyVar GlenohumeralExternalRotation = 0;

      AnyVar ElbowFlexion = 0.01;
      AnyVar ElbowPronation = 10.0;

      AnyVar WristFlexion =0;
      AnyVar WristAbduction =0;

      AnyVar HipFlexion = 0.0;
      AnyVar HipAbduction = 5.0;
      AnyVar HipExternalRotation = 0.0;

      AnyVar KneeFlexion = 0.0;

```

```

    AnyVar AnklePlantarFlexion =0.0;
    AnyVar AnkleEversion =0.0;
};

AnyFolder Left = {

```

This first section of the mannequin file contains the folder Posture of which you can only see a subset in the code above. The posture folder lets you specify anatomical joint angles in degrees, and when you subsequently load and run the model it will assume the posture you have specified. The bottom part of the the mannequin file contains this folder:

```

AnyFolder Load = {
    AnyVec3 TopVertebra = {0.000, 0.000, 0.000};

    AnyFolder Right = {
        AnyVec3 Shoulder = {0.000, 0.000, 0.000};
        AnyVec3 Elbow = {0.000, 0.000, 0.000};
        AnyVec3 Hand = {0.000, 0.000, 0.000};
        AnyVec3 Hip = {0.000, 0.000, 0.000};
        AnyVec3 Knee = {0.000, 0.000, 0.000};
        AnyVec3 Ankle = {0.000, 0.000, 0.000};
    };
    AnyFolder Left = {
        AnyVec3 Shoulder = {0.000, 0.000, 0.000};
        AnyVec3 Elbow = {0.000, 0.000, 0.000};
        AnyVec3 Hand = {0.000, 0.000, 0.000};
        AnyVec3 Hip = {0.000, 0.000, 0.000};
        AnyVec3 Knee = {0.000, 0.000, 0.000};
        AnyVec3 Ankle = {0.000, 0.000, 0.000};
    };
}; // Loads

```

This is a set of three dimensional vectors that allow you to apply external loads to various predefined points on the model.

The model has an additional feature concerning its posture control: The ankle angle values in the mannequin.any file are not used. The reason is that the model contains a balancing condition that requires it to keep its total center of mass directly above the global z axis on which the ankle points are also placed. To enable the model to accommodate the balance condition it must have some degree of freedom to adjust the center of mass, and this is done via the ankle joints.

With these basic properties of the model in mind, let us proceed to [Lesson 2](#) in which we shall give the model something to hold on to.

Lesson 2: Adding a segment

The first step of building the hand pump model is to add a segment which will eventually become the hand wheel driving the pump. Start by opening the HandPump.Main.any file in AnyBody. In the main file you can toggle between different versions of the body model and it can be advantageous to select a light version. This will allow us to get the model up and running without spending a lot of time on reloads. A bit down in the main file you will find the following:

```

AnyFolder HumanModel={

    //This model should be used when playing around with the model in the
    //initial modelling phase since leaving the normal muscles out, makes the
    //model run much faster. The model uses artificial muscles on each dof. in
    //the joints which makes it possible also to run the inverse analysis.

```

```

#include "../.../BRep/Aalborg/BodyModels/FullBodyModel/BodyModel_NoMuscles.any"

//This model uses the simple constant force muscles
//#include "../.../BRep/Aalborg/BodyModels/FullBodyModel/BodyModel.any"

//This model uses the simple constant force muscles for shoulder-arm and spine
//but the 3 element hill type model for the legs
//Remember to calibratate the legs before running the inversae analysis
//This is done by pressing Main.Bike3D.Model.humanModel.CalibrationSequence in the
//operationtree(lower left corner of screen)
//#include "../.../BRep/Aalborg/BodyModels/FullBodyModel/BodyModel_Mus3E.any"

```

Make sure that the first of the three red lines is active and the two latter are inactive, i.e. they have double slashes in front of them. Then load the model by pressing F7.

Before we add the wheel segment, let us spend just a few moments considering where to place it. The file structure of the application looks like this:



These files are organized according to the principle that the model is divided into three parts:

1. The model parts concerned with the human body. These are imported from the BRep part of the repository.
2. The model parts concerned with the environment. These are the parts that are modeled bottom-up for each new application.
3. A section connecting the body parts to the environment.

The wheel we are about to add is not a part of the human body. It logically belongs to the model's environment, and these parts are defined in the Environment.any file. Please open Environment.any:

```

AnyFolder EnvironmentModel = {

  /* *****
  This folder contains the definition of the Environment
  - GlobalRefFrame
  ***** */

  AnyFixedRefFrame GlobalRef = {
    #include "drawcoorsystem.any"
  }; //GlobalRef
};

```

As you can see, it is extremely simple containing only a global reference frame, which in this model plays the role of a floor to stand on. We shall add a hand wheel to the model, but first we shall define a point on the global reference frame about which the hand wheel will eventually revolve:

```

AnyFolder EnvironmentModel = {
    /* *****
    This folder contains the definition of the Environment
    - GlobalRefFrame
    ***** */

    AnyFixedRefFrame GlobalRef = {
        #include "drawcoorsystem.any"

        AnyRefNode Hub = {
            sRel = {0.4, 1.4, 0.0};
            AnyDrawNode drw = {};
        };
    }; //GlobalRef
};

```

When you reload the model and open a Model View Window you will see that a point has appeared in the form of a little grey ball in front of the chest. The next step is to define the wheel:

Place the cursor just below the definition of GlobalRef. Go to the Class Tab in the left pane Editor Window; unfold the class list and find AnySeg. Right-click the class and insert a class template. You will obtain this:

```

AnyFixedRefFrame GlobalRef = {
    #include "drawcoorsystem.any"

    AnyRefNode Hub = {
        sRel = {0.4, 1.4, 0.0};
        AnyDrawNode drw = {};
    };
}; //GlobalRef

AnySeg <ObjectName>
{
    //r0 = {0, 0, 0};
    //rDot0 = {0, 0, 0};
    //Axes0 = {{0, 0, 0}, {0, 0, 0}, {0, 0, 0}};
    //omega0 = {0, 0, 0};
    Mass = 0;
    Jii = {0, 0, 0};
    //Jij = {0, 0, 0};
    //sCoM = {0, 0, 0};
};

```

We fill in the blanks and add a draw segment:

```

AnySeg Wheel = {
    r0 = .GlobalRef.Hub.sRel;
    Mass = 5;
    Jii = {0.003, 0.003, 0.3};
    AnyDrawSeg drw = {};
};

```

Notice that we have given the wheel mass properties that causes the draw segment to take on a wheel shape. We shall also add two points to the wheel that can subsequently function as handles:

```

AnySeg Wheel = {
    r0 = .GlobalRef.Hub.sRel;
    Mass = 5;

```

```

Jii = {0.003, 0.003, 0.3};
AnyRefNode rHandle = {
  sRel = {0.2, 0, 0.1};
};
AnyRefNode lHandle = {
  sRel = {-0.2, 0, -0.1};
};
AnyDrawSeg drw = {};
};

```

Next we fix the wheel segment to the hub node by means of a revolute joint (notice that every time a new object is inserted it can be done from the Classes tree):

```

AnySeg Wheel = {
  r0 = .GlobalRef.Hub.sRel;
  Mass = 5;
  Jii = {0.003, 0.003, 0.3};
  AnyRefNode rHandle = {
    sRel = {0.2, 0, 0.1};
  };
  AnyRefNode lHandle = {
    sRel = {-0.2, 0, -0.1};
  };
  AnyDrawSeg drw = {};
};

AnyRevoluteJoint WheelHub = {
  AnyRefFrame &Hub = .GlobalRef.Hub;
  AnyRefFrame &Wheel = .Wheel;
  Axis = z;
};

```

Finally, let us define a driver to make the wheel rotate:

```

AnyRevoluteJoint WheelHub = {
  AnyRefFrame &Hub = .GlobalRef.Hub;
  AnyRefFrame &Wheel = .Wheel;
  Axis = z;
};

AnyKinEqSimpleDriver WheelTurn = {
  AnyRevoluteJoint &Hub = .WheelHub;
  DriverVel = {-pi};
};

```

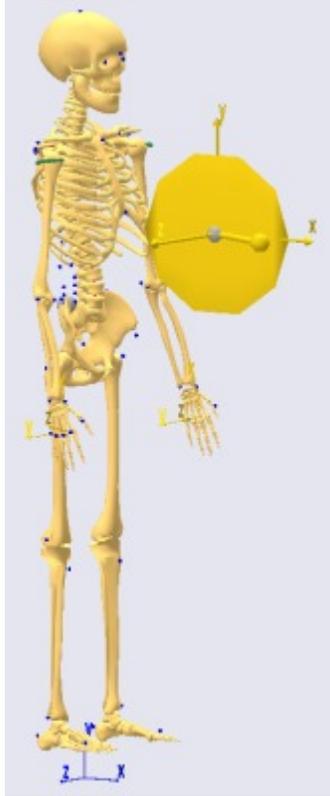
The model has now gone from being static to moving and to see it move we must increase the number of time steps in the model. This happens in the study section of the Main file:

```

AnyBodyStudy Study = {
  AnyFolder &Model = .Model;
  RecruitmentSolver = MinMaxSimplex;
  tEnd = 1.0;
  Gravity = {0.0, -9.81, 0.0};
  nStep = 10;
  MuscleEliminationTol = 1e-7;
}; // End of study

```

Please reload the model and run the kinematic analysis. You should see the wheel turning half a round.



Here's some emergency help if you are having problems making the model work: [HandPump.2.zip](#) contains the three modified files from this lesson.

The next step is to hook the hands up to the handles and get the arms moving [in Lesson 3: Kinematics](#).

Lesson 3: Kinematics

So far we have added a revolving segment - a hand wheel - to the standing model. In this lesson we shall deal with the kinematics in the sense that we are hooking the hand up to the handles on the wheel. This will make the arms move with the wheel as it turns and it is a convenient and simple way of realizing what would otherwise be a rather complex movement.

Before we begin it is worth noticing that we did a successful kinematic analysis at the end of the preceding lesson. This shows us that the model is kinematically determinate, so there is a balance between joint degrees of freedom and constraints in the model. So now that we wish to add constraints by hooking the hands up to the handles we must remove a similar number of the existing constraints. Otherwise the model will have redundant and mutually incompatible kinematic constraints and refuse to move or even assemble.

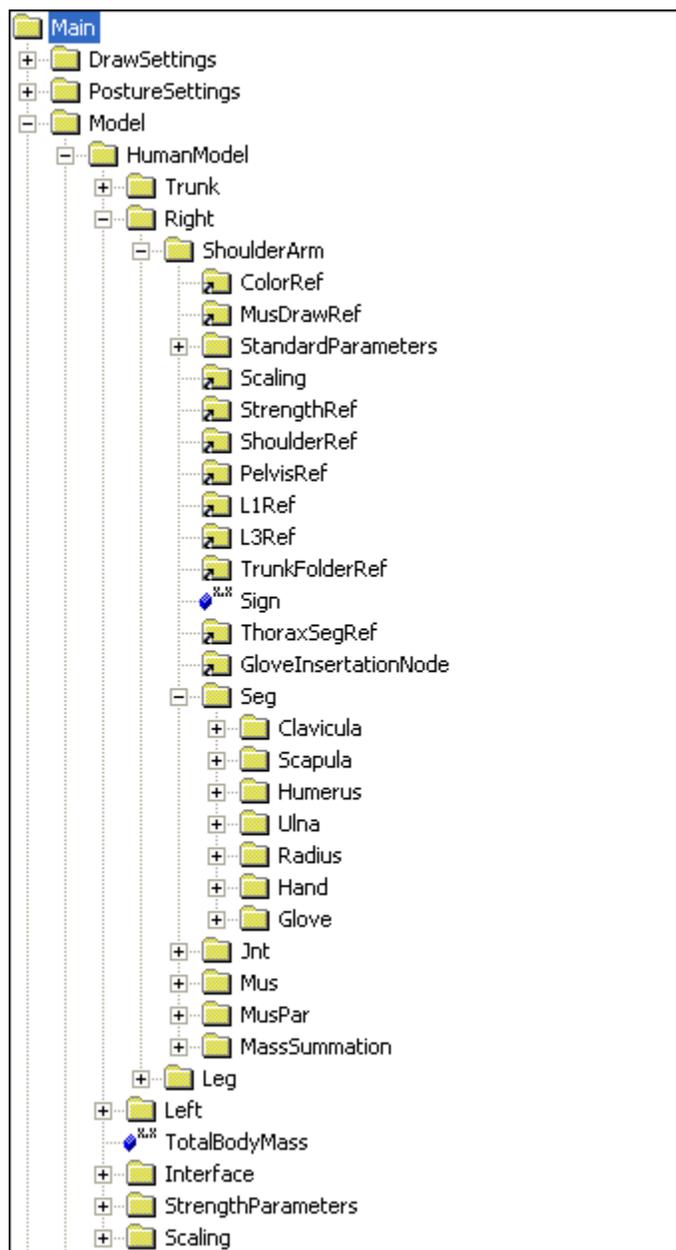
The model's arms are currently driven by:

- three joint angles in the shoulder (the gleno-humeral joint)
- one joint angle in the elbow
- one pronation angle of the forearm
- two joint angles in the wrist

If we attach a hand to a handle by a spherical joint we will be adding three constraints to the model, and we must correspondingly remove three of the constraints mentioned above. We cannot just remove three random constraints. For instance, we know that the model is going to have a variation of the elbow angle, so

we cannot leave the model with a specification of constant elbow angle. We also know that shoulder flexion and extension is going to vary through the movement. That will account for the second degree of freedom. Finally, when the elbow is flexed and the hand is holding on to the handle, shoulder internal and external rotation is impossible. So that constraint will also have to be removed.

Let us begin by defining the spherical joint between the right hand and the handle. If you unfold the model tree in the left-hand side of the editor window, then you can come obtain the following:



At the very bottom of this tree you find a glove segment as well as a hand. The glove is a remedy for the fact that we have a rigid hand in the model. Rigid segments are infinitely strong, and when you attach something very strong to the environment you can sometimes get unreasonable results. So we have added an extra glove segment to the hand. The connection between the hand and the glove has a finite strength that emulates the grip strength of a normal hand. This means that by attaching stuff to the glove rather than to the hand we eliminate the potential problem of the model abusing the strong hand.

The natural position of this joint would be in the jointsanddrivers.any file, because that is where we put the elements that connect the body to the environment. If you open this file you will see that it has a folder called Drivers that implements the joint angles specified in the mannequin file. But there is not a Joints folder. This is because the standing model does not have any actual joints with the environment. So we go to the top of the file and create a new folder for joints:

```
AnyFolder Joints = {
};

AnyFolder EnvironmentModel = {
```

We are going to make two spherical joints. The easiest way to do it is to create the first one with the object inserter and then copy it to make the second one. Place the cursor on the empty line between the two braces of the new Joints folder, pick the Classes tab, and unfold the class tree to locate the AnySphericalJoint. Right-click and insert a template:

```
AnyFolder Joints = {
  AnySphericalJoint <ObjectName>
  {
    AnyRefFrame &<Insert name0> = <Insert object reference (or full object
definition)>;
    AnyRefFrame &<Insert name1> = <Insert object reference (or full object
definition)>;
  };
};
```

We first define the necessary local names:

```
AnyFolder Joints = {
  AnySphericalJoint rhHandle = {
    AnyRefFrame &Glove = <Insert object reference (or full object definition)>;
    AnyRefFrame &Handle = <Insert object reference (or full object definition)>;
  };
};
```

The next step is to specify the two reference frames to be joined. In this case the two frames will be the glove of the right hand and the right handle. Both of these can be located in the object tree provided the model is loaded. Click the Model tab and expand the tree through the HumanModel, Right, an down to the Glove segment as shown in the figure above. Erase the <> and its contents on the right hand side of the equality sign, right-click the Glove segment in the tree, and insert the object name:

```
AnyFolder Joints = {
  AnySphericalJoint rhHandle = {
    AnyRefFrame &Glove = Main.Model.HumanModel.Right.ShoulderArm.Seg.Glove;
    AnyRefFrame &Handle = <Insert object reference (or full object definition)>;
  };
};
```

Similarly, locate the Handle node in the Wheel segment in the EnvironmentModel part of the tree and insert the name as the second reference frame:

```
AnyFolder Joints = {
  AnySphericalJoint rhHandle = {
    AnyRefFrame &Glove = Main.Model.HumanModel.Right.ShoulderArm.Seg.Glove;
    AnyRefFrame &Handle = Main.Model.EnvironmentModel.Wheel.rHandle;
  };
};
```

It is advisable when modifying models to make changes in small steps and verify that the model is working for each step. That way you can avoid agonies over mistakes that were made a long way upstream in the process. So, before we make the second connection between the left hand and the handle let us remove the now redundant constraints on the right arm and verify that it can move. We resolved in the introduction to this lesson to remove the joint drivers for elbow flexion, shoulder rotation, and shoulder flexion. We can find those drivers further down in the JointsAndDrivers file in this section:

```
// *****
// Drivers for the right arm
// *****

//Sterno clavicular joint driver
AnyKinEqSimpleDriver SCDriverRight ={
    AnyKinMeasureOrg &ref1
=..HumanModel.Interface.Right.SternoClavicularJointProtraction;
    AnyKinMeasureOrg &ref2
=..HumanModel.Interface.Right.SternoClavicularJointElevation;
    AnyKinMeasureOrg &ref3
=..HumanModel.Interface.Right.SternoClavicularJointAxialRotation;
    DriverPos = pi/180*{
        .JntPos.Right.SternoClavicularJointProtraction,
        .JntPos.Right.SternoClavicularJointElevation,
        .JntPos.Right.SternoClavicularJointAxialRotation
    };
    DriverVel = {0.0,0.0,0};
    Reaction.Type={Off,Off,Off};
};

//Glenohumeral joint
AnyKinEqSimpleDriver GHDriverRight={
    AnyKinMeasureOrg &ref1 =..HumanModel.Interface.Right.GlenohumeralAbduction;
    AnyKinMeasureOrg &ref2 =..HumanModel.Interface.Right.GlenohumeralFlexion;
    AnyKinMeasureOrg &ref3 =..HumanModel.Interface.Right.GlenohumeralExternalRotation;
    DriverPos=pi/180*{
        .JntPos.Right.GlenohumeralAbduction, //GH joint
        .JntPos.Right.GlenohumeralFlexion, //GH joint
        .JntPos.Right.GlenohumeralExternalRotation //GH joint
    };
    DriverVel = pi/180*{
        .JntVel.Right.GlenohumeralAbduction, //GH joint
        .JntVel.Right.GlenohumeralFlexion, //GH joint
        .JntVel.Right.GlenohumeralExternalRotation //GH joint
    };
    Reaction.Type={Off,Off,Off};
};

//Elbow flexion driver
AnyKinEqSimpleDriver ElbowFEDriverRight={
    AnyKinMeasureOrg &Elbow =..HumanModel.Interface.Right.ElbowFlexion;
    DriverPos=pi/180*{.JntPos.Right.ElbowFlexion};
    DriverVel = pi/180*{.JntVel.Right.ElbowFlexion};
    Reaction.Type={Off};
};
```

The elbow flexion driver is easy to remove simply by commenting it out. The glenohumeral driver has three separate degrees of freedom of which we can remove the flexion and the joint rotation. When we do so, we must remember to also remove their entries in the DriversPos, DriverVel and Reaction.Type specifications:

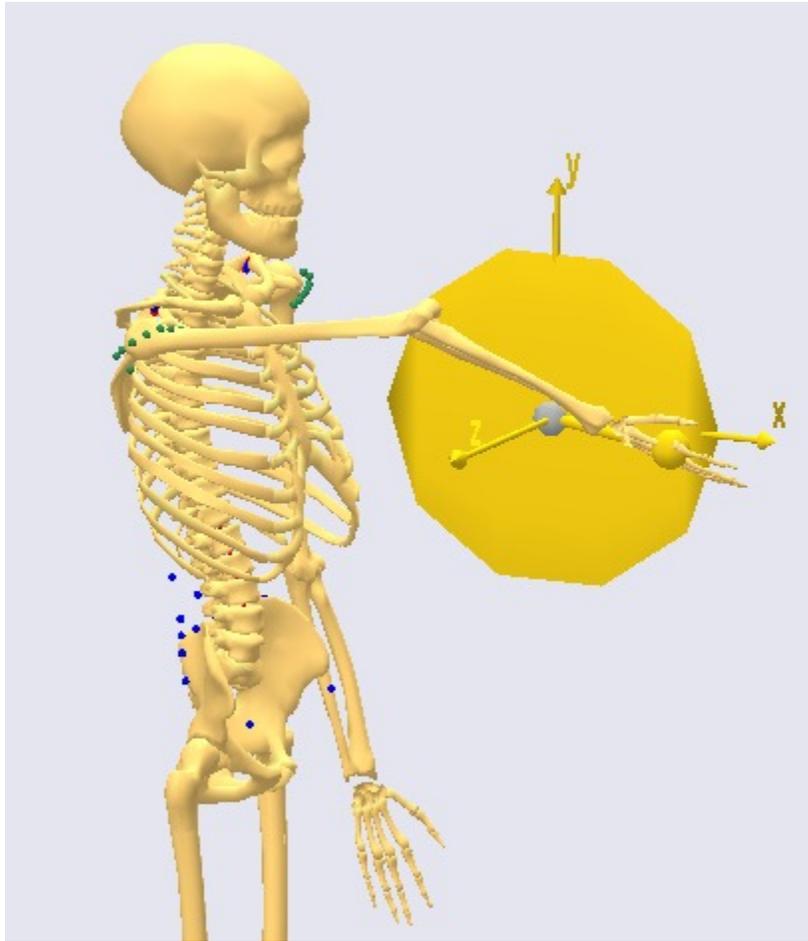
```
//Glenohumeral joint
AnyKinEqSimpleDriver GHDriverRight={
```

```

AnyKinMeasureOrg &ref1 =...HumanModel.Interface.Right.GlenohumeralAbduction;
// AnyKinMeasureOrg &ref2 =...HumanModel.Interface.Right.GlenohumeralFlexion;
// AnyKinMeasureOrg &ref3
=...HumanModel.Interface.Right.GlenohumeralExternalRotation;
// DriverPos=pi/180*{
// .JntPos.Right.GlenohumeralAbduction, //GH joint
// .JntPos.Right.GlenohumeralFlexion, //GH joint
// .JntPos.Right.GlenohumeralExternalRotation //GH joint
// };
// DriverVel = pi/180*{
// .JntVel.Right.GlenohumeralAbduction, //GH joint
// .JntVel.Right.GlenohumeralFlexion, //GH joint
// .JntVel.Right.GlenohumeralExternalRotation //GH joint
// };
// Reaction.Type={Off,Off,Off};
DriverVel={0};
Reaction.Type={Off};
};
//Elbow flexion driver
// AnyKinEqSimpleDriver ElbowFEDriverRight={
// AnyKinMeasureOrg &Elbow =...HumanModel.Interface.Right.ElbowFlexion;
// DriverPos=pi/180*{.JntPos.Right.ElbowFlexion};
// DriverVel = pi/180*{.JntVel.Right.ElbowFlexion};
// Reaction.Type={Off};
// };

```

Try reloading the model and run the SetInitialConditions operation. The operation may fail, or you may get a chocking result like this:



Ouch! How did that happen? Well, from a mechanical point-of-view, this solution is fully as good as the more anatomically compatible solution with the elbow bending the other way. Postures like this and failure to resolve the initial position can happen because the problem is nonlinear. This means that the solution (or lack thereof) depends on the starting position. So we must start the solution from a point that is closer to the result we want to get. This can be accomplished by imposing initial orientations on the segments. In hard-core AnyScript development this is done by means of the two segment properties `r0` and `Axes0`. However, the standing model on which this application is built conveniently controls the initial posture through the `mannequin.any` file. So we can make the necessary changes there:

```
AnyFolder Right = {
  //Arm
  AnyVar SternoClavicularJointProtraction=-23; //This value is not used for initial
position
  AnyVar SternoClavicularJointElevation=11.5; //This value is not used for initial
position
  AnyVar SternoClavicularJointAxialRotation=-20; //This value is not used for initial
position

  AnyVar GlenohumeralFlexion = 50;
  AnyVar GlenohumeralAbduction = 0;
  AnyVar GlenohumeralInternalRotation = 0;

  AnyVar ElbowFlexion = 40;
```

is set up to impose the same angles on the right and left hand sides. You can now run the KinematicAnalysis operation and see the model turning the wheel 180 degrees and the right arm following along. With that working, we can proceed to do exactly the same for the left arm. The first step is to add a joint, which we can copy from the one we just did for the right hand:

```
AnyFolder Joints = {
  AnySphericalJoint rhHandle = {
    AnyRefFrame &Glove = Main.Model.HumanModel.Right.ShoulderArm.Seg.Glove;
    AnyRefFrame &Handle = Main.Model.EnvironmentModel.Wheel.rHandle;
  };

  AnySphericalJoint lhHandle = {
    AnyRefFrame &Glove = Main.Model.HumanModel.Left.ShoulderArm.Seg.Glove;
    AnyRefFrame &Handle = Main.Model.EnvironmentModel.Wheel.lHandle;
  };
};
```

Notice the changes of 'Right' to 'Left' in the copy. The second step is to remove the redundant drivers on the left arm exactly as we did for the right arm:

```
//Glenohumeral joint driver
AnyKinEqSimpleDriver GHDriverLeft={
  AnyKinMeasureOrg &ref1 =...HumanModel.Interface.Left.GlenohumeralAbduction;
  // AnyKinMeasureOrg &ref2 =...HumanModel.Interface.Left.GlenohumeralFlexion;
  // AnyKinMeasureOrg &ref3
=...HumanModel.Interface.Left.GlenohumeralExternalRotation;
  // DriverPos=pi/180*{
  //   .JntPos.Left.GlenohumeralAbduction, //GH joint
  //   .JntPos.Left.GlenohumeralFlexion, //GH joint
  //   .JntPos.Left.GlenohumeralExternalRotation //GH joint
  // };
  // DriverVel = pi/180*{
  //   .JntVel.Left.GlenohumeralAbduction, //GH joint
  //   .JntVel.Left.GlenohumeralFlexion, //GH joint
  //   .JntVel.Left.GlenohumeralExternalRotation //GH joint
  // };
  // Reaction.Type={Off,Off,Off};
  DriverVel={0};
  Reaction.Type={Off};
};

//Elbow flexion driver
// AnyKinEqSimpleDriver ElbowFEDriverLeft={
//   AnyKinMeasureOrg &Elbow =...HumanModel.Interface.Left.ElbowFlexion;
//   DriverPos=pi/180*{.JntPos.Left.ElbowFlexion};
//   DriverVel = pi/180*{.JntVel.Left.ElbowFlexion};
//   Reaction.Type={Off};
// };
```

The left arm must also be positioned close to the posture is it going to take. Please make the following changes in the mannequin.any file:

```
AnyFolder Left = {
  //all values are set to be equal to the right side values
  //feel free to change this!

  //Arm
  AnyVar SternoClavicularProtraction=.Right.SternoClavicularProtraction;
  AnyVar SternoClavicularElevation=.Right.SternoClavicularElevation;
  AnyVar SternoClavicularAxialRotation=.Right.SternoClavicularAxialRotation;
```

```

AnyVar GlenohumeralFlexion = 0;
AnyVar GlenohumeralAbduction = .Right.GlenohumeralAbduction ;
AnyVar GlenohumeralExternalRotation = .Right.GlenohumeralExternalRotation ;

AnyVar ElbowFlexion = 100;

```

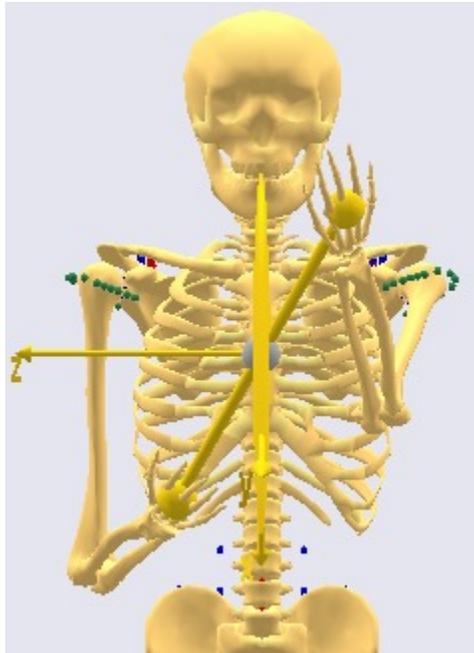
Now you should be able to run the kinematic analysis with both arms moving with the wheel. If you want to see an entire cycle, simply change tEnd in the study section in the main file from 1 to 2 seconds:

```

AnyBodyStudy Study = {
  AnyFolder &Model = .Model;
  RecruitmentSolver = MinMaxSimplex;
  tEnd = 2.0;
  Gravity = {0.0, -9.81, 0.0};
  nStep = 10;
  MuscleEliminationTol = 1e-7;
}; // End of study

```

Notice that you can furthermore control the pronation of the forearms by the setting in the mannequin file if you so desire. Notice also that, since we have retained the driver on the shoulder abduction, the lateral movement of the elbows may be unnatural. A natural movement can be imposed by information about the lateral elbow position from, for instance, a motion capture experiment.



Here is a helping hand if you did not succeed making the model in this lesson work: [HandPump.3.zip](#).

With the kinematics in place, let us proceed to the computation of forces: [Lesson 4: Kinetics](#).

Lesson 4: Kinetics

Having persuaded the model to move correctly we shall proceed to the task of imposing external forces and computing muscle and joint forces in the system.

The AnyBody Modeling System allows you to distinguish clearly between kinematics and kinetics, which is a

huge advantage when creating models like this one. In the real world, the muscles would be pulling on the bones, which causes the arms to exert forces on the handles, which subsequently creates the movement of the wheel. The distinction between kinematics and kinetics in AnyBody allows you to let the wheel rotation impose the kinematics of the entire system, i.e. reversely of how it happens in the real world, while the forces flow the correct way from the muscles to the handles.

To make this happen, we must make a couple of additions to the model. Both concern the definition of the wheel in the Environment.any file. When you open the file you can find the definition of the driver that makes the wheel revolve. To this driver we must add the following setting:

```
AnyKinEqSimpleDriver WheelTurn = {
  AnyRevoluteJoint &Hub = .WheelHub;
  DriverVel = {-pi};
  Reaction.Type = {Off}; // No motor in the driver
};
```

This setting ensures that the driver does not provide any torque to the wheel, and it is separation of kinematics and kinetics in a nutshell: The driver provides the wheel rotation, which further down the kinematic chain causes the arms to move too, but it does not provide any sort of torque, so other elements in the system must do the work. We have to set everything up so that those "other elements" are the muscles. Right now the muscles would not have a very difficult time providing the work because there wheel still has no resistance to work against. This we can provide by means of an applied torque. We shall presume that the arms are driving the wheel against a constant torque, which we can apply as an AnyForce to the hub:

```
AnyKinEqSimpleDriver WheelTurn = {
  AnyRevoluteJoint &Hub = .WheelHub;
  DriverVel = {-pi};
  Reaction.Type = {Off}; // No motor in the driver
};

AnyForce WheelTorque = {
  AnyRevoluteJoint &Hub = .WheelHub;
  F = {30};
};
```

AnyForce is a generic force object that imposes an external load on whatever kinematic measure you apply it to. If the measure is linear in nature, then the load is a force. If the measure is rotational as in the case of the revolute joint in the wheel, then the load becomes a torque. In the present case we are applying 30 torque units of load to the wheel, and because the wheel driver has no motor, this torque must be balanced by the muscles in the system.

There are just a couple of things to do to ice the cake. The first thing issue is that the original standing model has its forward/backward posture driven to maintain balance. This makes sense for a freely standing model, but probably not for a model holding on to a wheel. A more reasonable way to do it would be to control the distance between the thorax and the wheel hub. Let us initially remove the Center of Mass driver that is responsible for the balancing condition. This takes place in the JointAndDrivers.any file:

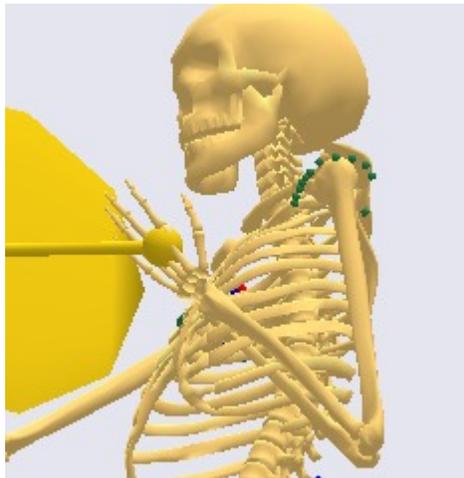
```
//Constrain the collective CoM to be right above the GlobalRef
// AnyKinEqSimpleDriver CoMDriver = {
//   AnyKinCoM CoM = {
//     AnyFolder &Body = Main.Model.HumanModel;
//   };
//   MeasureOrganizer = {0,2}; // Only the x and z directions
//   DriverPos = {0,0};
//   DriverVel = {0,0};
//   Reaction.Type = {Off,Off};
// };
```

This driver we replace by another driver that controls the two horizontal positions of the thorax with respect to the wheel hub. As you can see, this is pretty much a copy of the CoM driver that we just removed with the exception of the changed measure inside the driver. You can use the tree view to insert the long references to the wheel hub node and the thorax segment.

```
//Constrain thorax with respect to the wheel hub
AnyKinEqSimpleDriver WheelThorax = {
  AnyKinLinear Lin = {
    AnyRefFrame &Hub = Main.Model.EnvironmentModel.GlobalRef.Hub;
    AnyRefFrame &Thorax = Main.Model.HumanModel.Trunk.SegmentsThorax.ThoraxSeg;
  };
  MeasureOrganizer = {0,2}; // Only the x and z directions
  DriverPos = {-0.4, 0};
  DriverVel = {0,0};
  Reaction.Type = {Off,Off};
};
```

The DriverPos specification in this driver allows you to control how far the body should be from the wheel. Obviously the body cannot be so close that it touches the wheel and it cannot be so far away that it cannot reach the handles. The value of -0.4 will make the body roughly vertical. If you load the model and run the kinematic analysis, you will see the result. Try experimenting a bit with the distance if you like.

Closer investigation will reveal that the forearm pronation is a bit unrealistic for a hand wheel.



The simple way to remedy this situation is to change the forearm pronation in the mannequin.any file:

```
AnyFolder Right = {
  //Arm
  AnyVar SternoClavicularProtraction=-23; //This value is not used for initial
position
  AnyVar SternoClavicularElevation=11.5; //This value is not used for initial
position
  AnyVar SternoClavicularAxialRotation=-20; //This value is not used for initial
position

  AnyVar GlenohumeralFlexion = 50;
  AnyVar GlenohumeralAbduction = 0;
  AnyVar GlenohumeralExternalRotation = 0;

  AnyVar ElbowFlexion = 40.0;
```

```
AnyVar ElbowPronation = 50.0;
```

Finally, to not have too large time steps, let us define a slightly higher resolution in the AnyBodyStudy in the main file:

```
AnyBodyStudy Study = {
  AnyFolder &Model = .Model;
  RecruitmentSolver = MinMaxNRSimplex;
  tEnd = 2.0;
  Gravity = {0.001, -9.81, 0.001};
  nStep = 20;
  MuscleEliminationTol = 1e-7;
}; // End of study
```

With this completed, we are ready to attempt an inverse dynamic analysis. For this we need muscles in the model, so we switch the muscles back in by changing two lines in the main file:

```
AnyFolder HumanModel={

  //This model should be used when playing around with the model in the
  //initial modelling phase since leaving the normal muscles out, makes the
  //model run much faster. The model uses artificial muscles on each dof. in
  //the joints which makes it possible also to run the inverse analysis.
  //#include ".../BRep/Aalborg/BodyModels/FullBodyModel/BodyModel_NoMuscles.any"

  //This model uses the simple constant force muscles
  #include ".../BRep/Aalborg/BodyModels/FullBodyModel/BodyModel.any"
```

This type of loading of the model causes a torsional moment along the length axis of the body because one hand is pushing on the pedal while the other is pulling. This turns out to make it difficult for the fully extended knees as they are in the current model to carry the load, so it is advisable to flex the knees slightly by the knee flexion setting in the mannequin file:

```
AnyVar KneeFlexion = 5.0;
```

With these changes performed, please click the InverseDynamicAnalysis operation in the study tree and hit the run button. You should see the model turning the wheel against the imposed crank torque. Please beware that with more than 500 muscles in the model each step takes a considerable time.

That is pretty much all there is to it. You should now be able to load the model and run the InverseDynamicAnalysis to investigate the muscle actions, joint forces and so on.

Here's a set of files that work in case the model is giving you trouble: [HandPump.4.zip](#).



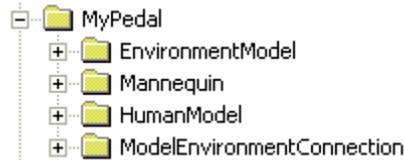
Modifications like these from an existing application to a new one probably accounts for 90% of the model development of AnyBody users. However, in some cases it is not possible to find a good existing application, and it can be advantageous to build your own model from the body parts in the repository.

The next lessons, starting with [Lesson 5](#), deal with such a case.

Lesson 5: Starting with a new model

In the previous lessons we have been constructing our model by modification of an existing application, namely the Standing Model. In some cases it may be difficult to find an existing model that is sufficiently similar to what you want to obtain. In such a case it can be reasonable to begin the modeling project from a new model rather than an existing model. This is what we shall explore in the forthcoming lessons. We shall design a model of a single leg stepping on a pedal. Such a model is much more numerically efficient than the model of the previous lessons, and therefore it makes no sense to begin the project from the standing model as we did before.

Let us first review the structure of the repository in slightly more detail. One of the objectives of its structure is to enable a clear division between the body parts and the applications we hook them up to. This comes through in the data structure of the model we are going to construct. Here is a brief overview of the principles behind that structure.



The model is primarily divided into three folders (a folder is a container of different objects much like a directory can contain files) as shown above. In fact, the structure contains a few more parts that we will get to later, but the elements shown above are the more important.

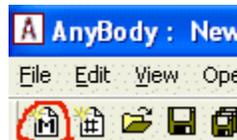
In the middle you see the "HumanModel". This is where we keep the body parts that we are importing from the BRep part of the repository. This folder contains objects such as segments (bones), joints, muscles, and ligaments. We also keep information about the scaling of the model in this folder.

It is just as important to notice what this folder does **not** contain: movement drivers, forces, and joints between the model and the environment. The external hardware parts of the models such as chairs, bicycles, tools, or, in the present case, a pedal are stored in the Environment.

To link the body model together with the environment we create a "ModelEnvironmentConnection" folder typically containing the joint between the objects of the two former folders.

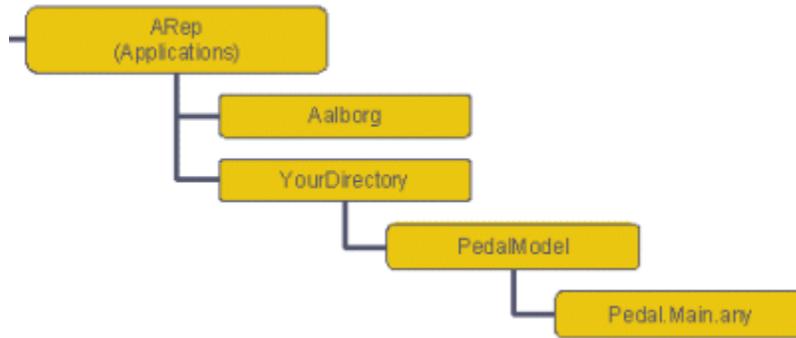
The "Mannequin" part of the model is used for specification of postures, and we shall return to this issue in more detail later.

Without further ado, let us start building the foot pedal model. The toolbar button "New Main" will generate an empty model that looks much like this (we have changed the name of the MyModel folder to MyPedal):

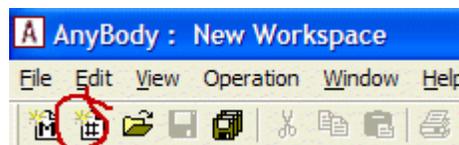


```
// This model demonstrates the construction of a foot pedal example
Main = {
  // The actual body model goes in this folder
  AnyFolder MyPedal = {
    // Global Reference Frame
    AnyFixedRefFrame GlobalRef = {
    }; // Global reference frame
  }; // MyPedal
  // The study: Operations to be performed on the model
  AnyBodyStudy MyStudy = {
    AnyFolder &Model = .MyPedal;
    RecruitmentSolver = MinMaxSimplex;
    Gravity = {0.0, -9.81, 0.0};
  };
}; // Main
```

The comments have been adapted to reflect the fact that we are going to construct a pedal example. Please press the save button (or Ctrl-S) and save the model in a new directory under ARep, for instance using the file name Pedal.Main.any. Notice that the use of the "Main" suffix is a good way to indicate that this is the starting point of the pedal application.



The model can be compiled, but it does not do much, and in any case we shall restructure it right away. As indicated above, we wish to separate the parts that deal with the environment into a dedicated file. Press the "New Include" button.



This gives you an empty window. Now fill the following into the new include file:

```
AnyFolder EnvironmentModel = {
};
```

This folder is for keeping stuff that forms the environment. In this case it is the global reference frame, i.e. ground, and the pedal that the foot is going to step on. In fact, let's move the global reference frame to this folder right away. Simply cut the GlobalRef definition from the Pedal.Main.any file and insert it into the include file (notice that new AnyScript code is written in red while existing code has the usual syntax highlighting):

```
AnyFolder EnvironmentModel = {
  // Global Reference Frame
  AnyFixedRefFrame GlobalRef = {
  }; // Global reference frame
};
```

It is time to save the new include file. Click the "Save" button or Ctrl-S and save it under the name of "Environment.any" in the same directory as the Main file.

The next step is to add an include statement in the Main file that incorporates the environment into the model:

```
Main = {
  // The actual body model goes into this folder
  AnyFolder MyPedal = {
    #include "Environment.any"
  }; // MyPedal
```

We now have the framework for adding the pedal to the model. We are presuming a pedal hinged in one end and the foot pushing in the other. We define the segment and the hinge in the Environment.any file:

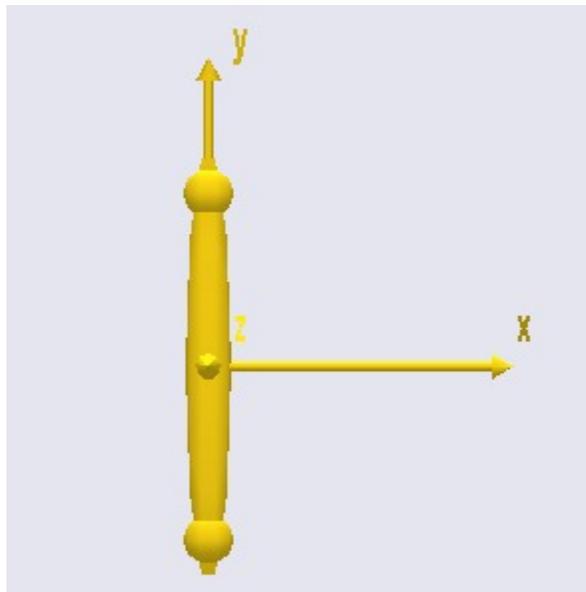
```
AnyFolder EnvironmentModel = {
  // Global Reference Frame
```

```

AnyFixedRefFrame GlobalRef = {
}; // Global reference frame
AnySeg Pedal = {
  Mass = 2;
  Jii = {0.05, 0.001, 0.05};
  AnyRefNode Hinge = {
    sRel = {0, -0.15, 0};
  };
  AnyRefNode FootNode = {
    sRel = {0, 0.15, 0};
  };
  AnyDrawSeg drw = {};
};
AnyRevoluteJoint HingeJoint = {
  Axis = z;
  AnyFixedRefFrame &Ground = .GlobalRef;
  AnyRefNode &Pedal = .Pedal.Hinge;
};
};

```

If you load the model and open a Model View, then you will see the new segment:



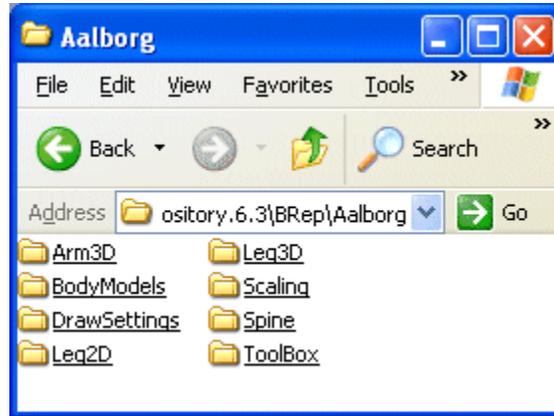
It is hinged to the origin of the global reference frame, but there is not much else to see. In the next lesson we shall look at how we can import a leg model from the repository to step on the pedal.

Next up is [Lesson 6: Importing a Leg Model](#).

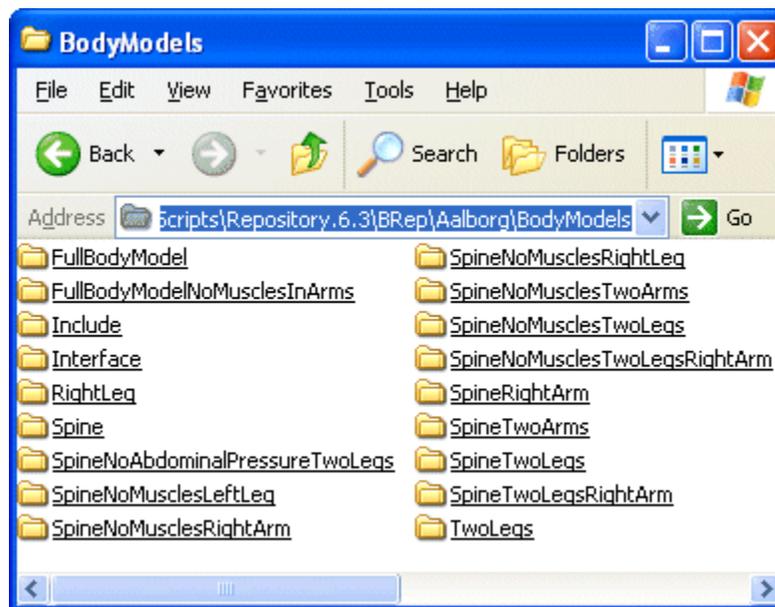
Lesson 6: Importing a Leg Model

Having defined the environment, the next step is to introduce a leg into the model. We are going to pick one from the repository. The repository has several layers from which you can pick models. At the low level you can pick individual body parts but will have to manually provide the necessary interfaces or handles to connect the body parts to each other and to the environment.

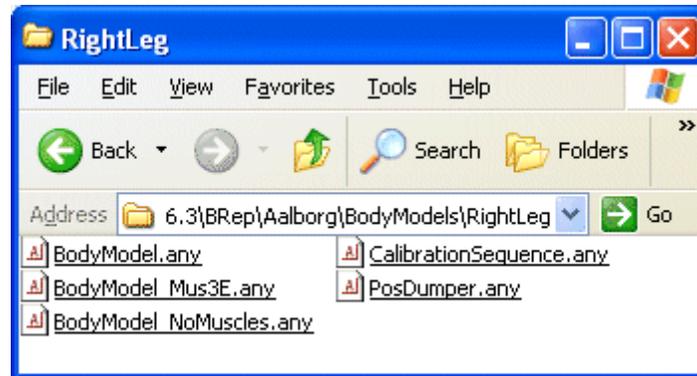
A much simpler solution is to use a set of popular, pre-defined assemblies of body parts that come with the necessary interfaces to hook them up to the environment. This is what we shall do here, and it is not much more than specifying an include file. If you open up the BRep branch of the repository and go to the Aalborg section, you will find the following directories:



Some of these directories are specific body parts, while others contain various useful utilities. The BodyModels directory is a bit of each. It contains the pre-defined assemblies of body models that you can easily insert into your model. Opening BodyModels reveals the following (please notice that this collection is subject to constant updates and hence changes a bit over time):



As the names indicate most of these directories contain one body model that you can include into your application. For the simple pedal example we are going to use the RightLeg model. Opening it up reveals that there is more to it than a single file:



Each of these body models comes in three different forms:

1. BodyModel.any is the basic version including simple muscle models, i.e. muscles that have constant strength regardless of length and contraction velocity.
2. BodyModel_Mus3E.any is the version with Hill-type, three-element muscles that take the complexities of contraction dynamics, tendon elasticity, and many other physiological properties into account.
3. BodyModel_NoMuscles.any is a version where all the anatomical muscles have been replaced by simple joint torque muscles. This is useful for development, because the model loads and runs much faster in this version, and for traditional joint-torque-type inverse dynamics.

To use a body model simply add an include statement for the version you want into the Main file of your application. In our case it goes like this:

```

Main = {
  // The actual body model goes in this folder
  AnyFolder MyPedal = {
    #include "Environment.any"

    AnyFolder HumanModel={
      #include "../BRep/Aalborg/BodyModels/RightLeg/BodyModel_NoMuscles.any"
    };
  }; // MyPedal

  // The study: Operations to be performed on the model
  AnyBodyStudy MyStudy = {
    AnyFolder &Model = .MyPedal;
    RecruitmentSolver = MinMaxSimplex;
    Gravity = {0.0, -9.81, 0.0};
  };
}; // Main

```

Notice that we have created a new folder named 'HumanModel' and inserted the include statement into it. We are using the model without muscles during the development because it loads much faster. The separate folder for the human model allows us to add a few necessary additional items. You will see the necessity of this if you try to load the model by pressing F7. This should produce the following error message:

```

ERROR(SCR.PRS9) : Repository.6.3/BRep/Aalborg/BodyModels/Include/SettingsTrunk.any(14) :
'Scaling' : Unresolved object

```

It appears that an object named 'Scaling' is missing from the model. All the body models in the repository are set up to expect some sort of scaling to be defined by the user. The repository comes with a number of different scaling laws, and it is possible for the advanced user to define new scaling laws. This, however, is a worthy subject of a separate tutorial, so here we shall just chose the simplest solution, which is to use the standard scaling. This really means that we do not scale at all but simply use the body models in the size

they were originally defined, i.e. roughly like a 50th percentile European male:

```
AnyFolder HumanModel={
  #include "../.../BRep/Aalborg/BodyModels/RightLeg/BodyModel_NoMuscles.any"
  #include "../.../BRep/Aalborg/Scaling/ScalingStandard.any"
};
```

Now we are at it, we also need to set the basif strength of muscles in the different body parts:

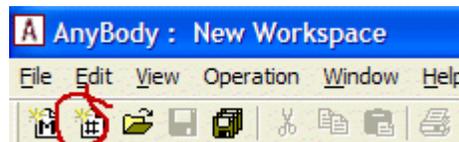
```
AnyFolder HumanModel={
  #include "../.../BRep/Aalborg/BodyModels/RightLeg/BodyModel_NoMuscles.any"
  #include "../.../BRepAalborg/Scaling/ScalingStandard.any"
  AnyFolder StrengthParameters={
    AnyVar SpecificMuscleTensionSpine= 90; //N/cm^2
    AnyVar StrengthIndexLeg= 1;
    AnyVar SpecificMuscleTensionShoulderArm= 90; //N/cm^2
  };
};
```

The strengths of the body parts scale differently. For the spine and shoulder complex the model needs a specific stress of the muscle tissue, while the legs need a strength index. However, in both cases a change of the numbers will scale the strength of the body part accordingly. This gives easy opportunity to, for instance, reduce the strength of the body when modeling an elderly individual.

When you load the model again you will get a new error message:

```
ERROR(SCR.PRS9) : Repository.6.3/BRep/Aalborg/BodyModels/Include/SettingsTrunk.any(36) :
'ColorRef' : Unresolved object
```

ColorRef is the local name of a folder inside the body models. It expects a folder defined in the model containing definitions of colors of the various objects in the model. All the applications in the repository use the same color setup, which is responsible for the graphical similarity between the different applications, i.e. bones, muscles and such with the same colors. To use the same settings here, click the New Include icon,



and fill the following into the new file:

```
AnyFolder DrawSettings ={

  //This is the color definitions of the nodes and segments
  AnyFolder Colors = {
    AnyVec3 AnyBodyRed = {149/256,51/256,55/256}; //AnyBody standard red
    AnyVec3 AnyBodyGreen = {47/256,131/256,80/256}; //AnyBody standard green
    AnyVec3 AnyBodyBlue = {82/256,85/256,111/256}; //AnyBody standard blue
    AnyVec3 AnyBodyYellow= {235/256,197/256,17/256}; //AnyBody standard yellow
    AnyVec3 AnyBodyPaleYellow = {248/256,204/256,115/256}; //AnyBody standard pale
    yellow

    AnyVec3 Nodes = AnyBodyPaleYellow;
    AnyVec3 Segments = AnyBodyPaleYellow;
  };
};
```

```

AnyFolder Muscle ={
  AnyVec3 RGB = .Colors.AnyBodyRed;
  AnyVar DrawOnOff = 1.0;
  AnyVar Bulging = 1.0;
  AnyVar ColorScale =1.0;
  AnyVec3 RGBColorScale = {0.957031, 0.785156, 0.785156};
  AnyVar MaxStress = 100000.000000; //N/m^2 //This number is for graphics only!
  AnyVar Transparency =1.0;
};

AnyFolder SegmentAxes ={
  AnyVec3 RGB ={0,0,1};
  AnyVec3 ScaleXYZ ={0.0001,0.00001,0.00001};
};

AnyFolder BML ={
  AnyVec3 ScaleXYZ ={0.0006,0.0006,0.0006};
  AnyVec3 RGB = .Colors.AnyBodyBlue;
};

AnyFolder JointAxesProximal = {
  AnyVec3 RGB = .Colors.AnyBodyRed;
  AnyVec3 ScaleXYZ = {0.015,0.015,0.015};
};

AnyFolder JointAxesDistal = {
  AnyVec3 RGB = .Colors.AnyBodyGreen;
  AnyVec3 ScaleXYZ = {0.01,0.01,0.01};
};

AnyFolder SegmentNodes ={
  AnyVec3 ScaleXYZ ={0.0005,0.0005,0.0005};
  AnyVec3 RGB = .Colors.AnyBodyRed;
};

AnyFolder WrapGeometry ={
  AnyVec3 RGB ={1,1,1};
};

AnyFolder DrawSettingsSupport={
  AnyFolder Lin={
    AnyVar ScaleFactor=0.004;
    AnyVec3 RGB = {0,0,1};
    AnyVar Thickness = 0.004;
    AnyVar HeadThickness = 2*Thickness;
    AnyVar HeadLength = 3*Thickness;
  };
  AnyFolder Rot={
    AnyVar ScaleFactor=0.08;
    AnyVec3 RGB = {1,0,0};
    AnyVar Thickness = 0.075;
    AnyVar HeadThickness = 2*Thickness;
    AnyVar HeadLength = 5*Thickness;
  };
};

AnyFolder DrawSettingsJointReactions={
  AnyFolder Lin={
    AnyVar ScaleFactor=0.0005;
    AnyVec3 RGB = {0,0,1};
    AnyVar Thickness = 0.01;
    AnyVar HeadThickness = 2*Thickness;
    AnyVar HeadLength = 3*Thickness;
  };
  AnyFolder Rot={

```

```

    AnyVar ScaleFactor=0.001;
    AnyVec3 RGB = {1,0,0};
    AnyVar Thickness = 0.01;
    AnyVar HeadThickness = 2*Thickness;
    AnyVar HeadLength = 5*Thickness;
};

AnyFolder Names={
    AnyVec3 RGB={0,0,1};
    AnyVec3 ScaleXYZ={0.01,0.01,0.01};
};

AnyFolder Marker={
    AnyVec3 Color={0,0,1};
    AnyVar Radius=0.005;
};
}; //DrawSettings

```

Then save the new file under the name "Drawsettings.any". The beauty of all this is that it allows you to very easily change many of the graphical settings of the entire model just by changing a few numbers in this file. For instance, if you want to give all the bones in the model a new color, then simply edit the blend of red, green and blue for the AnyBodyPaleYellow setting near the top of the file.

To use these settings, the following must be added to the Pedal.Main.any file:

```

Main = {

    #include "DrawSettings.any"

    // The actual body model goes in this folder
    AnyFolder MyPedal = {

```

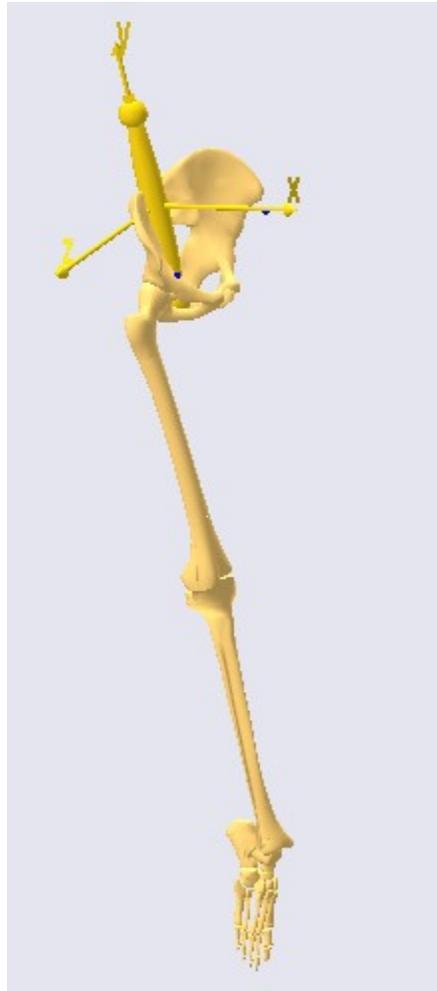
Try loading the model again. F7 should produce the encouraging message:

```

Model Warning: Study 'Main.MyStudy' contains too few kinematic constraints to be kinematically
determinate.
Evaluating model...
Loaded successfully.
Elapsed Time : 0.831000

```

The model view should show you the following picture:



The pedal seems to be located in the middle of the pelvis, which is really a symptom of the warning that the model contains too few kinematic constraints. We have not made any specifications yet of how everything in the model is connected. This will be the topic of [Lesson 7: Making Ends Meet](#).

Lesson 7: Making Ends Meet

So far we have accomplished to define an environment model with a simple pedal and a body model containing a pelvis and the right leg. What the application is still missing is specifications of how the different elements are connected and how the model moves. With kinematics it is usually a good idea to begin with an inventory of degrees of freedom (DOFs) in the model.

The pedal is simple: It is hinged to the global reference frame and therefore just has just one movement capability, namely a rotation about the hinge. The body model is more complicated. It is disconnected from everything and is therefore floating around in space. Furthermore it has a number of internal degrees of freedom that must be controlled: Three rotations in the hip, one rotation in the knee, and two rotations in the ankle. With the six DOFs of the entire body model in space and the single DOF of the pedal, this adds up to 13 DOFs. In other words, we need 13 constraints before the model is kinematically determinate.

This is what we plan to do:

1. The pelvis will be fixed completely at a point corresponding to the contact to a seat. This will do away with 6 DOFs leaving us with 7 more to specify.

2. The foot will be connected to the pedal by a spherical joint having 3 constraints. This leaves us with 4 more constraints to specify.
3. The ankle angle will be presumed fixed by two constraints. This leaves 2 DOFs to be constrained.
4. The lateral position of the knee will be specified by a driver. This leaves a single degree of freedom in the system.
5. Finally, we are going to drive the pedal angle. With the aforementioned constraints this will allow us to specify the posture of the entire system by this single driver.

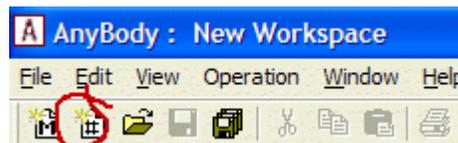
1. Fixing the pelvis to the global reference frame

We previously joined the pedal to the origin of the global reference frame. This means that the 'seat' to which we shall fix the pelvis must be displaced a suitable distance from the origin. In the Environment.any file, add the following to the definition of the GlobalReferenceFrame:

```
AnyFixedRefFrame GlobalRef = {
  AnyRefNode Hpoint = {
    sRel = {-0.7, 0.5, 0};
  };
}; // Global reference frame
```

The name Hpoint is a term used in the seating industry to characterize the position of the pelvis in a seat. Here we shall simply attach the pelvis to this point by means of a rigid connection.

All such specifications are traditionally put into a folder called ModelEnvironmentConnection, and for historical reasons it is placed in an include file called JointsAndDrivers.any. Hit the 'New Include' button



on the toolbar. It brings up an empty window where we can define the objects we need.:

```
// This file contains the connections between the model
// and the environment along with the motion drivers
AnyFolder Joints = {
  AnyStdJoint SeatPelvis = {
    AnyRefNode &Seat = ;
    AnySeg &Pelvis = ;
  };
};
```

The local pointer variables &Seat and &Pelvis need something to point to. The best way of locating the necessary points is to use the object tree at the left hand side of the editor window. Place your cursor in the editor window on the &Seat line just before the final semicolon. Then expand the three in the left hand side of the window through MyPedal, EnvironmentModel, GlobalRef to find the Hpoint that we defined previously. Right-click Hpoint and choose 'Insert Object Name'. The full name of the Hpoint is inserted at the position of the cursor.

We must repeat the procedure for the Pelvis. Place the cursor on the &Pelvis line just before the semicolon and subsequently expand the object tree through MyPedal, HumanModel, Trunk, SegmentsLumbar. Inside the lumbar segments folder you will find the PelvisSeg. Right-click and insert the object name. You should now have the following:

```
AnyFolder Joints = {
  AnyStdJoint SeatPelvis = {
```

```

AnyRefNode &Seat = Main.MyPedal.EnvironmentModel.GlobalRef.Hpoint;
AnySeg &Pelvis = Main.MyPedal.HumanModel.Trunk.SegmentsLumbar.PelvisSeg;
};
};

```

Save the file under the name JointsAndDrivers.any. Then insert the necessary include statement into the main file:

```

AnyFolder HumanModel={
#include "../.../BRep/Aalborg/BodyModels/RightLeg/BodyModel_NoMuscles.any"
#include "../.../BRepAalborg/Scaling/ScalingStandard.any"
AnyFolder StrengthParameters={
AnyVar SpecificMuscleTensionSpine= 90; //N/cm^2
AnyVar StrengthIndexLeg= 1;
AnyVar SpecificMuscleTensionShoulderArm= 90; //N/cm^2
};
};

AnyFolder ModelEnvironmentConnection = {
#include "JointsAndDrivers.any"
};

```

Hit F7 to reload the model. The model still loads in the same position as before. If you run the SetInitialConditions operation, the body model may move backward with the pelvis to the point you have specified (You may have to click the model view to update the picture). This brings up the challenge of getting the model elements aligned reasonably at load time. This is an important topic because the model will be unable to resolve the initial conditions when we add more constraints if all the segments are loaded in a big mess on top of each other.

For the purpose of initial alignment, most applications have a file called InitialPositions.any. It contains specifications of positions and rotations of all segments in the model at load time. It is possible to type reasonable positions manually into this file, but it is much easier to use the version from the standing model we used in the first lessons in this tutorial. It allows us to set the load-time positions of the model by means of anatomical joint angles, which is more intuitive for most users.

As a first step, go to /ARep/Aalborg/StandingModel, and make copies of the two files InitialPositions.any and Mannequin.any. Paste these files into the directory of the model you are working on here. Then insert a couple of new include statements into the main file:

```

AnyFolder MyPedal = {
#include "Environment.any"
#include "Mannequin.any"

AnyFolder HumanModel={
#include "../.../BRep/Aalborg/BodyModels/RightLeg/BodyModel_NoMuscles.any"
#include "../.../BRepAalborg/Scaling/ScalingStandard.any"
AnyFolder StrengthParameters={
AnyVar SpecificMuscleTensionSpine= 90; //N/cm^2
AnyVar StrengthIndexLeg= 1;
AnyVar SpecificMuscleTensionShoulderArm= 90; //N/cm^2
};
};

AnyFolder ModelEnvironmentConnection = {
#include "JointsAndDrivers.any"
#include "InitialPositions.any"
};
}; // MyPedal

```

When you load the model you will get an error in the InitialPositions.any file:

```
ERROR(SCR.PRS9) : Repository.6.3/ARep/Aalborg/BBTutorial/InitialPositions.any(5) : 'ref' : Unresolved object
```

Double-click the line number, and the file opens with the cursor placed at the infamous line. The error is that the file is referring to a folder called Model, which in our application is called MyPedal. Change the name in the two subsequent lines:

```
AnyFolder &ref=Main.MyPedal.HumanModel;
AnyFolder &JointPos=Main.MyPedal.Mannequin.Posture;
```

and reload again. This time you get another error in the same file. This time it is in a line dealing with the thorax. The standing model comprises the entire body, while the pedal model only has a pelvis and one leg. Therefore, we must erase all sections in the file that do not deal with the pelvis or the right leg. When you are done, the file should have only these definitions:

```
AnyFolder &ref=Main.MyPedal.HumanModel;
AnyFolder &JointPos=Main.MyPedal.Mannequin.Posture;
ref.Trunk.SegmentsLumbar.PelvisSeg.r0
{JointPos.PelvisPosX,JointPos.PelvisPosY,JointPos.PelvisPosZ};
ref.Trunk.SegmentsLumbar.PelvisSeg.Axes0=
RotMat((pi/180)*JointPos.PelvisRotZ ,z)*
RotMat((pi/180)*JointPos.PelvisRotY ,y)*
RotMat((pi/180)*JointPos.PelvisRotX ,x);

//Right leg
ref.Right.Leg.Seg.Thigh.Axes0
ref.Trunk.SegmentsLumbar.PelvisSeg.Axes0*
ref.Trunk.SegmentsLumbar.PelvisSeg.HipJointRight.RotNode.ARel*
RotMat((pi/180)*JointPos.Right.HipAbduction,x)*
RotMat((pi/180)*JointPos.Right.HipExternalRotation,y)*
RotMat((pi/180)*JointPos.Right.HipFlexion,z)*
ref.Right.Leg.Seg.Thigh.HipJoint.RotNode.ARel';

//shank
ref.Right.Leg.Seg.Shank.Axes0
ref.Right.Leg.Seg.Thigh.Axes0*
ref.Right.Leg.Seg.Thigh.KneeJoint.ARel*
ref.Right.Leg.Seg.Thigh.KneeJoint.RotNode.ARel*
RotMat((-pi/180)*JointPos.Right.KneeFlexion,z)*
//RotMat(pi,y)*
ref.Right.Leg.Seg.Shank.KneeJoint.RotNode.ARel'*
ref.Right.Leg.Seg.Shank.KneeJoint.ARel';

//Foot
ref.Right.Leg.Seg.Foot.Axes0
ref.Right.Leg.Seg.Shank.Axes0*
ref.Right.Leg.Seg.Shank.AnkleJoint.ARel*
ref.Right.Leg.Seg.Shank.AnkleJoint.RotNode.ARel*
RotMat((pi/180)*JointPos.Right.AnklePlantarFlexion ,z)*
RotMat((pi/180)*JointPos.Right.AnkleEversion ,y)*
ref.Right.Leg.Seg.Foot.AnkleJoint.RotNode.ARel'*
ref.Right.Leg.Seg.Foot.AnkleJoint.ARel';
```

Now reload the model again. This time it should work, and you will get the following picture:



We can now forget about the InitialPositions.any file. All positioning from now on takes place in the Mannequin.any file. Open it up and make the following changes:

```
AnyFolder Mannequin = {
  AnyFolder Posture = {
    //This controls the position of the pelvis wrt. to the global reference frame
    AnyVar PelvisPosX = -0.7;
    AnyVar PelvisPosY = 0.5;
    AnyVar PelvisPosZ = 0;
  }
}
```

What we have done here is to specify the load-time position of the pelvis to the place where we have the seat. After reload you should be able to see in the model view that the body model has moved to a new position. It is also a good idea to specify the initial joint angles so that the foot comes closer to the pedal. This can be done further down in the Mannequin file:

```
AnyFolder Right = {
  //Arm
  AnyVar SternoClavicularProtraction=-23; //This value is not used for initial
  position
  AnyVar SternoClavicularElevation=11.5; //This value is not used for initial
  position
  AnyVar SternoClavicularAxialRotation=-20; //This value is not used for initial
}
```

position

```

AnyVar GlenohumeralFlexion = -0;
AnyVar GlenohumeralAbduction = 10;
AnyVar GlenohumeralExternalRotation = 0;

AnyVar ElbowFlexion = 0.01;
AnyVar ElbowPronation = 10.0;

AnyVar WristFlexion = 0;
AnyVar WristAbduction = 0;

AnyVar HipFlexion = 110.0;
AnyVar HipAbduction = 5.0;
AnyVar HipExternalRotation = 0.0;

AnyVar KneeFlexion = 100.0;

```

On reload you will see that the body now loads in pretty much the desired position. Notice that this is only to bring the body close to where it will eventually be. It is not necessary to align the model exactly with the pedal. The kinematic constraints will take care of this once they are properly defined.



2. Connecting the foot to the pedal

The foot will be connected to the pedal by a spherical joint. This is defined inside the JointsAndDrivers file in the following way:

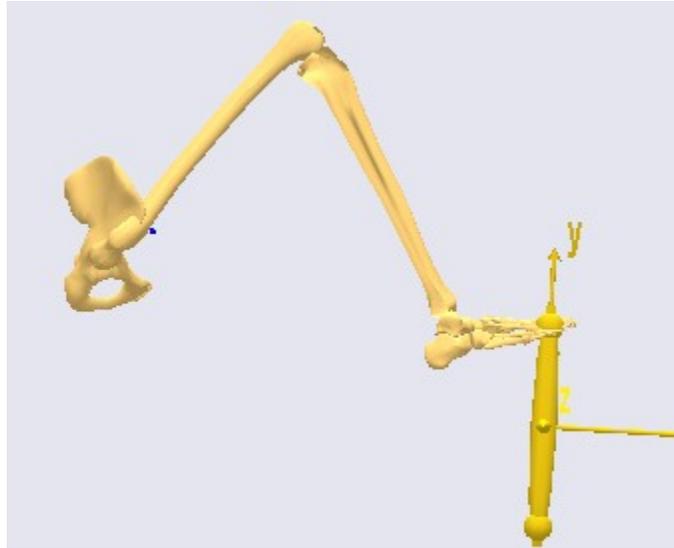
```

AnySphericalJoint PedalFoot = {
  AnyRefNode &Pedal = Main.MyPedal.EnvironmentModel.Pedal.FootNode;
  AnyRefNode &Foot = Main.MyPedal.HumanModel.Right.Leg.Seg.Foot.MetatarsalJoint2Node;
};

```

We have cheated just a little. It is possible to define new nodes on the foot for attachment to a specific place, but we have taken the cheap-and-dirty solution of picking an existing point close to where we presume the contact with the pedal will be. The MetatarsalJoint2Node is a good approximation.

You will not see any change when you reload the model, but if you run the SetInitialConditions operation, you might get this (notice you may have to click the model view window to update the picture):



Notice that the leg has moved slightly to honor the constraint that the foot must be on the pedal.

3. Setting the ankle angle

The ankle in this body model is a universal joint, which means that it has two degrees of freedom. We wish to constrain these two degrees of freedom to predefined values. This can be done by a so-called simple driver. In the JointsAndDrivers file we shall introduce a driver section below the Joints folder:

```
AnyFolder Joints = {
  AnyStdJoint SeatPelvis = {
    AnyRefNode &Seat = Main.MyPedal.EnvironmentModel.GlobalRef.Hpoint;
    AnySeg &Pelvis = Main.MyPedal.HumanModel.Trunk.SegmentsLumbar.PelvisSeg;
  };
  AnySphericalJoint PedalFoot = {
    AnyRefNode &Pedal = Main.MyPedal.EnvironmentModel.Pedal.FootNode;
    AnyRefNode &Foot =
Main.MyPedal.HumanModel.Right.Leg.Seg.Foot.MetatarsalJoint2Node;
  };
};
AnyFolder Drivers = {
};
```

We then insert the simple driver into the Drivers folder:

```
AnyFolder Drivers = {
  AnyKinEqSimpleDriver AnkleDriver = {
    AnyUniversalJoint &Ankle = Main.MyPedal.HumanModel.Right.Leg.Jnt.Ankle;
    DriverPos = {};
    DriverVel = {0, 0};
  };
};
```

Most of this came about the same way as we have done previously: The definition of the AnyKinEqSimpleDriver (and indeed its complex name) came from the object inserter in the Classes tree at the left hand side of the editor window. The complete name of the ankle joint was inserted from the object tree. The joint is going to be static, so the DriverVel specification was also easy to do. What is remaining is

two degrees of freedom is which. Fortunately, the model is already loaded, and we can get the current values for the ankle angles from the object tree. Click your way through the tree to HumanModel->Right->Leg->Jnt->Ankle, and double-click the Pos property. The current angles are dumped in the message window:

```
Main.MyPedal.HumanModel.Right.Leg.Jnt.Ankle.Pos = {1.570796, 0};
```

Now we know which value to assign to the joint angle driver:

```
AnyFolder Drivers = {
  AnyKinEqSimpleDriver AnkleDriver = {
    AnyUniversalJoint &Ankle = Main.MyPedal.HumanModel.Right.Leg.Jnt.Ankle;
    DriverPos = {1.570796, 0};
    DriverVel = {0, 0};
  };
};
```

The model should load again with no significant difference.

4. Fix the lateral position of the knee

Imagine your pelvis on a seat and your foot resting on a point like the model is right now. You can still move your knee sideways either medially or laterally rotating the leg about an axis through the foot contact point and the hip joint. We must constrain this movement, and the easiest way to do it is by fixing the knee laterally.

We shall do this by another simple driver in conjunction with a linear measure. Let us add another driver to the Drivers folder:

```
AnyFolder Drivers = {
  AnyKinEqSimpleDriver AnkleDriver = {
    AnyUniversalJoint &Ankle = Main.MyPedal.HumanModel.Right.Leg.Jnt.Ankle;
    DriverPos = {1.570796, 0};
    DriverVel = {0, 0};
  };

  AnyKinEqSimpleDriver KneeDriver = {
    DriverPos = {0};
    DriverVel = {0};
  };
};
```

This empty driver needs something to drive. We are going to create a linear measure between the global reference frame and the knee:

```
AnyKinEqSimpleDriver KneeDriver = {
  AnyKinLinear GlobKnee = {
    AnyRefFrame &Glob = Main.MyPedal.EnvironmentModel.GlobalRef;
    AnyRefFrame &Knee = Main.MyPedal.HumanModel.Right.Leg.Seg.Thigh.KneeJoint;
  };
  DriverPos = {0};
  DriverVel = {0};
};
```

The AnyKinLinear is really a vector between the two points it refers to, i.e. in this case the position of the knee in the global reference frame. However, we only wish to drive one of the coordinates of this vector, namely the lateral coordinate. This is the z coordinate, which in an AnyScript model has number two, because numbering begins at 0. To drive only this one coordinate, we insert a measure organizer:

```
AnyKinEqSimpleDriver KneeDriver = {
  AnyKinLinear GlobKnee = {
    AnyRefFrame &Glob = Main.MyPedal.EnvironmentModel.GlobalRef;
    AnyRefFrame &Knee = Main.MyPedal.HumanModel.Right.Leg.Seg.Thigh.KneeJoint;
  };
  MeasureOrganizer = {2};
  DriverPos = {0};
  DriverVel = {0};
};
```

This has the effect of neglecting the x and y coordinates of the vector returned by the linear measure. You should be able to load the model again, but there is no visible difference.

5. Drive the pedal

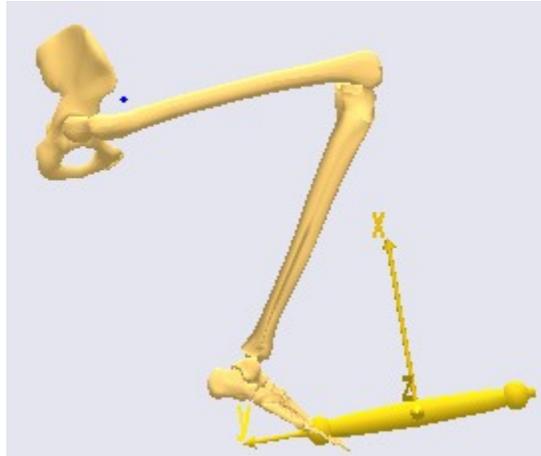
The final step is to drive the movement of the pedal. It is hinged to the origin of the coordinate system, and we shall add a driver to the joint angle pretty much like we did with the ankle and the knee.

```
AnyKinEqSimpleDriver KneeDriver = {
  AnyKinLinear GlobKnee = {
    AnyRefFrame &Glob = Main.MyPedal.EnvironmentModel.GlobalRef;
    AnyRefFrame &Knee = Main.MyPedal.HumanModel.Right.Leg.Seg.Thigh.KneeJoint;
  };
  MeasureOrganizer = {2};
  DriverPos = {0};
  DriverVel = {0};
};

AnyKinEqSimpleDriver Pedal = {
  AnyRevoluteJoint &Hinge = Main.MyPedal.EnvironmentModel.HingeJoint;
  DriverPos = {100*pi/180};
  DriverVel = {45*pi/180};
};
```

This puts the pedal in an initial 100 degree angle compared to vertical. It also specifies a movement with an angular velocity of 45 degrees per second, but let us postpone the investigation of that for later.

For now, hit F7 again to reload the model. Notice that the system no longer complains about the model being kinematically indeterminate. Run the SetInitialConditions operation to get things connected. With a little luck you will get this picture:



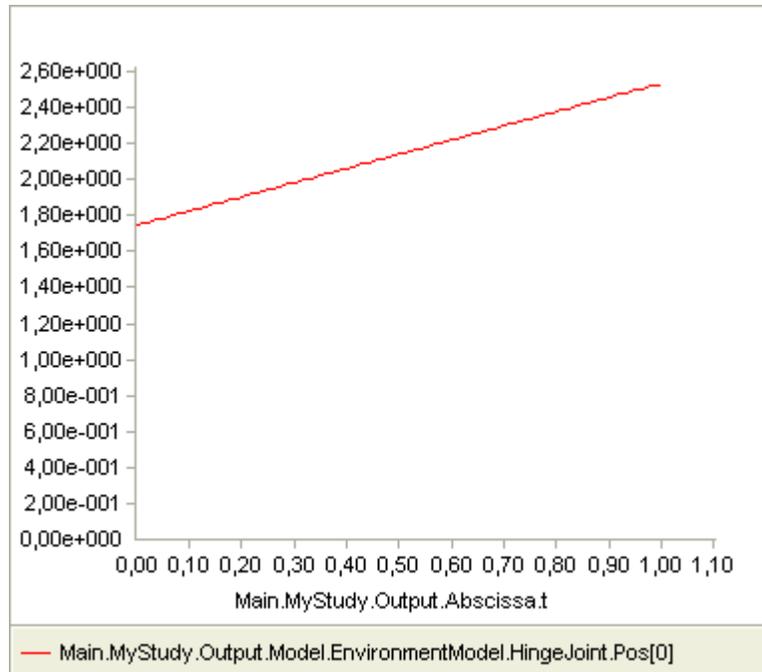
With the model kinematically determinate we can proceed and run the KinematicAnalysis operation. Doing so will show you the movement of the entire system as the pedal is rotating.

[Now that the kinematics is in order, let us move on to the kinetic analysis in Lesson 8 and see what the model is good for.](#)

Lesson 8: Kinetics - Computing Forces

With the kinematic analysis in place we are ready to compute forces and investigate ergonomic properties of the pedal arrangement. We shall presume that the pedal is loaded by a spring, the force of which the leg must overcome when stepping on the pedal. AnyScript has a ligament class, which can be used to create springs of various types. Please refer to the [ligament tutorial](#) for further information. However, here we shall take a simpler approach and simply define the spring force directly.

A force can be added to any kinematic measure by means of the AnyForce class. Because the concept of kinematic measures is general, the AnyForce class attains the type given by the kinematic measure. If the measure is a length, then an AnyForce is a force, and if it is an angle, the AnyForce automatically becomes a moment. In the present case we shall add the AnyForce to the kinematic measure of the pedal's hinge. Let us initially study the measure. Run the KinematicAnalysis again, open a ChartFX 2D View, and browse your way through the tree to `Main.MyStudy.Output.Model.EnvironmentModel.HingeJoint.Pos`. You should see the following graph:



The analysis runs in time from zero to one second, and the pedal angle develops in this time from 100 degrees (1.74 rad) to 145 degrees (2.53 rad). Let us presume that the pedal is loaded by a linear spring that is slack at 0 degrees and increases its moment linearly with the rotation of the hinge. We might be wondering: What would be a comfortable spring stiffness for a pedal like that? Not having much experience with pedal design it might be difficult to imagine just how stiff the spring should be, and we could find ourselves developing a series of hardware prototypes with different springs and perhaps conducting subjective investigations with test subjects. A simple task like this could potentially be very time consuming and expensive.

Let us do it with AnyBody instead. We shall start out by declaring an AnyForce to play the role of the spring. Since this is not a part of the body it is logical to place it in the Environment.any file. Here's what to add:

```
AnyRevoluteJoint HingeJoint = {
    Axis = z;
    AnyFixedRefFrame &Ground = .GlobalRef;
    AnyRefNode &Pedal = .Pedal.Hinge;
};
AnyForce Spring = {
    AnyRevoluteJoint &Hinge = .HingeJoint;
    F = -0.0*.HingeJoint.Pos;
};
```

This looks easy, does it not? The AnyForce contains a reference to the HingeJoint. Since the degree of freedom in HingeJoint is rotational, the force is automatically turned into a moment and applied it to the hinge. The specification of F is the actual size of the force. We have made it proportional to the HingeJoint.Pos, which is the hinge angle, and we have initially set the spring stiffness to 0.0, to investigate the effect of having no spring before we start adding a spring force. Notice, by the way, the minus sign in front of spring constant. It has no importance now, but when we start adding non-zero stiffnesses it will signify that the spring force goes against the angle, i.e. pushes back onto the foot.

There are just a couple of things we need to do before we can do the InverseDynamicAnalysis operation and compute the forces: All the drivers we added in the previous lesson have motors built into them. This means that whatever force or moment is necessary to perform the movement will be provided by the drivers, and there will be nothing for the muscles to do. Motors in drivers are technically reaction forces, and they can be

turned off inside the driver:

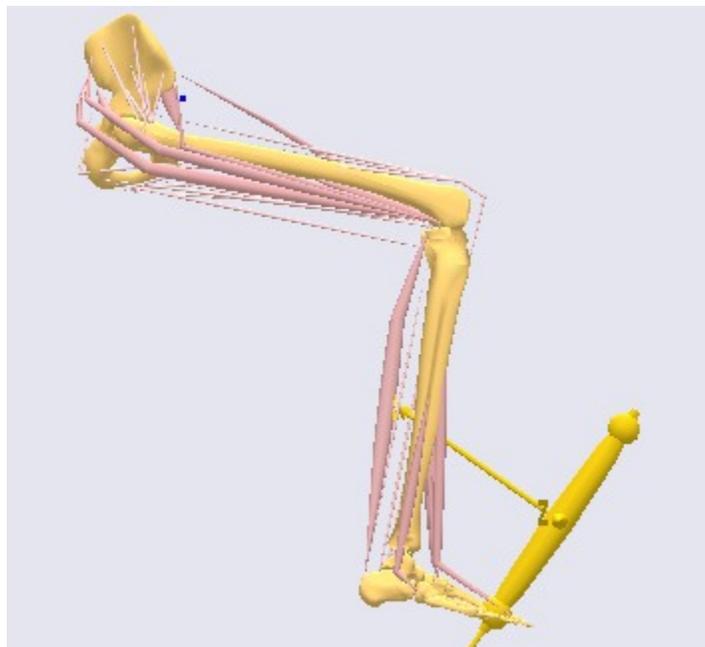
```
AnyFolder Drivers = {
  AnyKinEqSimpleDriver AnkleDriver = {
    AnyUniversalJoint &Ankle = Main.MyPedal.HumanModel.Right.Leg.Jnt.Ankle;
    DriverPos = {1.570796, 0};
    DriverVel = {0, 0};
    Reaction.Type = {Off, Off};
  };
  AnyKinEqSimpleDriver KneeDriver = {
    AnyKinLinear GlobKnee = {
      AnyRefFrame &Glob = Main.MyPedal.EnvironmentModel.GlobalRef;
      AnyRefFrame &Knee = Main.MyPedal.HumanModel.Right.Leg.Seg.Thigh.KneeJoint;
    };
    MeasureOrganizer = {2};
    DriverPos = {0};
    DriverVel = {0};
    Reaction.Type = {Off};
  };

  AnyKinEqSimpleDriver Pedal = {
    AnyRevoluteJoint &Hinge = Main.MyPedal.EnvironmentModel.HingeJoint;
    DriverPos = {100*pi/180};
    DriverVel = {45*pi/180};
    Reaction.Type = {Off};
  };
};
```

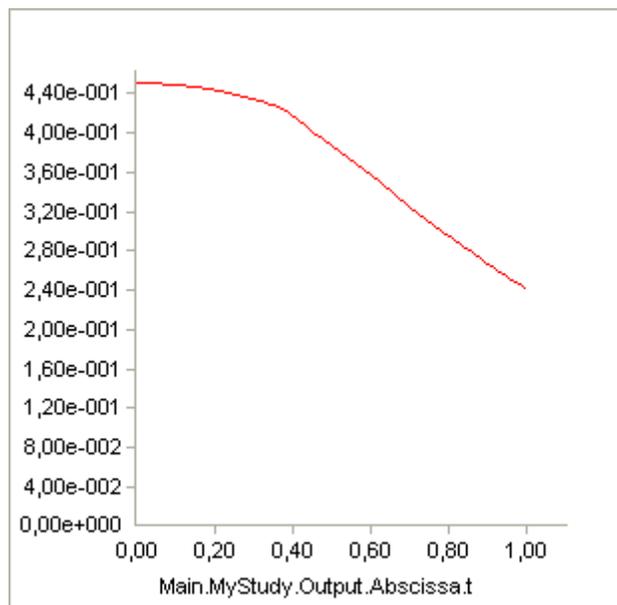
There is one more thing we have to do: The model has no muscles. This can be rectified by a simple change in the included body model in the main file:

```
AnyFolder HumanModel={
  #include "../.../BRep/Aalborg/BodyModels/RightLeg/BodyModel.any"
  #include "../.../BRepAalborg/Scaling/ScalingStandard.any"
  AnyFolder StrengthParameters={
    AnyVar SpecificMuscleTensionSpine= 90; //N/cm^2
    AnyVar StrengthIndexLeg= 1;
    AnyVar SpecificMuscleTensionShoulderArm= 90; //N/cm^2
  };
};
```

Now, reload the model and run the InverseDynamicAnalysis. The model should look like this:



Notice that the muscle forces are illustrated by the bulging of the muscles. In the ChartFx view near the top of the tree you can find the MaxMuscleActivity. It expresses the load on the body in percent of its strength. Plotting this property in the ChartFx View gives you the following result:

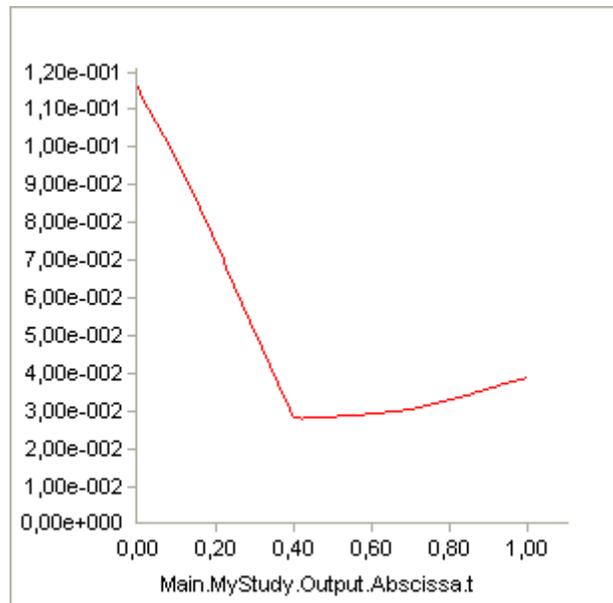


Obviously holding the leg out in the air like that without the support of a pedal spring and holding up the weight of the pedal as well is rather strenuous and in fact requires about 44% of the body's strength.

Now, let us study the effect of spring stiffness. We initially try:

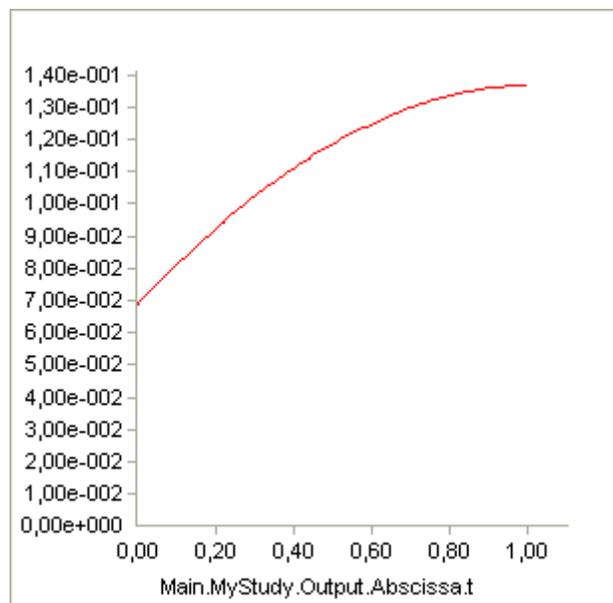
```
F = -10*.HingeJoint.Pos;
```

This produces the activity curve:



Obviously the level is much lower now starting at just 12%, so the spring really seems to help. Let us try to double the stiffness:

```
F = -20*.HingeJoint.Pos;
```



This appears to be equally good in terms of activity level and has the added quality of increasing muscle activity or effort for increasing angle. This can make it easier for the operator to control the pedal and thereby enhance the operability.

The completed model is available here: [PedalDemo.zip](#).

The AnyBody Modeling System is all about making this type of investigation easy. The mechanical model we have put together in four simple lessons has a complexity worthy of a Ph.D. project if you develop it bottom up. In AnyBody, this is a matter of a few hours of work when using the predefined models of the repository.

Let's continue to [Lesson 9: Model Structure](#).

Lesson 9: Model Structure

This section contains recommendations on construction of body parts to make them compatible with the model structure of the [AnyScript Repository](#).

Building an AnyScript model of a body part or the complete body is much like any other complex construction work in the sense that it requires planning and coordination. This is particularly true if different people divide the task between them and later assemble the model. These are the general recommendations:

The Repository uses the ISB coordinate system.

The International Society of Biomechanics is endorsing the use of a particular convention for coordinate axes in the human body, and so are we. These recommendations are published in these references:

[Wu G, Cavanagh PR.: ISB recommendations for standardization in the reporting of kinematic data. J Biomech 1995 Oct;28\(10\):1257-1261](#)

[Wu G, Siegler S, Allard P, Kirtley C, Leardini A, Rosenbaum D, Whittle M, D'Lima DD, Cristofolini L, Witte H, Schmid O, Stokes I.: ISB recommendation on definitions of joint coordinate system of various joints for the reporting of human joint motion-part I: ankle, hip, and spine. J Biomech 2002 Apr; 35\(4\):543-548.](#)

Conventions like these are always debatable. For instance, ISB recommends a vertical y axis, where many users probably feel that a vertical z axis is natural. But there is a distinct benefit to having a standard, so most of the models in the repository adhere to the ISB recommendation.

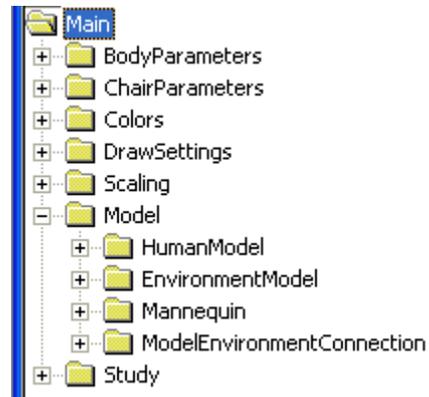
The Repository uses SI Units

SI units are based on meters, kilograms and seconds. They are consistent and therefore eliminate the possibility of miscalculations due to hidden conversion factors. For instance, a seemingly consistent use of millimeters instead of meters in a model may lead to the devious error of square root 1000 in some types of calculations. The AnyBody Modeling System expects all angles to be specified in radians. If you feel more comfortable working with degrees you can use expressions to convert to radians like this example where we specify an angle of 30 degrees:

```
AnyVar KneeAngle = 30*Pi/180;
```

Bodies and environments

When you load a model from the repository and investigate its tree, you will find that it is structured with one folder for the body parts (HumanModel), one folder for the environment (EnvironmentModel), and one folder for the connection between the human model and the environment (ModelEnvironmentConnection).



The idea behind this system is to make the human model and the environment model as independent of each other as possible.

Some models also have a folder called Mannequin for control of posture.

Validation of models

Somewhere on the way to the decision of using a biomechanical model you have probably asked yourself the question: Will I be able to trust the results I get?

This is a very relevant question indeed. Computer models are just that: a model of reality, and there will always be some amount of approximation involved. The good news is that with careful modeling and the 'right model for the right problem' you can get very close to reality with the AnyBody Modeling System because it is tailor-made for the complexity of musculoskeletal systems.

Investigation of the accuracy of the model goes under the term 'validation', and this is what we will be dealing with in this tutorial. More precisely, you can expect to find the following in this tutorial:

1. Clever ideas for validation methods.
2. Examples of models that have been validated previously.

What can go wrong?

Well, lots, actually. But it is helpful to try to categorize the matter into a few sources of error.

- Errors sources in the model
- Errors sources in the basic assumptions
- Errors sources in the software

Errors sources in the model

An AnyScript model contains a lot of data, and they are all infested with some degree of inaccuracy: Geometry and mass properties of segments, assumptions about the kinematics and reactions of joints, properties and attachment points of muscles, and much more.

It has been said about biomechanics that there is a 'right' model for each case. For instance, there is little point in using a complex muscle model if you have little information about the muscle properties, for instance fiber lengths and pennation angles. Another consideration is the level of subject-specific accuracy. Is the purpose of the model to simulate a particular individual, or should it reflect a cross section of the population?

Model data uncertainties

In general, the models in the [AnyScript Model Repository](#) are based on data reported in the literature. They often come from studies of one or few subjects or cadavers, and the data has little or no statistical significance. You will find the references of the data listed in the comments in the individual AnyScript files. However, the fact that a specific fiber length or muscle insertion point has been found in an individual cadaver does not mean that the value is valid for every individual or even typical.

In conclusion there is no guarantee that the values in models from any library are valid for the case you may want to analyse, and the best advice is to approach the matter with a critical mind. If results look suspicious in some part of the model, consider whether this can be due to the model input. Some typical cases are:

- The muscle primarily responsible for carrying the load over a joint does not have sufficient strength. This can happen even in well-tested models if an unusual loading, posture or support condition that was never tested before is imposed.
- The model has attained a posture in which the moment arm of a primary muscle erroneously becomes zero or negative. This can happen, for instance, if a wrapping muscle slides off its wrapping surface. The variation of muscle length with the joint angle reflects the moment arm, so if the moment arm is too small, then the muscle will have little length variation when the joint is articulated.
- If the model makes use of a muscle model with strength/length variation and passive stiffness, then a tendon length that is poorly calibrated to the model can cause malfunction of its muscle. A too long tendon will cause its muscle to have little or no strength in its usual operation interval. A too short tendon will cause a muscle to exert passive force and likely cause muscles on the other side of the joint to work more than they are supposed to. Please notice that AnyBody has facilities for calibrating tendon lengths. [The muscle modeling tutorial](#) has in-depth information about these issues.

Boundary conditions

Input to inverse dynamics is movement and boundary conditions, and these can have more influence on the result than most inexperienced modelers would expect. In fact, they are the principal source of error in many models. The human body is remarkable in its ability to make the best of the available supports, and this often creates the illusion that supports are solid while they really are not.

Consider a hand gripping a handle firmly. Apparently, the hand is rigidly connected to the handle, and you might be inclined to define a model connection between the two elements reflecting this notion. However, hands have limited strength to hold on with, and handle surfaces have limited friction to offer. If the model contrary to reality offers an effortless connection between the hand and the handle, then the model is likely to exploit this as we shall see later.

Movement data

Recorded movement input such as motion capture data is usually in the form of positions over time. But inertia forces in the model are derived from accelerations, and to obtain accelerations, the positional data must be differentiated twice thus increasing noise and inaccuracies by two orders of magnitude. This is the topic of the first lesson of this tutorial, starting at the bottom of this page.

Errors sources in the basic assumptions

As mentioned a couple of times already, the AnyBody Modeling System is based on inverse dynamics. This means that - for a given point in time - the system solves the equilibrium equations and resolves the interior muscle and joint forces. Since these time steps are solved independently of each other, the state can in principle shift abruptly from one step to the next, whereas, in reality, a change of muscle tone requires a bit of time. Force development in a muscle is the result of an electric signal from the central nervous system,

very quick and the system predicts very rapid changes of muscle activation, then the result may not be realistic.

Another possible source of error is the distribution of force between the muscles. The body has more muscles than strictly necessary to carry most loads, so is infinitely many different combinations of muscle forces will balance the external loads. The way AnyBody picks the right one is by an optimality criterion. The system presumes that the body wants to make the best of its resources. The user has some amount of control over this criterion, but in its basic form it is a minimum fatigue criterion that distributes the loads as evenly as possible between the muscles taking their individual strengths into account. Please refer to [A Study of Studies](#) for more detailed information.

So the system basically presumes that the body has the knowledge and the desire to activate muscles optimally. This is supported by a lot of research, but the precise criterion employed by the body is a matter of continuous discussion. Furthermore, the ability to instantly choose the optimal muscle recruitment most likely requires that the movement is skilled and that the required changes of muscle activation are not faster than the electro-chemical process of muscle contraction can accommodate.

Errors in the software

All software has bugs, and very probably this is also the case for the AnyBody Modeling System. However, in terms of muscle recruitment, the validity of the software was validated independently in 2004 in a Ph.D. thesis by Erik Forster from the University of Ulm, Germany. The thesis is available from the list of publications in the AnyBody Research Project, www.anybody.aau.dk/publications.htm. The basic idea was to program an independent special-purpose application for gait simulation and then compare it to an identical gait model in AnyBody. If the results were identical, it would prove the correctness of the algorithms of both systems. The result was that the output data of the two systems were identical on all but a tiny fraction of the data. Closer investigation of this tiny fraction revealed that different algorithms - although mathematically similar - can produce slightly deviating results due to round-off errors.

When compared to the modeling errors and approximations due to the recruitment assumptions, errors in the software are much less likely to disturb the result of the computation significantly.

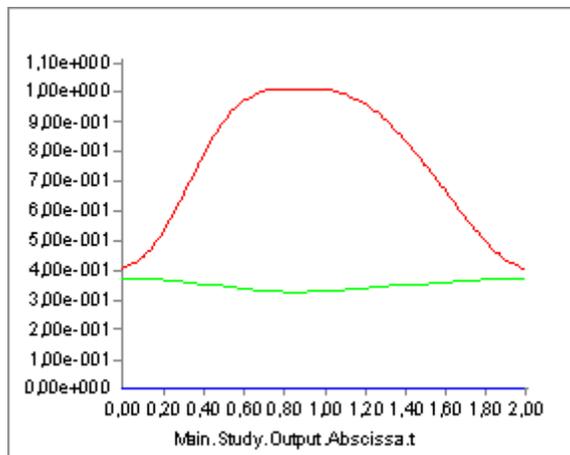
Methods of validation

The expression 'garbage in - garbage out' is very much valid for biomechanical simulation. The quality of the output can never be better than the input. This means that the first step of any validation is to check the quality of the input. Input comes in the form of movements and applied forces, where the former is the more difficult. A rough check of the specified movements can be obtained by running a kinematic analysis and charting the positions, velocities and above all accelerations of characteristic points and segments in the model as illustrated for the rowing model above. Notice that proximal body parts tend to be heavier than distal body parts, so larger accelerations are plausible in the distal parts.

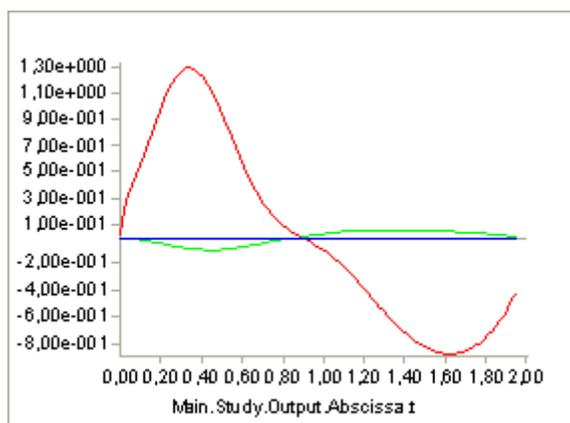
Gravity = 9.81 m/s^2 is a good measure to compare your values to. If the accelerations oscillate or attain unrealistic values, then the input positional information definitely needs careful reviewing and probably smoothing with a low-pass filter.

Kinematic input

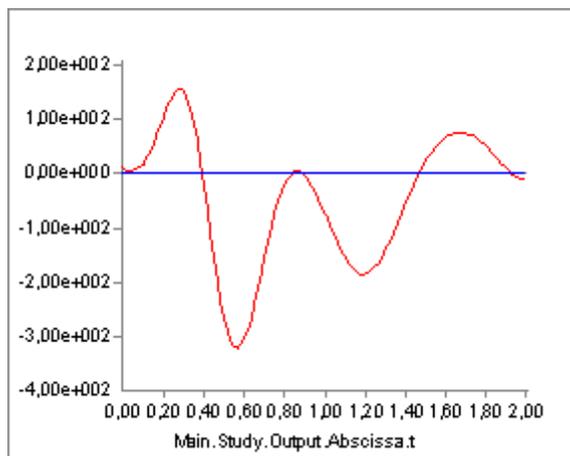
The picture below shows the thorax position variation over time recorded by digitizing images from a video capture (model courtesy of the Technical University of Vienna) of ergometer rowing. The red curve is the horizontal position, and the green curve is the vertical position. The lateral position remains zero and is the blue curve. It looks very reasonable, and it does not seem to be infested with significant noise.



To find velocities, the system automatically differentiates positional data with respect to time and we get the following:



It still looks reasonable except for a suspicion that the maximum velocity around 12 m/s may be a bit high over such a short distance. The system differentiates the velocity function to obtain the accelerations, which subsequently according to the second law of Newton will generate forces:



This graph still looks nice and smooth, but notice the values: The maximum acceleration is around 300

m/s² or 30 g. Notice that this is for the thorax and not a distal segment like a hand or a foot. It is not realistic, and it is in fact an artifact produced by the amplification of small errors in the positional signal through the two subsequent differentiations.

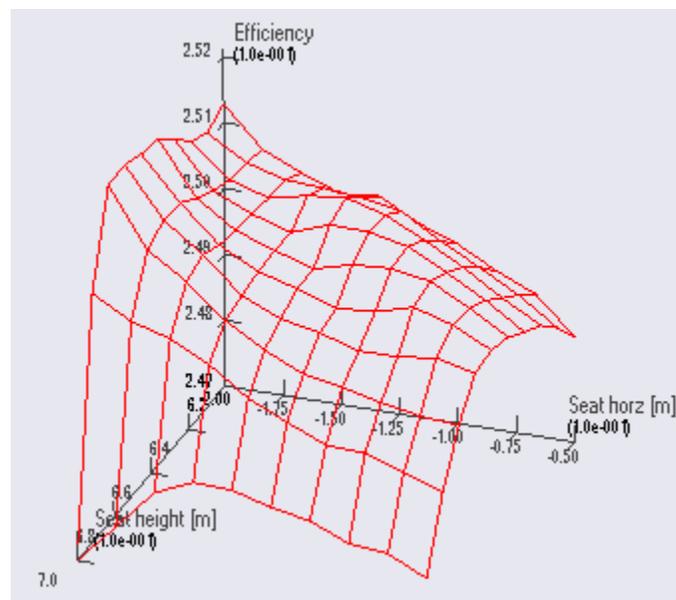
If you work with recorded movement data, then it is very important to check that the accelerations are within reasonable limits. The movement is input in inverse dynamics, and if the accelerations are unrealistic, then the muscle and joint forces will be too.

Too high accelerations are usually due to lack of smoothness of the recorded motion data. The solution is often to apply smoothing with a low pass filter to reduce the unrealistic accelerations.

Parameter studies and optimization

The AnyBody Modeling System has a nice mechanism that allows you to perform investigations of the model's reaction to its parameters and even to automatically find the set of parameters that causes a given behavior of the model. Some examples of applications are:

- Systematic investigations of the model's sensitivity to a group of parameters such as a muscle insertion point, muscle strength, or external support point.
- Posture and movement prediction.
- Optimization of muscular strength for a particular sports performance.
- Optimization of the layout of a bicycle for a particular person.
- Answering research questions such as: Could a T. rex jump? With optimization you can find the movement pattern that maximizes, for instance, the jump height given the body weight and limitations on muscular strength.



Parameter study: Metabolic efficiency of a bicycle as a function of seat height and seat horizontal position.

This functionality is provided through two complementary [studies](#):

The **AnyParamStudy** performs an exhaustive search of the variable space computing the model's reaction to every combination of the variables within a given interval. For instance, a parameter study could investigate the metabolic efficiency of a bicycle depending on the horizontal and vertical position of the saddle. The advantage of this study is that it gives you the ultimate overview of the system's behavior. The

disadvantage is that the number of computations grows exponentially with the number of parameters. A two-parameter problem with five values of each parameter leads to $5 \times 5 = 25$ analyses, which is usually no problem to do, while a five parameter problem will lead to $5^5 = 3125$ analyses, which obviously is a more time-consuming undertaking, at least for larger models.

The **AnyOptStudy** performs a systematic search within a parameter space using optimization techniques of solutions that fulfill certain criteria. For instance, you could ask the study to find the saddle position that maximizes the metabolic efficiency of the bicycle while keeping the maximum muscle activity below a certain upper limit. The advantage of this study is that it does not need to compute all combinations of the parameters and therefore can handle spaces with multiple parameters within a reasonable time. The disadvantage is that it does not provide the overview of the design space that you get from a parameter study.

This tutorial devotes one lesson to each of the two study types:

1. Defining a parameter study
2. Optimization studies

Without further ado, let us get the parameter study defined in [lesson 1](#).

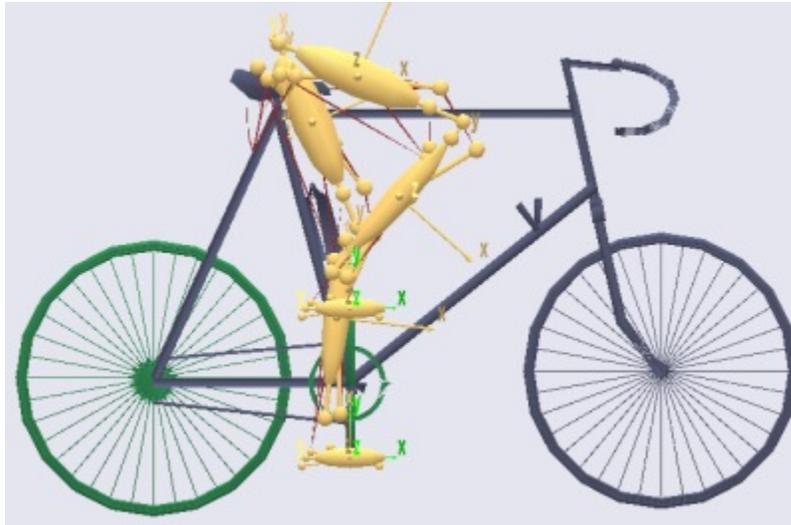
Defining a parameter study

A parameter study is a systematic way to vary a number of model parameters and have the system automatically run one or several analyses for each combination of parameters.

For instance, you may want to know how the forces affecting a joint prosthesis depend on the implanted position. Or you may be interested in finding the standing posture by which you can hold a heavy box as easily as possible between your hands. Or how the position of a handle influences the muscular effort of operating it.

Or you may be interested in knowing how the seat height and horizontal position influence the muscle effort and metabolism of the rider. This is precisely what we shall do in this tutorial. To make life a bit easier for you, we have prepared a bicycle model you can download and play around with. [Please click here](#) to download a zip file and unpack it to some pertinent place on your hard disk.

The bicycle model is pretty much the 2DBike that you may know from [the model repository](#). In fact, the structure of the model is as in the repository, so we have maintained the traditional division between the BRep directory containing the human body model and the ARep directory containing the bicycle. You will find the main file, OptTutorial.main.any, in OptimBike\ARep\Aalborg\OptTutorial (Notice the file OptTutorial.final.main.any in the same location; this is a file that contains most of the additions we make in the lessons of this tutorial). Please open The AnyBody Modeling System and load the main file. Opening a model view window should give you this picture:



As you can see the model is very simple. It has two legs and a pelvis that is rigidly fixed to the seat. The feet are attached to the crank mechanism, and the crank is loaded by a sinusoidal torque and constant angular velocity producing a mean mechanical output of 165 W. It has a total of 18 muscles - nine on each leg. You can control the design parameters of the bicycle and the way the rider propels the pedals by means of the variables at the top of the main file. It might be a good idea to play a bit around with the variables and run some analyses. Try, for instance, to raise and lower the seat. Notice that if you raise the seat more than a few centimeters, the model has trouble reaching the pedals. This is really a kinematical problem, but it causes momentarily very high muscle activities and, if you raise the seat further, makes the kinematical analysis break down because the feet lose the contact with the pedals.

The crank torque profile of a bicycle rider changes when the seat is moved horizontally because the location of the cycle's dead center changes. To account for this, a special feature has been set up in this model to adjust the phase shift of the crank torque profile to the seat position such that the minimum crank torque occurs when the pedals point towards the hip joint regardless of where the saddle is positioned.

Some general terminology

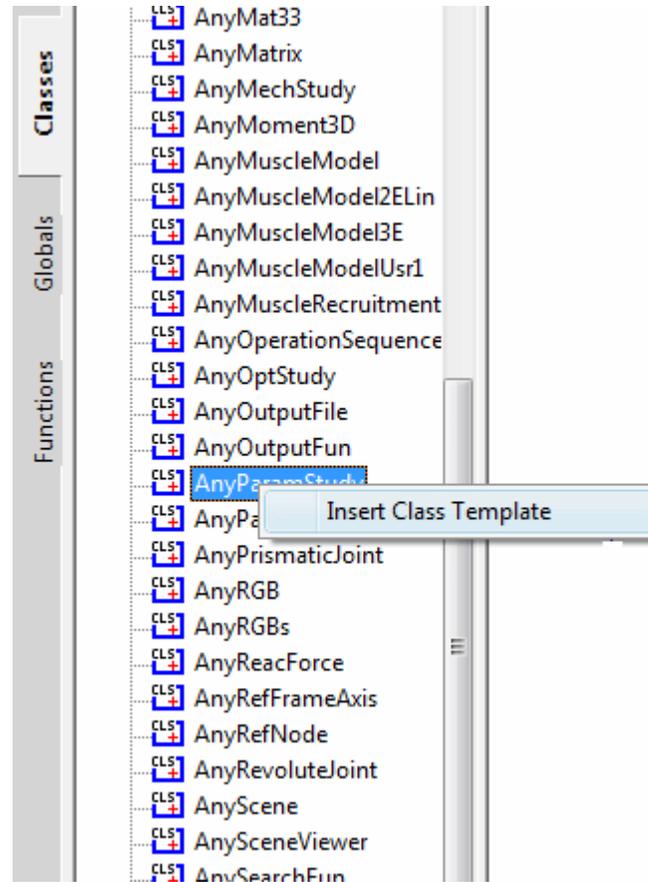
Before we proceed with the definition of a parameter study it might be useful to introduce the terminology used by AnyBody for parameter and optimization studies:

- A design variable is an independent parameter controlling some aspect of the model, for instance the seat height, the pedal length, the pelvic angle, the crank torque variation, the cadence, the strength of a muscle, and so on. In short, just about any property you can set in the AnyScript model. A design variable is always a single number and it must be associated with upper and lower variation limits, but it is allowed to construct the model such that many properties depend on each variable. For instance, you might want to define a variable controlling the soleus muscle strength and then let the soleus muscle in both legs depend on it. In this way you can distinguish between dependent and independent parameters, and only independent parameters can be used as design variables. The AnyScript class defining a design variable is called AnyDesVar.
- A design measure is a dependent parameter that results from an analysis with given values of design variables. Typical examples would be the maximum muscle activity, the metabolism, the mechanical work, the mechanical power generated by a specific muscle, or the force in a joint. The AnyScript class for definition of design measures is the AnyDesMeasure.

These two classes are common to parameter studies and optimization studies, so the two types obviously share several concepts. Let us proceed with the definition of a parameter study. Actually, both these studies come from the same family of classes having the AnyDesStudy as common parent; we commonly refer to these studies as design studies. Within this kinship, they also share the definition of the "analysis" to be performed when evaluating the design measures for a certain set of design variables. The "analysis" is in

fact an AnyScript operation (AnyOperation), called Analysis, which is a member of all design studies. To state an optimization or a parameter study properly, the design variables, the design measures, and the analysis must all be defined.

Definition of a parameter study



A parameter study is as the name indicates a study. Therefore its natural position in the model is below the existing AnyBodyStudy. We can insert a new parameter study by means of the object inserter mechanism from the class tree. Place the cursor below the definition of the AnyBodyStudy Study, click the Classes tab in the tree view, locate the AnyParamStudy, right-click, and insert a template of the class. You should get the following result:

```
AnyBodyStudy Study = {
    AnyFolder &Model = .Model;

    RecruitmentSolver = MinMaxOOSolSimplex;
    Gravity = {0.0, -9.81, 0.0};

    tEnd = Main.BikeParameters.T;
};

AnyParamStudy <ObjectName>
{
    //LogFile = "";
    /*Analysis =
```

```

{
  //AnyOperation &<Insert name0> = <Insert object reference (or full object
definition)>;
};*/
  nStep = ;
  AnyDesVar &<Insert name0> = <Insert object reference (or full object definition)>;
  //AnyDesVar &<Insert name1> = <Insert object reference (or full object definition)>;
  AnyDesMeasure &<Insert name0> = <Insert object reference (or full object
definition)>;
  //AnyDesMeasure &<Insert name1> = <Insert object reference (or full object
definition)>;
};

```

As you can see, this requires a bit of additional specifications and general tidying up:

```

AnyParamStudy ParamStudy = {
  Analysis = {
    //AnyOperation &<Insert name0> = <Insert object reference (or full object
definition)>;
  };
  nStep = ;
  AnyDesVar &<Insert name0> = <Insert object reference (or full object definition)>;
  //AnyDesVar &<Insert name1> = <Insert object reference (or full object definition)>;
  AnyDesMeasure &<Insert name0> = <Insert object reference (or full object
definition)>;
  //AnyDesMeasure &<Insert name1> = <Insert object reference (or full object
definition)>;
};

```

Here's a brief explanation of the different components of a parameter study:

Parameter	Function
Analysis	This is a specification of the operation(s) to perform to provide the data we are studying in the parameter study. This will typically be an InverseDynamicAnalysis operation, but it could also be simply an evaluation of some mathematical expression, or it could be a combination of multiple operations, for instance various calibrations followed by an inverse dynamic analysis.
nStep	This is a specification of how many steps to evaluate in the parameter study for each parameter.
AnyDesVar	The study must declare at least one of these. It is the parameter(s) that are varied in the study and for combinations of which the model is analyzed. You can define as many as you like, but please beware that the number of analyses in the parameter study is the product of steps for each AnyDesVar, so the time consumption grows exponentially with the number of AnyDesVars.
AnyDesMeasure	Each of these objects specifies a property that is the result of the analysis and which must be collected for further inspection as the study proceeds. You can define as many of these as you like.

Let us insert the necessary specifications to perform a parameter study on the saddle position of the bicycle:

```

AnyParamStudy ParamStudy = {
  Analysis = {
    AnyOperation &Operation = ..Study.InverseDynamicAnalysis;
  };
};

```

As you can see, this is a pointer to the inverse dynamic analysis of the existing AnyBodyStudy in the bicycle model. This specification simply means that to evaluate the parameters we want to investigate in this parameter study, we must execute the analysis of the bicycle. This may seem obvious in a simple model like this one, but many AnyScript models contain multiple studies and each study contains multiple operations.

The next specification deals with the parameters to vary:

```
nStep = ;
AnyDesVar SaddleHeight = {
    Val = Main.BikeParameters.SaddleHeight;
    Min = Val - 0.05;
    Max = Val + 0.03;
};
AnyDesVar SaddlePos = {
    Val = Main.BikeParameters.SaddlePos;
    Min = Val - 0.07;
    Max = Val + 0.10;
};
AnyDesMeasure <Insert name0> = <Insert object reference (or full object definition)>;
//AnyDesMeasure <Insert name1> = <Insert object reference (or full object
definition)>;
};
```

Please notice here that we have removed the '&'s that were inserted in the template in front of the variable names. Instead of pointing at AnyDesVars defined elsewhere we include the entire definition right here in the study, and this is actually the usual way to do it. Each AnyDesVar gets three properties set. The first one is called 'Val' and is simply set equal to an existing parameter in the model. The best way to understand this statement is to think of Val as a reference variable that is equalized in the first case with the SaddleHeight, which is a parameter defined at the top of the main file. At any time in the parameter study, Val will be equal to the saddle height as one should expect from the assignment. But in this special case, the assignment also goes the other way: It lets the parameter study control the value of what is on the right hand side of the equality sign, in this case the SaddleHeight parameter. We have similarly defined a second parameter, SaddlePos, which allows the parameter study to vary the horizontal saddle position. This two-way linkage between Val and another variable in the model implies certain restrictions on what assignments AnyScript allows for this particular case. The referred variable must be a scalar quantity, i.e. either a scalar or an element of a larger structure (e.g. vector or matrix). Secondly, it must be an independent scalar quantity, i.e., it cannot depend (by expressions) on other variables; otherwise there would exist an ambiguity. Alternatively to linking another independent variable in the model, Val can be initialized with constants. In this case, Val will be the only instance of the design variable and the model must depend directly on Val. This latter use is a somewhat restricted exploitation of AnyDesVar and is typically not practical when studies of existing models are to be carried out.

The next step is to define the properties we wish to study, i.e. the dependent parameters or "design measures" of the model. As you know, after running an operation from a study the results are available in the Output branch of the tree view of the operation and they can be plotted, dumped and copied to the clipboard and so on. Now we are defining a study that will execute operations from other studies and assemble the results for later investigation. We might even want to make mathematical operations on these results, combine results from different operations, and so on. To do this we must refer to the result we wish to store for further processing. There is just one semantic problem: The results do not exist until we have performed the analysis, but we must refer to them already when we author (and load) the model.

To solve this problem we must go back to the AnyBodyStudy Study, from where we want to lift the results, and declare an object that will allow us to refer to computational results before they are actually made. The object is of class AnyOutputFun, and we shall add it to the existing AnyBodyStudy:

```
// The study: Operations to be performed on the model
AnyBodyStudy Study = {

    AnyFolder &Model = .Model;

    RecruitmentSolver = MinMaxOOSolSimplex;
    Gravity = {0.0, -9.81, 0.0};

    tEnd = Main.BikeParameters.T;
    nStep = 50;
```

```

AnyOutputFun MaxAct = {
    Val = .MaxMuscleActivity;
};
};

```

This allows us to refer to `Study.Output.MaxMuscleActivity` before it actually gets created.

`AnyOutputFun` is actually a class of mathematical function that returns the output (when existing) associated with the `Val` member. So here we have created a function called `MaxAct` that takes no arguments and returns the output data for `.MaxMuscleActivity`. Notice that `AnyOutputFun` must be declared inside a study in order to resolve the association with the output data structure of the particular study.

We can now use the output function, `MaxAct`, in our design measure simply by calling the function in the assignment of the `Val` member of the `AnyDesMeasure`:

```

AnyDesVar SaddlePos = {
    Val = Main.BikeParameters.SaddlePos;
    Min = Val - 0.07;
    Max = Val + 0.10;
};
AnyDesMeasure MaxAct = {
    Val = max(..Study.MaxAct());
};

```

Notice the definition. The `MaxAct` function for each `InverseDynamicAnalysis` operation returns a vector of maximum muscle activities in the model. The vector has as many components as the study has time steps, i.e. 50 in the present case. In the definition of the `AnyDesMeasure` we want to save only the largest value of each of the vector, so we wrap the call of the `MaxAct` function in another `max` function. `AnyScript` gives you a number of such data processing functions and we shall study others further down. Please refer to the reference manual for further details.

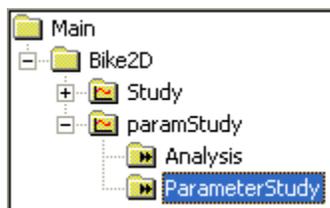
One thing is missing before we can try the whole thing out: We must specify how many steps we want the parameter study to perform for each parameter. As in `AnyBodyStudies` this is done by the `nStep` variable, but where `nStep` in an `AnyBodyStudy` is an integer variable, it is a vector with one component for each `AnyDesVar` in an `AnyParamStudy`. We shall be modest at first and choose only five steps in each direction. And so, the final `AnyParamStudy` looks like this:

```

AnyParamStudy ParamStudy = {
    Analysis = {
        AnyOperation &Operation = ..Study.InverseDynamicAnalysis;
    };
    nStep = {5,5};
    AnyDesVar SaddleHeight = {
        Val = Main.BikeParameters.SaddleHeight;
        Min = Val - 0.05;
        Max = Val + 0.03;
    };
    AnyDesVar SaddlePos = {
        Val = Main.BikeParameters.SaddlePos;
        Min = Val - 0.07;
        Max = Val + 0.10;
    };
    AnyDesMeasure MaxAct = {
        Val = max(..Study.MaxAct());
    };
};

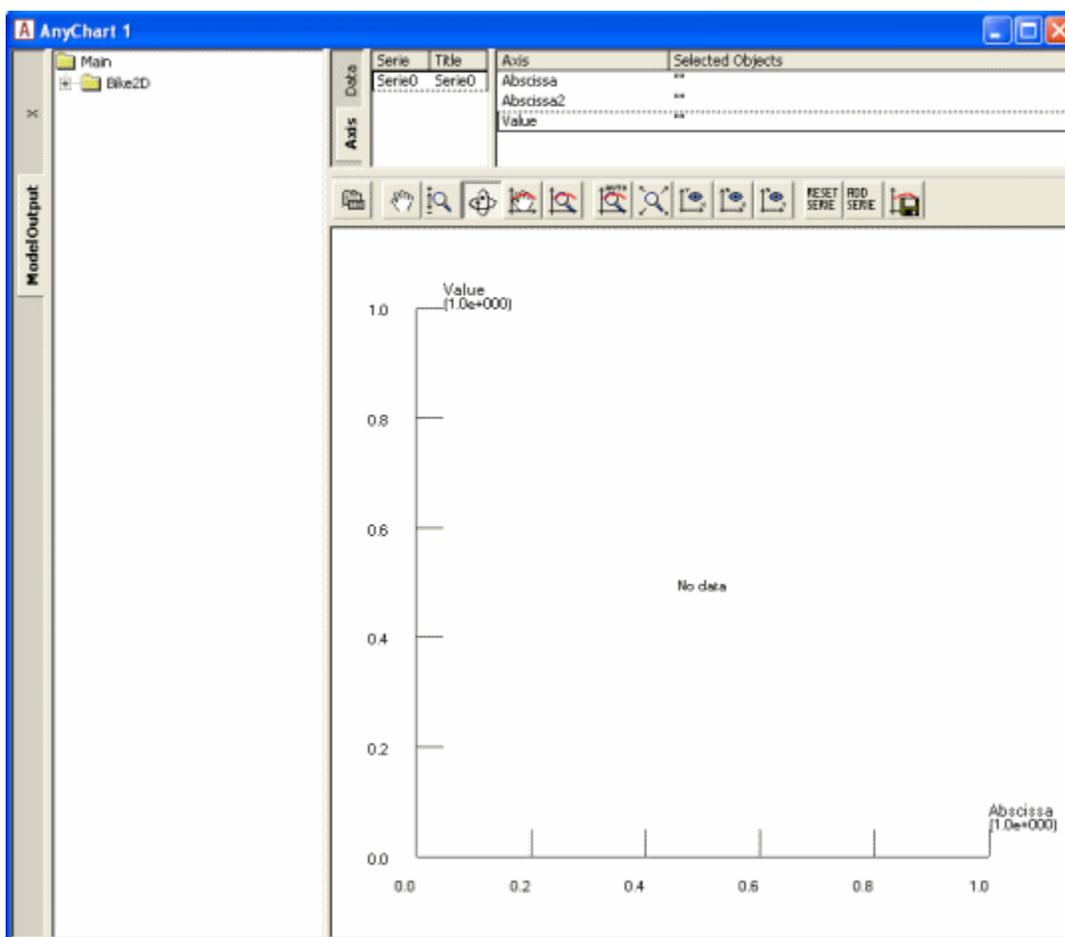
```

It is finally time try it out. If you have typed everything correctly, then you should be able to load the model and expand the Operations Tree in the left hand side of the Main Frame to this:

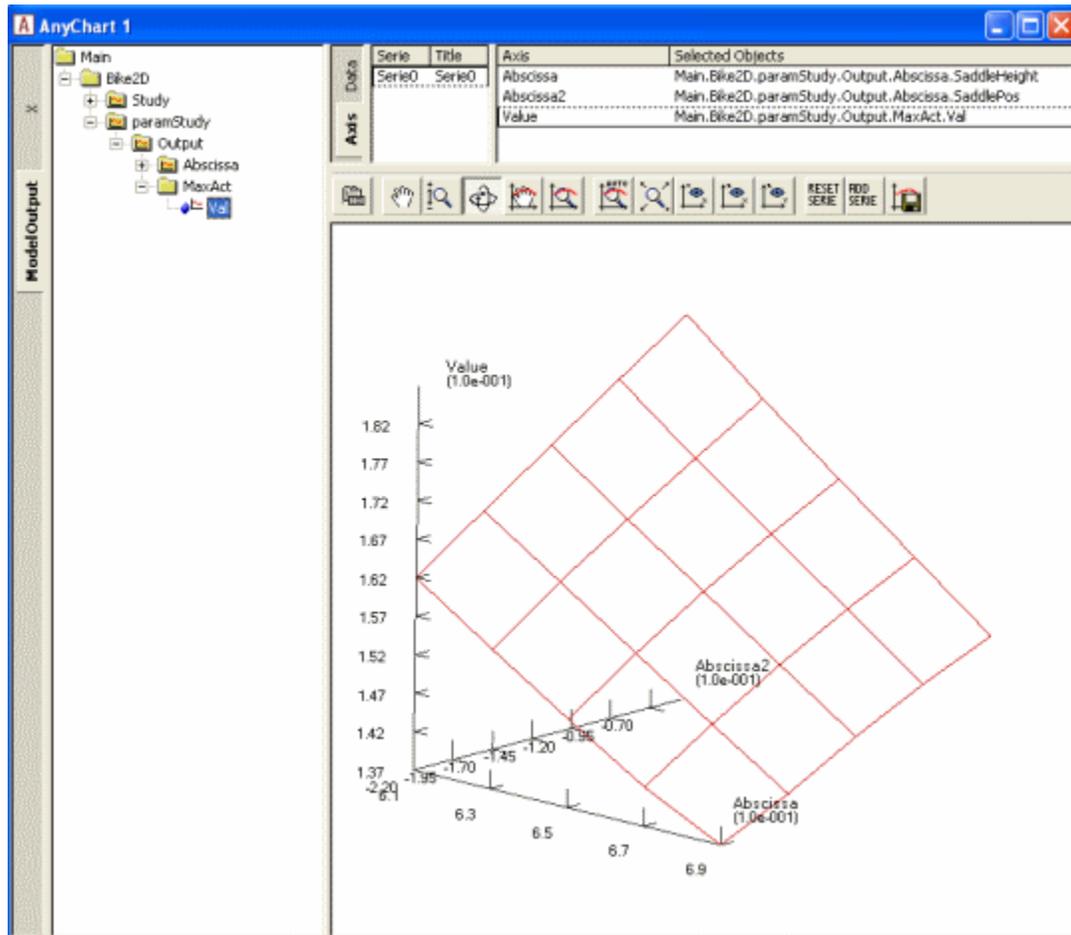


Make sure you have a Model View window open. Select ParameterStudy as indicated and hit the "Run" button. You should see the model starting to cycle, and if you watch the vicinity of the saddle carefully, you will see that the hip joint is changing its position on a 5 x 5 grid. With a reasonably fast computer it should take a minute or less to do the 25 analyses after which the computations stop. Congratulations! You have completed your first parameter study.

The obvious way to visualize the results of a study with two parameters is as a 3-D surface. AnyBody has a window to make that type of plots. Please click Window -> AnyChart 2D/3D (new). A new window containing a coordinate system and the usual model tree appears:



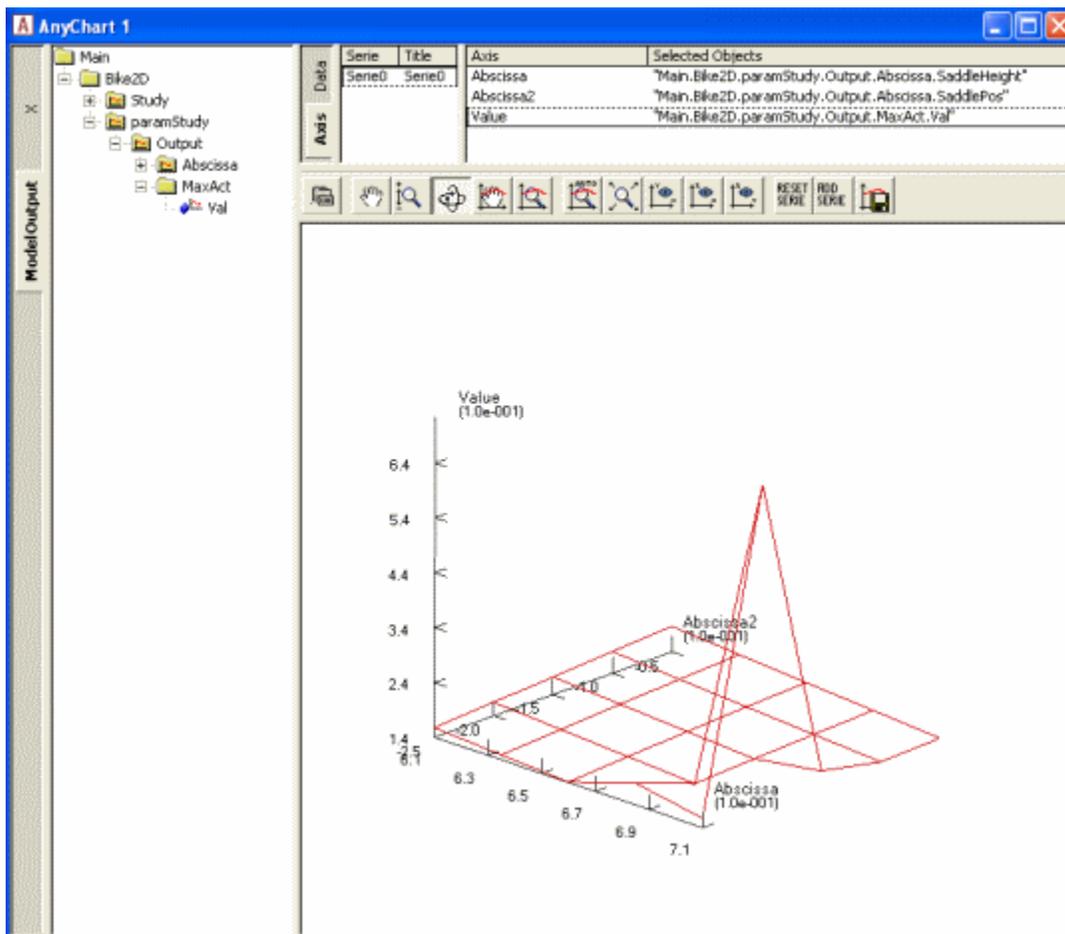
The toolbar of this window indicates a kinship with the Model View window. Indeed, if you select the rotation button in the toolbar and drag the mouse with the left button down inside the coordinate system you will notice that the system rotates just like an ordinary Model View. Now, expand the Bike2D node in the tree until you can click the ParamStudy->Output->MaxAct->Val property. The coordinate system automatically attains a second abscissa axis and you can see a nice surface like this:



The surface shows the maximum muscle activity over the cycle for each of the 25 combinations of parameters and provides a very nice overview of the behavior of the model. The surface reveals that the highest and most backward position is the best. Why not try higher and more backward, then? It is very simply to do:

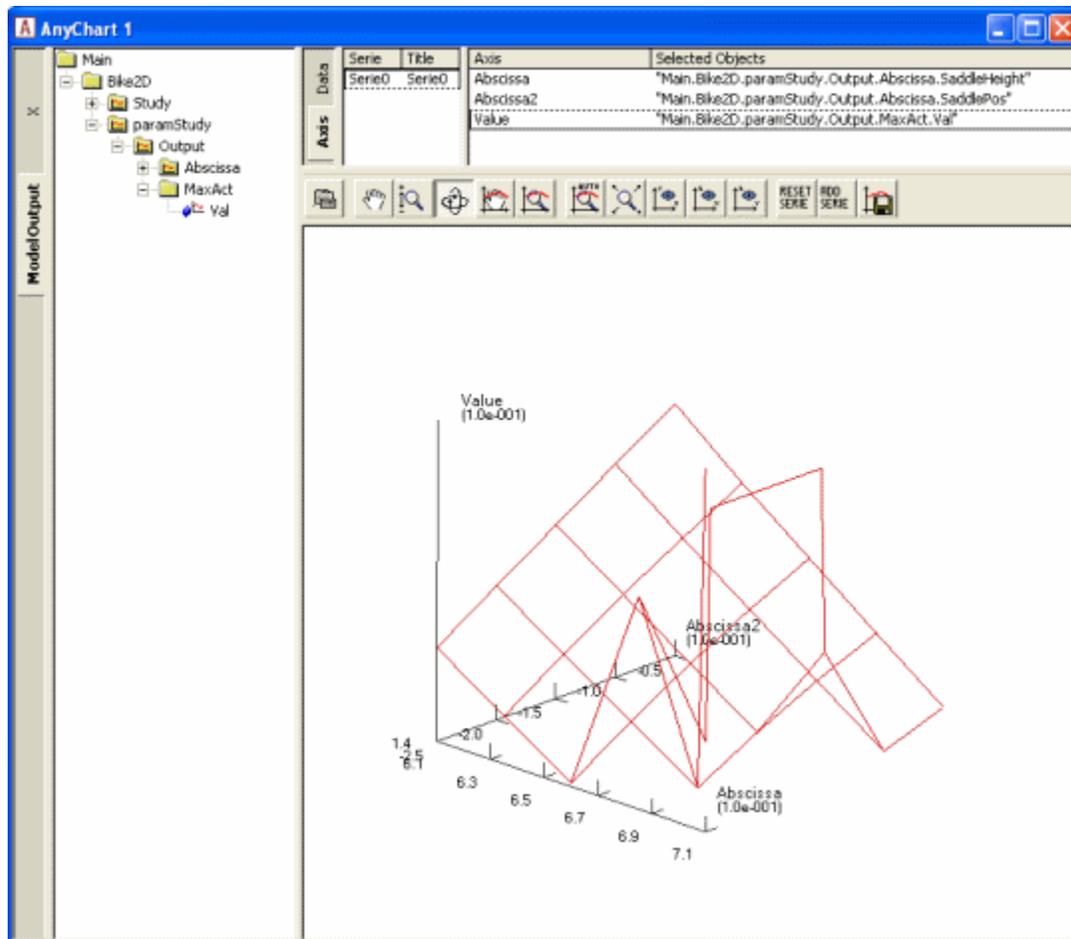
```
AnyDesVar SaddleHeight = {
    Val = Main.BikeParameters.SaddleHeight;
    Min = Val - 0.05;
    Max = Val + 0.05;
};
AnyDesVar SaddlePos = {
    Val = Main.BikeParameters.SaddlePos;
    Min = Val - 0.10;
    Max = Val + 0.10;
};
```

combinations you may notice muscles beginning to bulge more and momentarily attain the color of magenta. This is the system's way of demonstrating that the muscles have been loaded above 100% of their strength. The reason why this happens is that, as the seat rises, the model gets into positions where it is difficult for the feet to reach the pedals. Just before the feet cannot reach the pedals the knee movements are accelerated causing large inertia forces in the system. All this happens a bit more drastically in an ideal rigid body model than it would in real life where joints have a bit of slack, segments are slightly elastic, and the prescribed kinematics may be compromised. You can see very clearly what happens if you go back to the AnyChart View and study the new surface:



The surface is now completely dominated by the one combination, which is difficult for the model to do. You can still see the surface shape if you change the scale of the value axis. This and all other settings are

available if you click the  button in the toolbar. Doing so will produce a window with a tree view in which you can select ValueAxis->Max. Try setting Max to 0.2 and you should obtain the following:



What this study reveals is that in terms of muscle activity to drive the bicycle a high seat is advantageous, but there seems to be a very sharp limit where the leg gets close to not being able to reach the pedals, and this should not be exceeded. One additional remark in this context is that this bicycle model has a predefined ankle angle variation whereas a real human can compensate for a higher seat by letting the ankle operate in a more plantar-flexed position.

Before we finish this section, let us take a look at a particularly important feature of AnyScript mathematics: The ability to compute integral properties. AnyBody has a simple way of approximating the metabolism of muscles based on the simulation of each muscle's mechanical work. Metabolism is technically a power measured in Watt, and the sum of the individual muscle metabolisms will give us an estimate of the total metabolism involved in the bicycling process. It is fairly simple to add up the muscle metabolisms in the AnyBody study:

```
// The study: Operations to be performed on the model
AnyBodyStudy Study = {

    AnyFolder &Model = .Model;

    RecruitmentSolver = MinMaxOOSolSimplex;
    Gravity = {0.0, -9.81, 0.0};

    tEnd = Main.BikeParameters.T;
    nStep = 50;
```

```

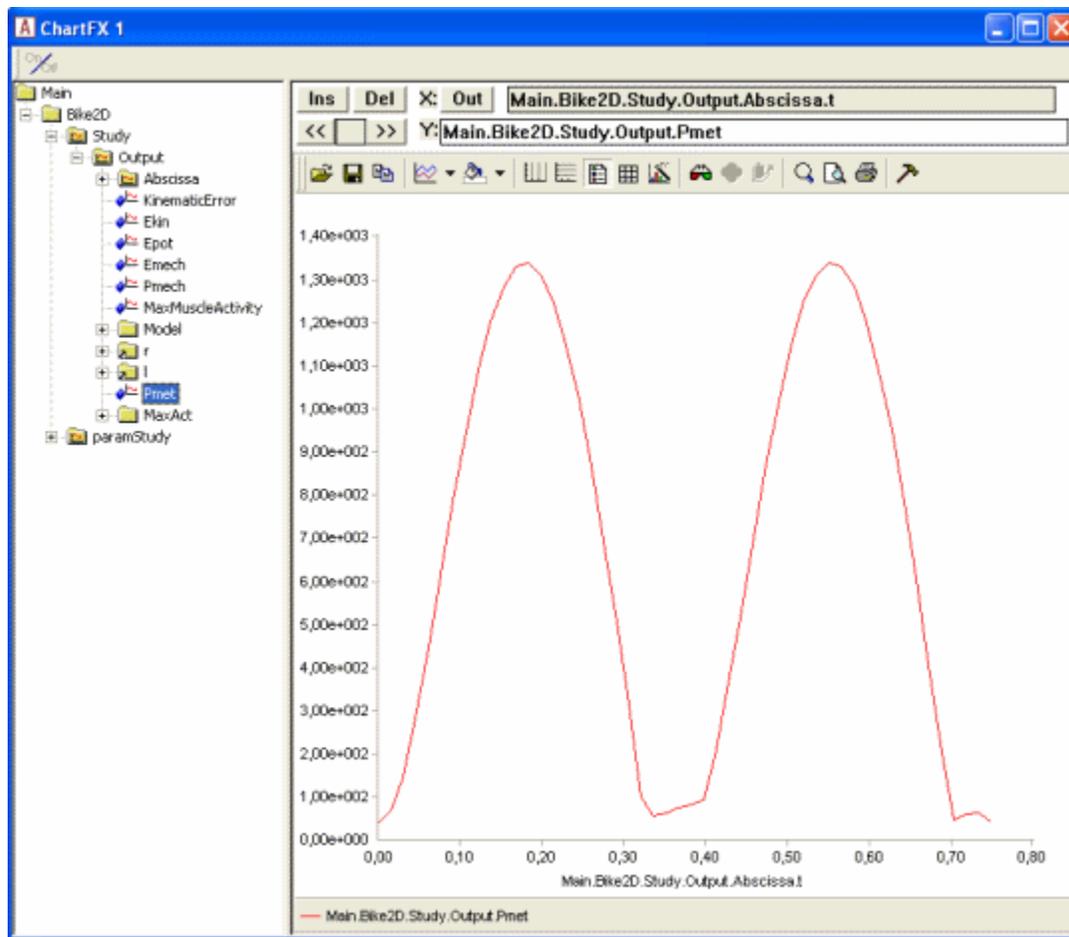
// Useful variables for the optimization
AnyFolder &r = Main.Bike2D.Model.Leg2D.Right.Mus;
AnyFolder &l = Main.Bike2D.Model.Leg2D.Left.Mus;
AnyVar Pmet = r.Ham.Pmet+r.BiFemSh.Pmet+r.GlutMax.Pmet+r.RectFem.Pmet+
r.Vasti.Pmet+r.Gas.Pmet+r.Sol.Pmet+r.TibAnt.Pmet+
l.Ham.Pmet+l.BiFemSh.Pmet+l.GlutMax.Pmet+l.RectFem.Pmet+
l.Vasti.Pmet+l.Gas.Pmet+l.Sol.Pmet+l.TibAnt.Pmet;

AnyOutputFun MaxAct = {
    Val = .MaxMuscleActivity;
};

};

```

Notice that we have defined the r and l variables for convenience to limit the size of the expressions. If you run the InverseDynamicAnalysis (go on and try!) you will find the new variable mentioned in the list of output, and you can chart it in a ChartFX View:



The area under this curve is the total metabolism combusted over a crank revolution. To compute this we must introduce two more elements. The first one is an AnyOutputFun as we have seen it before. The purpose of this function is to make it semantically possible to refer to the output of the Pmet variable before it has actually been computed:

```

// Useful variables for the optimization
AnyFolder &r = Main.Bike2D.Model.Leg2D.Right.Mus;

```

```

AnyFolder &l = Main.Bike2D.Model.Leg2D.Left.Mus;
AnyVar Pmet = r.Ham.Pmet+r.BiFemSh.Pmet+r.GlutMax.Pmet+r.RectFem.Pmet+
r.Vasti.Pmet+r.Gas.Pmet+r.Sol.Pmet+r.TibAnt.Pmet+
l.Ham.Pmet+l.BiFemSh.Pmet+l.GlutMax.Pmet+l.RectFem.Pmet+
l.Vasti.Pmet+l.Gas.Pmet+l.Sol.Pmet+l.TibAnt.Pmet;

AnyOutputFun MaxAct = {
    Val = .MaxMuscleActivity;
};
AnyOutputFun Metabolism = {
    Val = .Pmet;
};

```

The second missing element is the actual integration of the function. This we perform in the parameter study where we define the AnyDesMeasure:

```

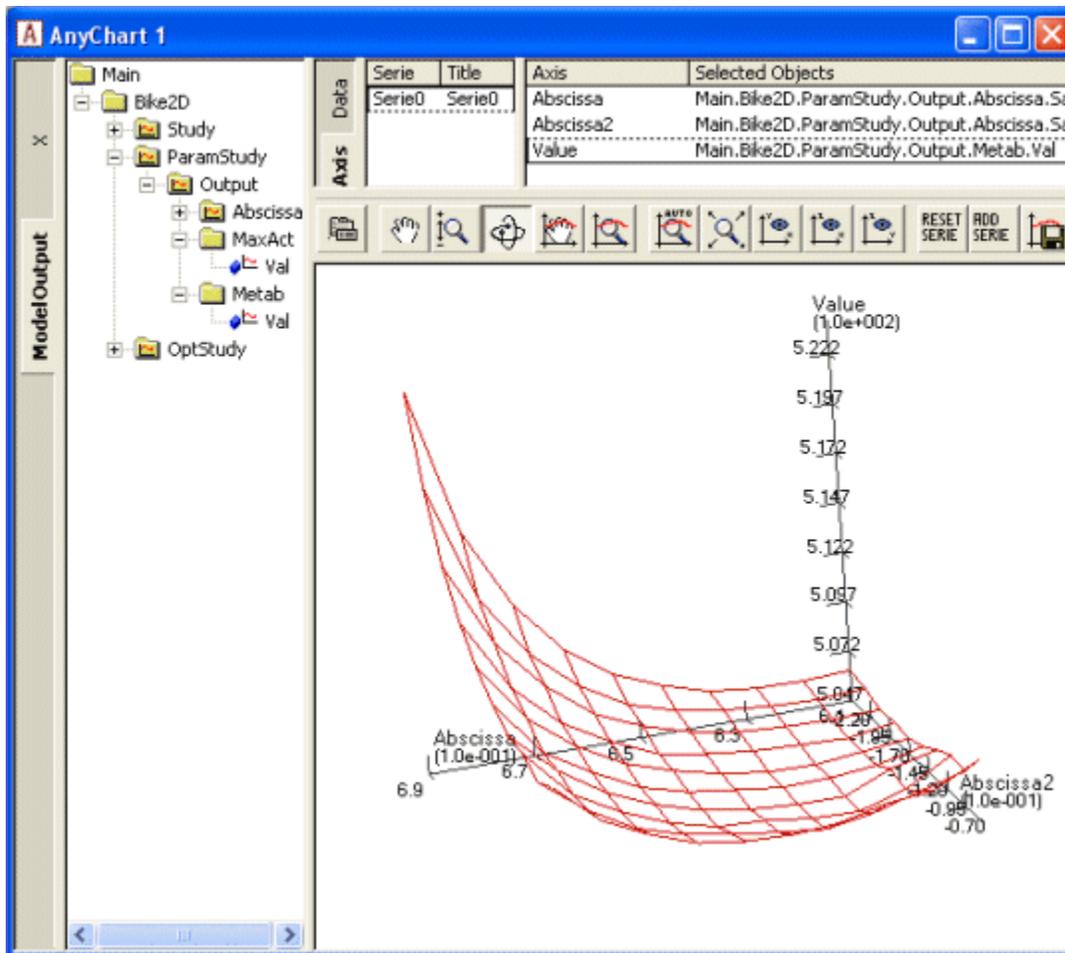
AnyParamStudy ParamStudy = {
    Analysis = {
        AnyOperation &op = ..Study.InverseDynamicAnalysis;
    };
    nStep = {10,10};
    AnyDesVar SaddleHeight = {
        Val = Main.BikeParameters.SaddleHeight;
        Min = Val - 0.05;
        Max = Val + 0.03;
    };
    AnyDesVar SaddlePos = {
        Val = Main.BikeParameters.SaddlePos;
        Min = Val - 0.07;
        Max = Val + 0.10;
    };

    AnyDesMeasure MaxAct = {
        Val = max(..Study.MaxAct());
    };
    AnyDesMeasure Metab = {
        Val = secint(..Study.Metabolism(),..Study.tArray);
    };
};

```

The secint function performs a numerical integration of the first argument against the second argument. Each argument must be an array and the number of components in the two arguments must be the same.

Notice the other two changes: We have changed the variable limits back to what they were before and we have decided to be a little more adventurous and have specified 10 variable steps in each direction. It is time to run the parameter study again. The new Metab variable is now available in the list under the ParamStudy in the AnyChart window and can be plotted:



We shall return to the capabilities of the AnyChart in more detail in the [next lesson](#), which deals with the definition of optimization studies.

Optimization studies

The parameter study introduced in the preceding lesson provides a complete overview of the design space, but the study is only feasible when the problem has few independent parameters, preferably one or two. In the previous lesson we considered a problem with two parameters and 5 steps in each direction of the design space leading to $5^2 = 5 \times 5 = 25$ analyses. If the problem had 10 parameters we would be facing $5^{10} = 9.7$ million analyses, which is an entirely different matter in terms of computation times. The truth is that such so-called full factorial parameter studies are computationally infeasible when the problem has more than very few independent parameters. So what to do?

The solution is to use a method that picks the combinations to compute carefully and only has to evaluate a few of them. One class of such methods is optimization. An optimization algorithm systematically searches through the design space for the combination of parameters that minimizes the value of a function of the parameters, the so-called objective function. Some algorithms also allow the definition of constraint functions, which are dependent parameters that must be maintained below a certain upper limit.

The AnyBody Modeling System provides a study to handle optimization problems. The mathematical definition of the problem it solves is as follows:

Minimize

$$g_0(x_1..x_n)$$

Subject to

$$g_i(x_1..x_n) \leq 0$$

$$L_j \leq x_j \leq U_j$$

where g_0 is called the objective function, $x_j, j=1..n$ are the design variables, and $g_i, i=1..m$ are the constraints. The definition of an optimization problem in AnyBody is therefore a question of appointing independent parameters as design variables and dependent parameters as the objective function and constraints. Please notice that m could be zero in which case we have a problem that is only constrained by the simple bounds on the variables.

In an optimization terminology, the parameter study from the preceding lesson could be defined as:

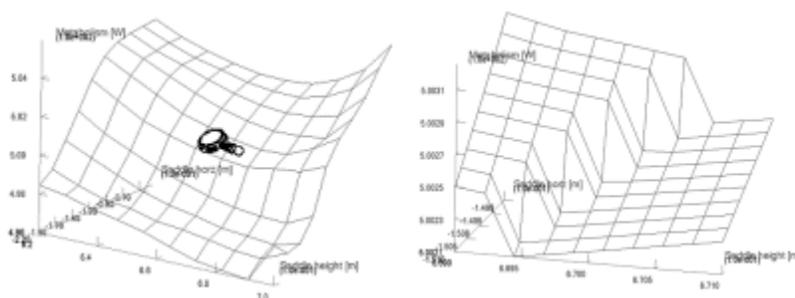
Minimize

Metabolic energy consumption

Subject to

*Saddle height within predefined limits
Saddle horizontal position within predefined limits*

In fact, this is precisely what we are going to do, but before we proceed, let us briefly look at the properties of a typical musculoskeletal objective function and how the optimization algorithm solves the problem.



The two pictures above both show the result of a parameter study. The picture on the right is the section indicated by the magnifying glass on the left amplified by 50 times. As you can see, the seemingly smooth objective function has a microscopic jump. In other words the function is non-smooth and in fact discontinuous at certain points. Not all design measures have such discontinuities, but some do. The figure also indicates that the function is smooth in between these discontinuities. Optimization algorithms are trying to navigate on multi-dimensional hyper-surfaces with such qualities and must consequently be robust against a certain amount of non-smoothness. The optimization algorithm in AnyBody is indeed capable of doing this in most cases. It is a special version of a so-called feasible directions algorithm, which seeks out the optimum in two-step loops. The two steps are:

1. Decide on a search direction.
2. Perform a linear search to find the minimum along the chosen direction.

This means that it is only necessary to perform analyses of the function values at the points that the algorithm actually visits and not all points in a predefined grid as we did in the parameter study. It also means that the algorithm depends on the smoothness of the surface when it decides on a direction to take in step 1, but once the direction has been chosen, the line search in step 2 can be done with methods that do not predispose smoothness.

Now that we know what to expect, we can proceed to the actual definition of the optimization study. The previous definition of the parameter study will help us a lot because an optimization study has almost exactly the same structure. So the first step would be to simply copy the parameter study:

```
AnyParamStudy ParamStudy = {
  Analysis = {
    AnyOperation &Operation = ..Study.InverseDynamicAnalysis;
  };
  nStep = {5,5};
  AnyDesVar SaddleHeight = {
    Val = Main.BikeParameters.SaddleHeight;
    Min = Val - 0.05;
    Max = Val + 0.03;
  };
  AnyDesVar SaddlePos = {
    Val = Main.BikeParameters.SaddlePos;
    Min = Val - 0.07;
    Max = Val + 0.10;
  };
  AnyDesMeasure MaxAct = {
    Val = max(..Study.MaxAct());
  };
};
```

```
AnyParamStudy ParamStudy = {
  Analysis = {
    AnyOperation &Operation = ..Study.InverseDynamicAnalysis;
  };
  nStep = {5,5};
  AnyDesVar SaddleHeight = {
    Val = Main.BikeParameters.SaddleHeight;
    Min = Val - 0.05;
    Max = Val + 0.03;
  };
  AnyDesVar SaddlePos = {
    Val = Main.BikeParameters.SaddlePos;
    Min = Val - 0.07;
    Max = Val + 0.10;
  };
  AnyDesMeasure MaxAct = {
    Val = max(..Study.MaxAct());
  };
  AnyDesMeasure Metab = {
    Val = secint(..Study.Metabolism(), ..Study.tArray);
  };
};
```

We proceed to change a few parameters:

```
AnyOptStudy OptStudy = {
  Analysis = {
```

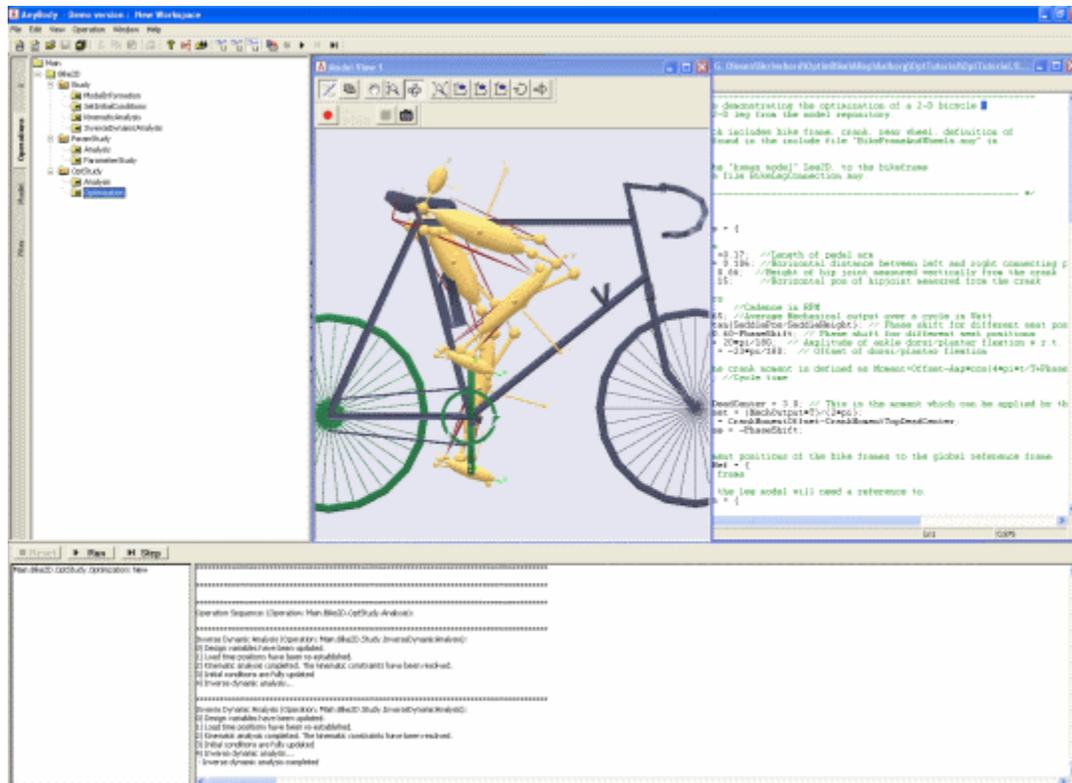
```

AnyOperation &Operation = ..Study.InverseDynamicAnalysis;
};
AnyDesVar SaddleHeight = {
  Val = Main.BikeParameters.SaddleHeight;
  Min = Val - 0.05;
  Max = Val + 0.03;
};
AnyDesVar SaddlePos = {
  Val = Main.BikeParameters.SaddlePos;
  Min = Val - 0.07;
  Max = Val + 0.10;
};
AnyDesMeasure Metab = {
  Val = secint(..Study.Metabolism(),..Study.tArray);
  Type = ObjectiveFun;
};
};

```

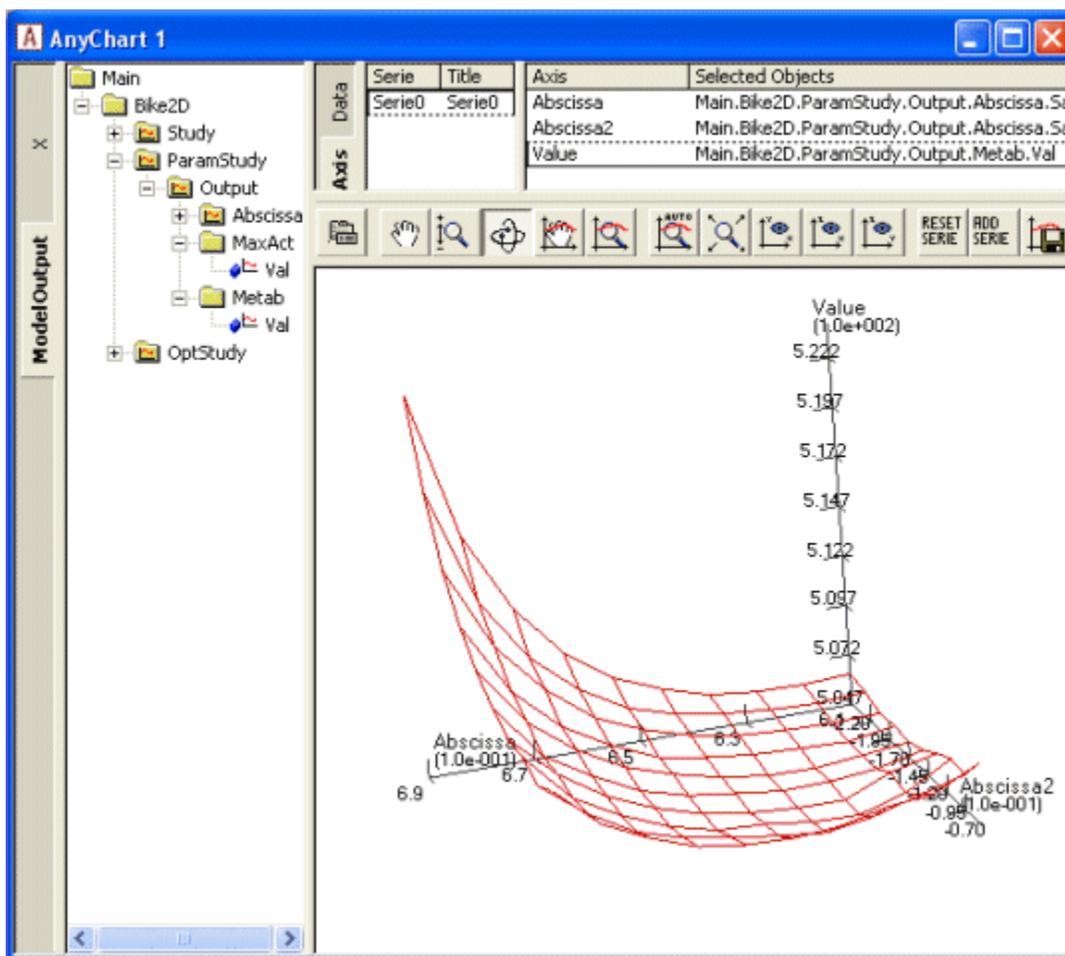
Please notice that the AnyDesMeasure MaxAct was removed, and so was the entire line with the nStep specification. The optimization study does not use any particular step size but rather adapts its steps automatically to find the accurate position of the optimum. This is another advantage of optimization over a parameter study. Finally, we have added a type specification to the Metab object specifying that this is the objective function of the problem.

This is the definition of an optimization problem that will vary the saddle height and horizontal position to minimize the metabolism. Let us run it and see what happens. Load the model in and please make sure that you have a Model View window open so that you can see the difference in the way the seat position is varied compared to the parameter study.

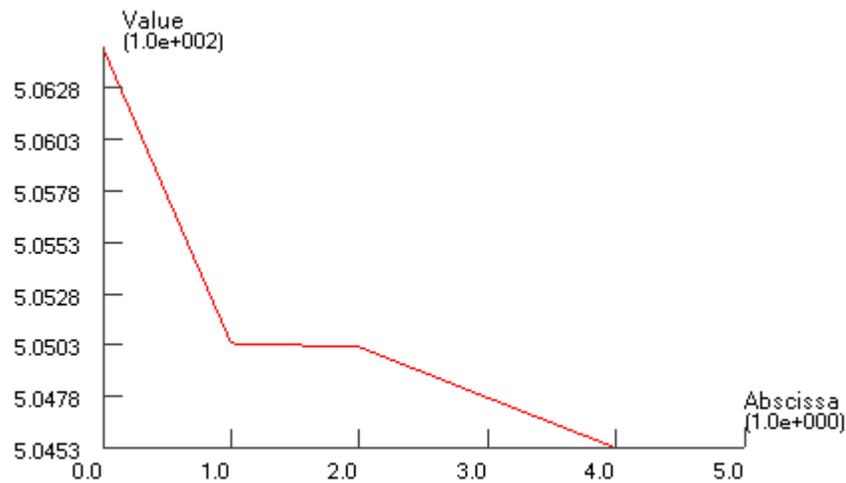


If the model loads you should get a screen picture similar to the one above this text. Expand the OptStudy branch in the operations tree, click Optimization once and then the Run button. The model starts cycling and after a few rounds you will notice the saddle position changing, but not in a systematic grid like in the parameters study. What you will see is gradual changes back and forth in different directions until the changes wear off and the position converges. Every time you see the step counter below the Run button changing number it is an indication that the optimizer has picked a new optimization direction to try. You should see the number increasing in slow steps up to six before the process stops and the system announces that it is finished. Please notice that the changes of saddle position in the last several steps is very minute, which is typical for optimization: the first steps bring large changes and large improvements, while the last many steps only improve slightly.

Now we are going to study the results in more detail using the AnyChart window. Do you still have the AnyChart window from the previous lesson with the Metabolism parameter study open? It should look like this:



If not, please run the ParamStudy again and plot the surface. When you have this surface ready, please open another AnyChart window by clicking Window->AnyChart 2D/3D (new). In the new window, please expand the tree down to Main.Bike2D.OptStudy.Output.Metab. Then click the Val variable under Metab. This produces a simple 2-D graph showing the development of the metabolism over the 5 iterations:



The graph confirms that the vast majority of the improvement is obtained in a couple of iterations and the final iteration contributes only by a minor, almost insignificant adjustment. Such iterations with insignificant improvements occur due to the convergence criterion, i.e., the criterion that stops the optimization process. The optimizer does not detect mathematically that the objective function has an optimum value; it merely detects that the changes of the found solution are small from one iteration to the next. Therefore, the optimization process will always end with one (or more) steps with insignificant changes.

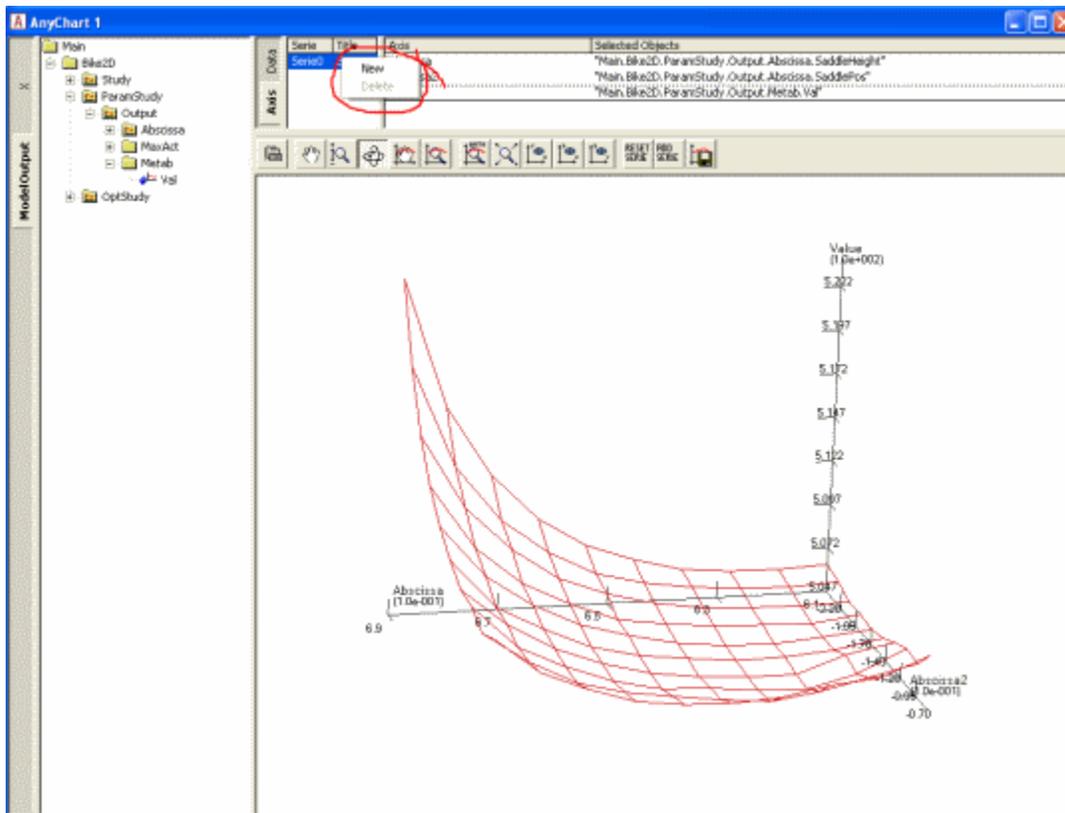
The optimal solution in the Model View looks like this:



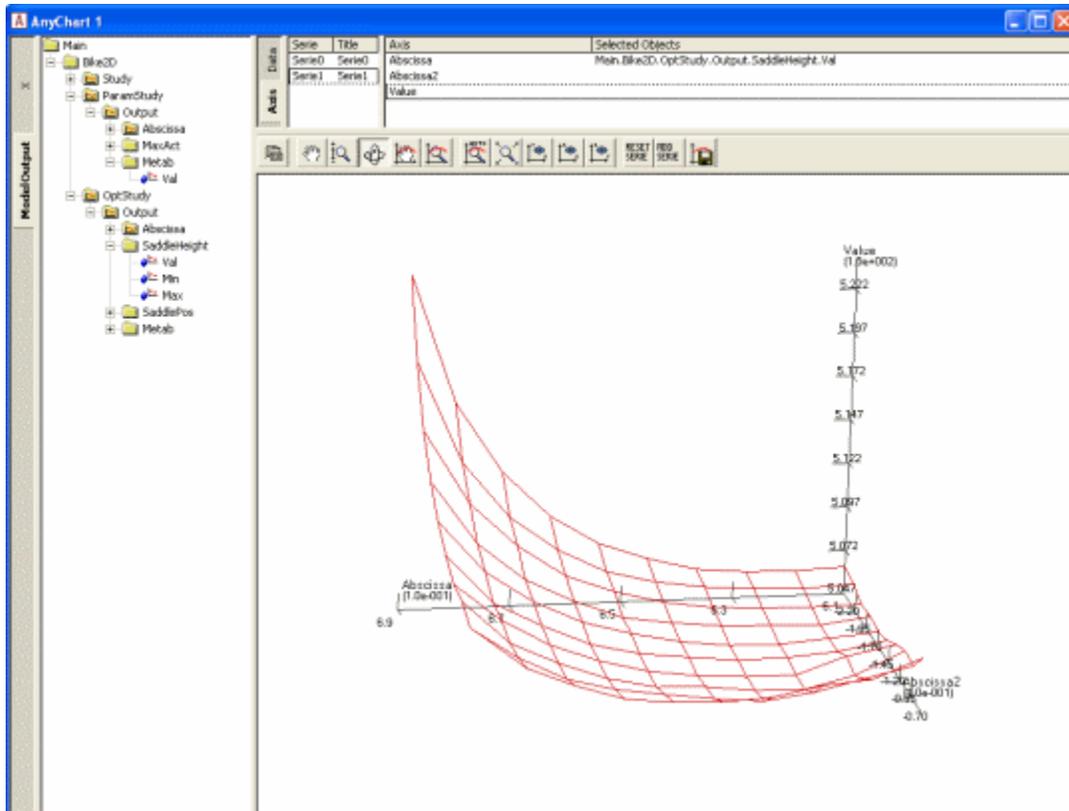
Just above the Metab variable in the tree you can find the two independent variables, SaddleHeight and SaddlePos, and they can be graphed the same way revealing that their convergence is less monotone over the iterations. This is also quite usual for optimization processes.

An interesting way to investigate the convergence is to plot it in the variable/objective space rather than over the iterations. This is what we need the window with the parameter study surface for. At the top of this window you will find panels listing series and data to be plotted. Please right-click in the series window and

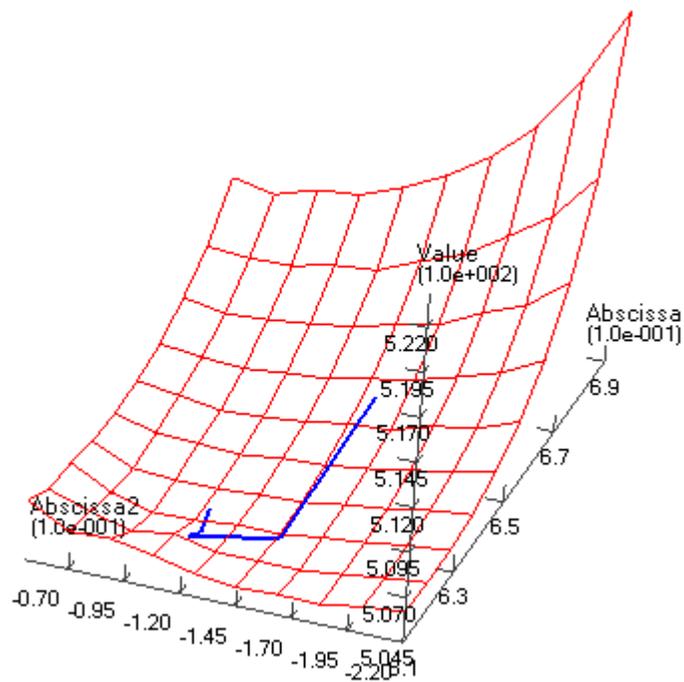
select "New":



This will give you a blank "Series 1". When you highlight it by clicking with the mouse you will see the list of Selected Objects in the right-hand pane is empty. We are going to fill in the SaddleHeight and SaddlePos variables from the OptStudy as Abcissa and Abcissa2, respectively. This is done by selecting Abcissa and Abcissa2 in turn and then expanding the OptStudy branch until the SaddleHeight.Val and SaddlePos.Val, respectively, can be selected:

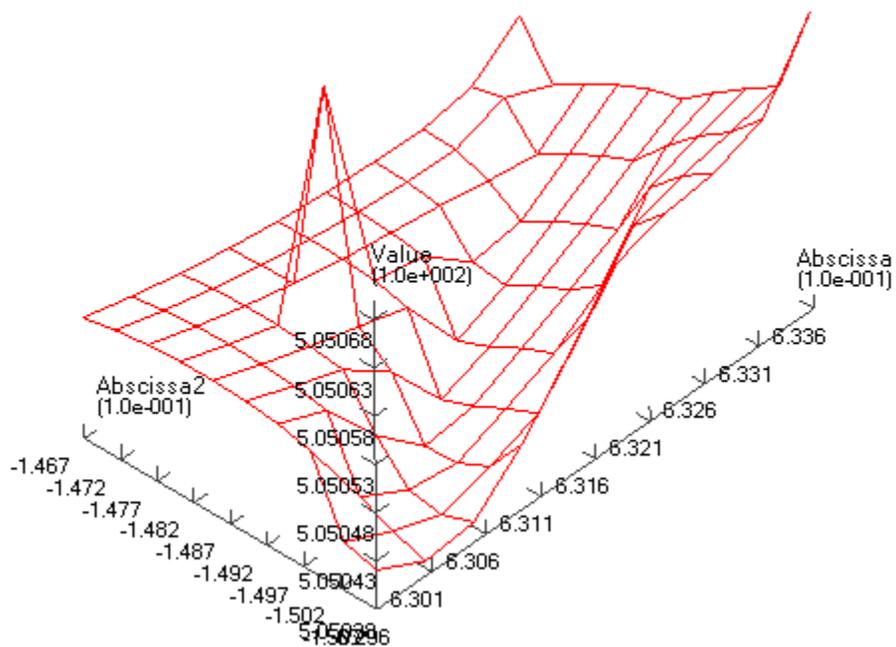


Finally, in the Value field select OptStudy.Metab.Val and look carefully at the plot. You will see that an additional polyline has been added. It originates approximately at the middle of the surface and shows the path the optimization process has taken through the design space to the minimum point. You can change the color of the line by clicking the leftmost button (Properties) in the toolbar directly over the graphics pane. This gives you access to all the settings and lets you control the appearance of graphs in detail. In the picture below we have selected RGB = {0,0,1}, i.e. blue, for Series1 and Thickness = 2:



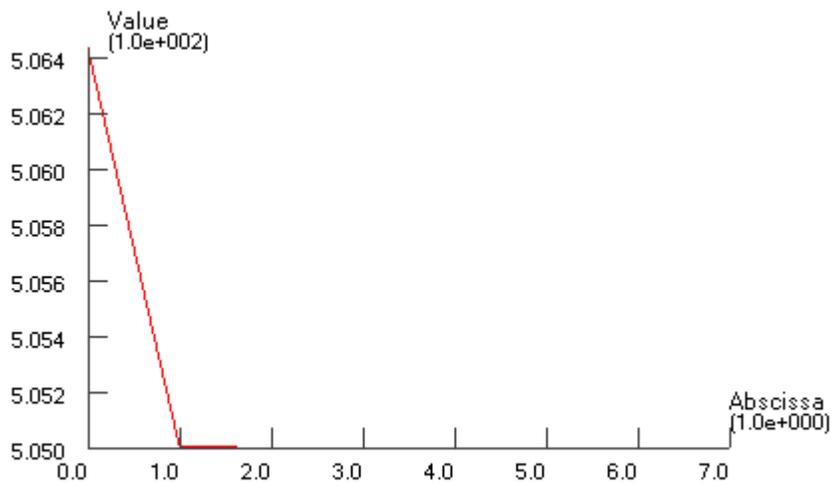
This plot illustrates the convergence history in the "landscape" of the objective function. Here we can see the reasons for the convergence being as it is. Actually, the optimum value lies in a relatively flat region and therefore the exact mathematical location of the optimum may be of a more academic importance than practical relevance since we can find many design point with almost the same objective function value.

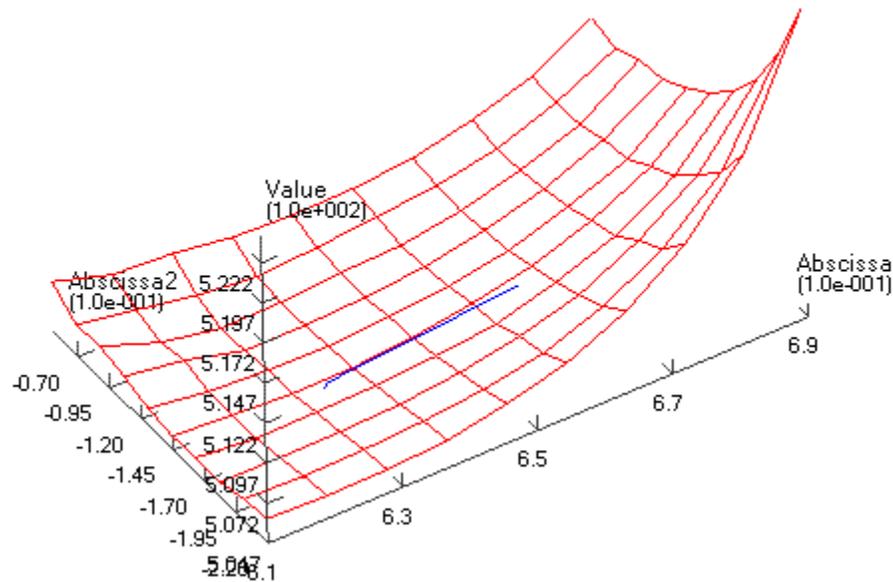
"A flat optimum", like this, can occasionally cause problems for the optimization process to provide exact convergence because it is difficult to distinguish between insignificant changes due to flatness or convergence. Furthermore, one more obstacle for finding the exact optimum is present in the given case. The objective function is not as smooth as the parameter study with the relative crude grid indicates. Below you see the result of a parameter study, we have prepared for a small 2 by 2 mm design area in the vicinity of the end-point of the first optimization step.



This reveals a somewhat jacket surface and a distinct (local) valley of the objective function. Minor changes of the input to the optimization process, whether it be the starting point or design variable bounds, can actually make the optimization process dive into this local valley and get stuck in there.

An optimization process that gets stuck in this local minimum could have a convergence history like in the plots shown below





Notice how the final objective function value is slightly higher than the previous optimization result. Notice also how only the first iteration out of 7 provides significant improvement of the objective function. This step brings the design value down into to the valley. The remaining iterations zigzags in the bottom of the valley without being able to get up and out and without providing any visible improvement. Finally, the convergence criterion is fulfilled. It can be mentioned that the convergence criterion requires both objective and design changes to be small.

In the beginning of this lesson, we mentioned that the optimization problem formulation also handles constraints. They can be used for all sorts of purposes. For instance we notice that the optimal solution is a rather low saddle position, cf. the picture above. Suppose that for some reason, this position is too low. We, therefore, want to ensure that the distance between the crank and the seat is not too small, for instance larger than 0.66 m. This can be formulated very nicely as a constraint like this:

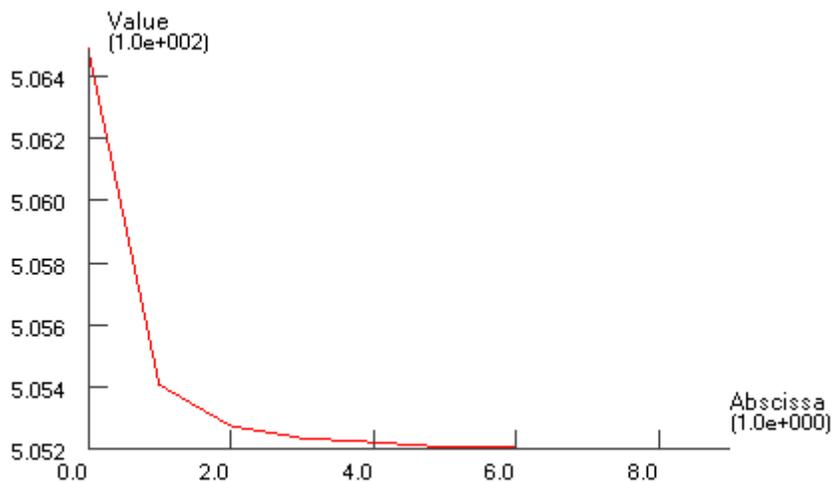
```
AnyDesMeasure Metab = {
  Val = secint(..Study.Metabolism(),..Study.tArray);
  Type = ObjectiveFun;
};
AnyDesMeasure SeatDist = {
  Val = (.SaddleHeight.Val^2+.SaddlePos.Val^2)^0.5 - 0.66;
  Type = GreaterThanZero;
};
```

Notice that constraints are defined as AnyDesMeasures of type LessThanZero or GreaterThanZero. In the mathematical formulation of the optimization problem stated in the beginning of this lesson, we have only less-than-or-equal-to constraints, but there is only a minus sign in difference of making a greater-than-or-equal-to into a less-than-or-equal-to constraint. You can put this minus sign manually or you can use Type = GreaterThanZero, which is equivalent. Notice that equality constraints are in principle also a possibility, but currently the optimization solvers in AnyBody do not handle this type of constraints. Moreover, it is most often possible to handle equality constraints by means of inequality constraints, because the objective function's gradient will put pressure on the constraint from one side; thus, it is merely a matter of determining the proper type of inequality constraint.

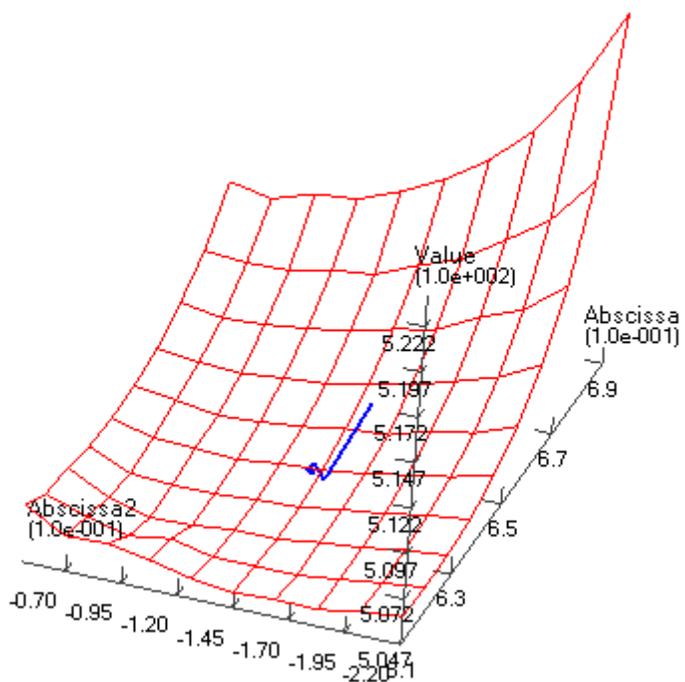
Notice also that the constraint is just an AnyDesMeasure, so anything you could conceivably use as an objective function can also be a constraint. In this case, the constraint is a simple mathematical combination of variables, but in general it can also be properties such as muscle forces, joint reactions, point locations,

segment velocities, and any other model property that the system can compute.

Enough talk; let's try the optimization with the constraint added. Please load the model again, select the optimization operation, and click the run button. The optimization process will have the following convergence picture:

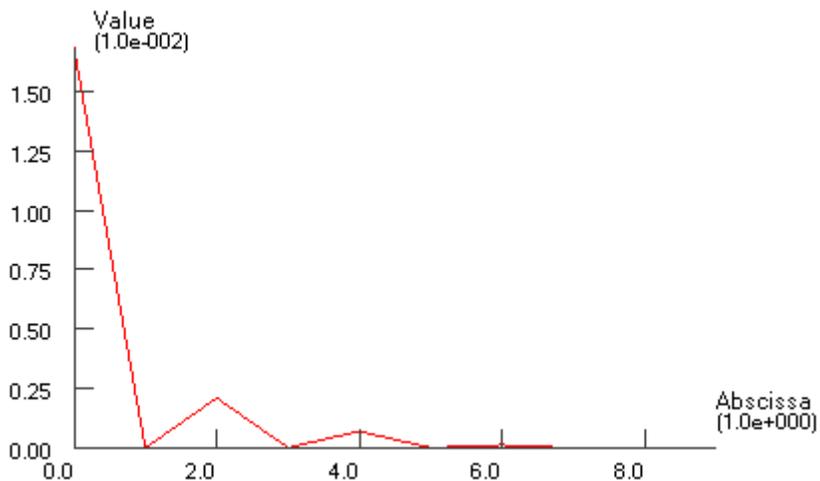


If you also re-run the parameter study, you can get this picture of the convergence:



We see that the result is indeed a compromise since the objective function value cannot be reduced as much

as in the unconstrained case. The path of the design values bounces off the constraint and finally it gets stuck on the constraint even though the objective function still has a downwards inclination. The constraint lies like a wall through the design space. We can see the convergence path along the constraint by plot the constraint value, i.e., the SeatDist.Val. This looks like:



where it is obvious how the optimizer hits the constraint, bounces off, hits again, etc. and finally it converges. At no point in time, the constraint value becomes negative, which was exactly what we prescribed in its definition.

A final look at the result could be the picture of the model after this constrained optimization, which shows a visible difference compared to the unconstrained solution: The hip position is now higher, i.e., longer from the crank and to achieve this it is further forward, see the picture below:



This completes the introduction to optimization studies.

Trouble shooting AnyScript models

If you think mechanics is simple, it's probably just because you haven't worked with three-dimensional space yet. The laws of mechanics are pretty easy to comprehend as long as stuff is moving on a one-dimensional line. When you go to two dimensions, complications such as rotational inertia and centrifugal forces start to play a role, but the equations are still not very difficult. The third dimension is what complicates things enormously and even to the point that mere kinematics becomes a matter for university scholars. It is quite literally rocket science.

A system like AnyBody is a tremendous help in this situation because it sets up and handles all the equations inside the system and relieves you of the task of actually handling the mathematics. But the system does not prevent you from creating models where the syntax or semantics of the model is invalid, where segments cannot reach their joints, where the kinematics is undefined, or where there are not enough muscles to balance the forces in the system. You are likely to run into all these problems.

More precisely, you can get the following types of errors:

- Load-time errors - when the AnyScript model is syntactically erroneous
- Run-time errors - when a successfully loaded model refuses to be analyzed.

Load-time errors

A load-time error occurs when you load a model by pressing F7 or the M<-S icon on top of each window. This causes the system to attempt a compilation of the model you have in the window, and any errors occurring in this respect are load-time errors.

Load-time errors are problems with the syntax of the AnyScript model you have authored. Such a model must honor a number of very formal semantic rules to be valid, and if it fails the test of any of those, you will get a load-time error.

Each possible error that can occur is associated with an error message, and the system will print the message in the message window at the bottom of the screen, for instance like this:

```
ERROR : C:\MyDocuments\AnyScripts\Main.any(42) : AnyVar : unexpected
```

or like this:

```
ERROR : C:\MyDocuments\AnyScripts\Main.any(45) : cannot open file : DrawSetting.any
```

or this:

```
ERROR : C:\MyDocuments\AnyScripts\Main.any(133) : EOF : unexpected
```

As you can see, error messages adhere to a certain structure. The first part after ERROR is the file in which the system encountered the error. Notice that this may be a different file from the one you were loading because the main file may spawn to include files during the loading of the model.

After the file name you find a number in parenthesis. This is the number of the line where the error occurred. If you double-click the file name or the number, the file opens, and the cursor is placed at the line in question. Be sure to click the file name or line number and not the error message.

After the line number comes the actual specification of the error. With good descriptive error messages and easy access to the error location you should have the problem fixed in no time. Unfortunately things are not

always that nice. First of all, the error messages are not always very descriptive. This is a problem the AnyBody Modeling System shares with any other computer language compiler in the market. It is not because programmers specifically want to bother their users. The problem is simply that error messages are generated by a very formal semantic analysis. This makes them very different from the natural human expression of the problem, and they can be difficult for the user to understand. But you can get used to them and people have been known to even grow fond of their conciseness.

The second and more serious problem is that the error may occur in a totally different location from where it really is. Let's take an example: Suppose by mistake you have included the wrong file like this:

```
#include "TheWrongFile.any"
```

somewhere in the model. When the compiler spawns to the wrong file it is likely to meet statements or references to objects that do not exist. The compiler will report an error in WrongFile.any, but the real error is in the file that included WrongFile.any.

Here are some typical errors and their consequences:

Forgotten semicolon	<p>Every statement in AnyScript must be terminated by a semicolon, and it is easy to forget. The consequence is that the compiler will proceed to the next line and probably report that it has encountered something unexpected there. By closer investigation, the next line may be fully in order, and you get confused. The problem was really on the former line.</p> <p>Notice also that end braces must also have a semicolon after them.</p>
Unbalanced braces	<p>Braces { } are used to group things together in AnyScript. They must be coherent and balanced, and if you have one too few or one too many it can completely change the structure of the code, and you can get strange error messages. The best remedy is to use consistent indentations in the code. This makes it easy to follow the brace level and spot mistakes.</p> <p>The AnyScript editor can indent your code automatically. If you select all the text and press Alt-F8, all lines are indented according to the brace level, and this often makes it much easier to see where the problem is. Beware that the missing brace can be in an include file.</p>
Mix-up of decimal points and commas	<p>Some nationalities use decimal commas, and some use decimal points. The AnyBody Modeling System consistently uses decimal points regardless of the nationality settings in your computer. If you type a comma in place of a decimal point, you will get a syntax error.</p>
Mix-up of 'O' and '0'	<p>Beware that there is a difference between the letter 'O' and the digit zero, '0'.</p>
Mix-up of 'l' and '1'	<p>Beware that there is a difference between the letter 'l' and the digit one, '1'.</p>
Inconsistent use of capitals	<p>AnyScript is case-sensitive, so these two statements refer to different variables:</p> <pre>MyVariable = 1; Myvariable = 1;</pre> <p>This also means that predefined class names such as AnyVar or AnyFolder must be written with correct capitalization.</p>
Missing reference operator	<p>If by mistake you assign two folders to each other:</p> <pre>AnyFolder MyFolderCopy = MyFolder;</pre>

	<p>you will get the error message: Folder assignment expected for this object.</p> <p>What the message means is that this type of assignment is not allowed. You may argue that the error message is misleading because '=' is indeed an assignment operator. However, operators in AnyScript are polymorphic, and they are interpreted in the context of the variables they operate on, and for two folders no proper assignment operator exists. So, while rhetorically correct, what the statement really means is that you are missing an ampersand, '&'. Assignment of folders to each other must be by reference like this.</p> <pre>AnyFolder &MyFolderCopy = MyFolder;</pre>
Missing expected members	<p>Some classes in AnyScript have members that must be initialized. For instance, this declaration</p> <pre>AnySeg arm = { Mass = 12; };</pre> <p>will produce the error: Obligatory initialization of member : AnyVec3 Jii is missing.</p> <p>The reason is that AnySeg has a property called Jii which must be given a value before the definition is complete. Similarly, some objects have properties that are untouchable. This declaration: <pre>AnySeg arm = { t = 12; };</pre> <p>also causes an error: t : Initialization denied.</p> <p>because t is a protected variable. It is set automatically by the system and cannot be assigned a value by the user.</p> </p>

Run-time errors

Run-time errors occur during analysis of a successfully loaded model. Their nature and remedies are completely dependent on the nature of the study. Please refer to the tutorial "[A study of studies](#)" for further information.