

Integrated module for analysis / synthesis
/ matching - First version
CHARM D12 deliverable
Report - Universitat de les Illes Balears

Contents

1. Introduction
2. Validation and registration in the context of CHARM
3. The integrated environment for 3D reconstruction and validation
 - 3.1. Introduction
 - 3.2. General description of the interface
 - 3.3 File formats of the reconstruction module
 - 3.4 File formats of the validation module
 - 3.5 Data structure
 - 3.6 Visualisation controllers
 - 3.6.1 Video controllers
 - 3.6.2 Zoom controllers
4. User manual
 - 4.1 Reconstruction module
 - 4.1.1 Loading files
 - 4.1.2 Camera calibration
 - 4.1.3 Reconstruction
 - 4.2. Registration/validation module
 - 4.2.1. Loading an arm
 - 4.2.2. Trajectory loading
 - 4.2.3. Centre of masses and principal directions loading
 - 4.2.4. Saving reconstructions
 - 4.2.5. Play synchronising
 - 4.2.6. Video controllers
 - 4.2.7. Quitting
 - 4.3 Error messages
5. Spatial registration and validation results

1. Introduction

Deliverable D12, **Integrated module for analysis / synthesis / matching**, constitutes the module for the CHARM project validation, aiming at analysing the correspondence of images coming from real sources (medical origin, video sequences) with synthetically generated ones using CHARM methods and thus assessing somehow the results of the project as a whole. Partial inspiration for this deliverable comes from the work performed for the second year deliverable D8, **An interface for matching**, where some of the validation problems were approached in a prototype way.

Due to the current limitations of the CHARM results, in particular the unfeasibility of simulating the behaviour of a sufficient number of muscles and other tissues through finite element methods, the final validation has been performed by comparing trajectories of 3D bones corresponding to a real movement, and reconstructed from fluoroscopies taken from different perspectives, with simulated trajectories of some bones using the 3D models obtained from the Visual Human Dataset and with movements driven by the control methods developed by CHARM.

In this report we describe:

- the environment for 3D reconstruction of objects from the real sources used for CHARM validation namely image sequences obtained through video cameras and fluoroscopies, using stereoscopy;
- the validation environment where these images are compared with the simulated ones, specifically the tools for comparing the trajectories of the real and simulated cases, and the registration problems analysed;
- and finally we discuss the validation results and perspectives.

In an appendix we discuss some more advanced methods for moving images analysis which have not been yet integrated in the module, due to time constraints in the project, which limited the extension to which more advanced methods could be tested and integrated.

We recall that this deliverable is complementary of the deliverable replacing D11, **Test sequences for validation**, where the setting of the experiences for the obtention of the sequences, the methods used for camera calibration and 3D reconstruction, both of video and fluoroscopy sequences, and the results obtained are discussed

But first we discuss the validation questions as perceived in the context of the CHARM project and, specifically, in this deliverable.

2. Validation and registration in the context of CHARM

The aim of CHARM is to obtain better synthetic animation of humans by developing new methods; different modalities of moving 3D images are analyzed and/or synthesized and have to be compared in order to validate these methods. The type of images for use in CHARM range from 3D reconstructions obtained from real sources, such as MR, CAT, fluoroscopies or video, to synthetically generated movements coming from physically based simulations, namely, on biomechanics and high-level motion control.

The validation / registration problem of CHARM can be compared to the introduction of graphics techniques in the medical context, where tomographic images are used in concert with each other, so that the correlation of 3D tomographic diagnostic images obtained from different modalities such as PET or MR, or from the same modality in different times has become clinically significant in recent years. It was natural for the CHARM partnership to take this graphics approach and enhance it, exploiting current hardware and software developments for the use of multi-modal moving 3D images. In the clinical approach the questions are image matching and the associated registration problems - registration means determining the geometric relationship between multi-modal image data sets in order to perform the best possible superposition of the images -. The CHARM validation questions are slightly different.

Comparing images from different sources and checking for the accuracy and correspondence of the different representations is one of the approaches for testing whether our models represent an effective progress in synthesizing human animation. This problem is somehow different from the medical image matching where in the clinical context the aim of matching can be, for instance, registering scans of the same patient with each other and with CT scans or relate them to a standard atlas in order to perform the best possible superposition of the images. In our context we are interested in getting the appropriate reference frames (both spatial and temporal) which allow the study of coincidences and discrepancies among multi-modal images, because it is in the accuracy of the methods of synthetic generation of deformation and movement what we are interested in assessing.

We take mainly this visualisation approach, which allows clinicians and other non-technical users to assess the validity of the results of the project by visual comparison of different modalities of moving 3D images, and we also aim at providing some more analytical tools to test also the results. This approach gets its strength both from graphics and the current medical approaches, while the objectives are different from the clinical approach, namely, the best matching is not the optimum, but the most accurate comparison with a suitable referencing.

3. The integrated environment for 3D reconstruction and validation

3.1. Introduction

The environment developed by UIB for the CHARM project integrates the tasks of 3D reconstruction of moving objects from "real" image sequences, and the validation of the results by comparing (mainly perceptually at the current stage, but helped by some automatised tools) multi-modal image sequences, after the temporal synchronisation and spatial registration of the different sources. The resulting environment is composed of two modules, the first one is the reconstruction module, for 3D reconstruction of objects from frames of the same object from different perspectives, with the capability of generating sequences of reconstructed bones in Inventor format, together with a file containing essentially the trajectories of the movement. After performing calibration of the cameras, by operator identification of corresponding points for the different camera images (helped by epipolar lines), a sequence of reconstructed objects is generated in Inventor format. The second module is the validation module, which shares the common aspects of the interface with the former but which is separated from it for optimising memory and loading management. The trajectory file from the reconstruction module is used to generate the animation sequence of the shoulder-arm in a window, which will be compared with another movement which is loaded in another window, this time synthetically generated with CHARM methods, for the validation. The validation module can load independent bones reconstructions, provided the reconstructions are in the CHARM developed format based on Inventor. Some automatised help tools are also shown. As indicated earlier, the final validation takes place only on some bones movement, both reconstructed from fluoroscopies, and simulated on the VHD-based data.

3.2. General description of the interface

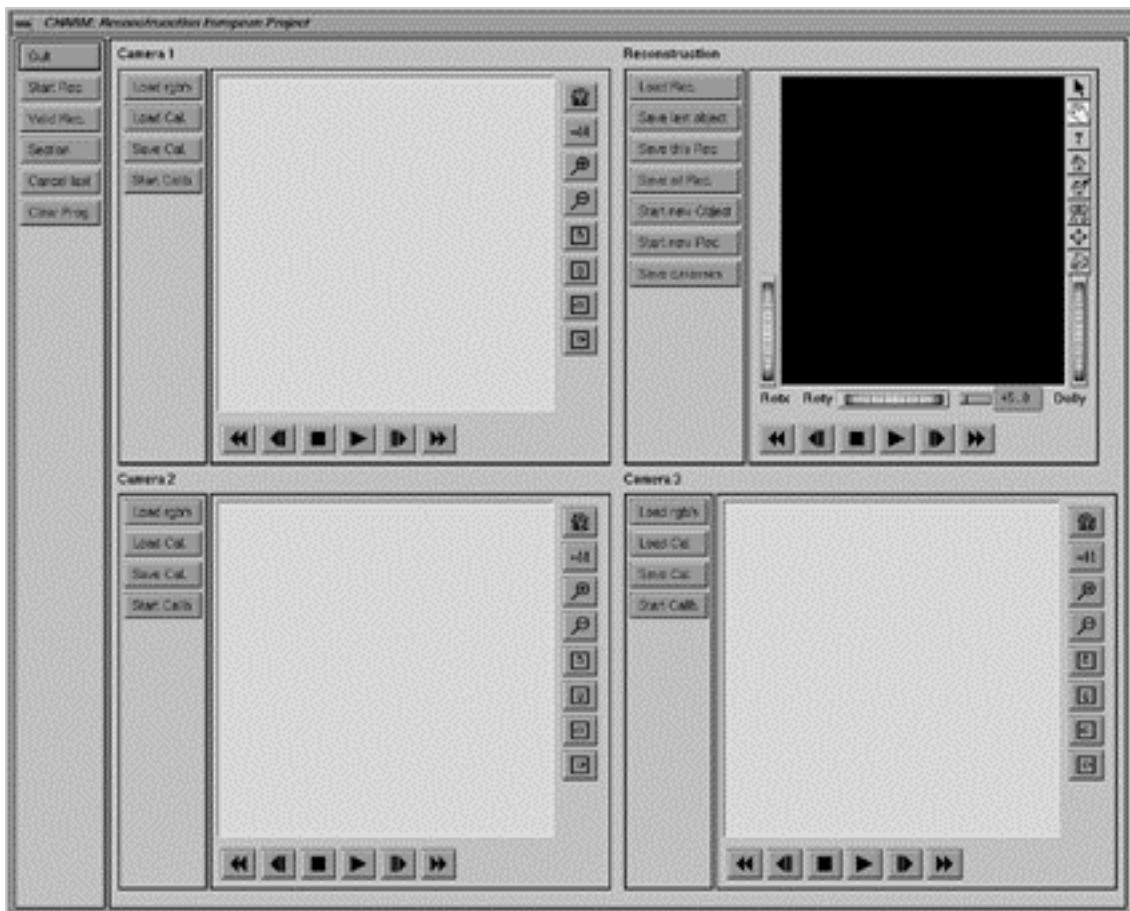
The interface for the environment, especially the calibration/reconstruction module, has been chosen to appear very similar to the interface for matching developed as CHARM D8, although the functionalities and underlying structures are widely different.

The reasons for keeping a seemingly looking environment are twofold. On one hand, the tiled window system for D8 was seen as very convenient for novice users and we favored keeping the similarities, which gives an advantage to the user, helping in its familiarisation with the tasks although they are different.

On the other hand, as the main functionality of this module is getting a reconstructed 3D object from different views, it seemed convenient to follow the quite standard interface used for 3D modelling in commercial packages for image synthesis and animation, where the users

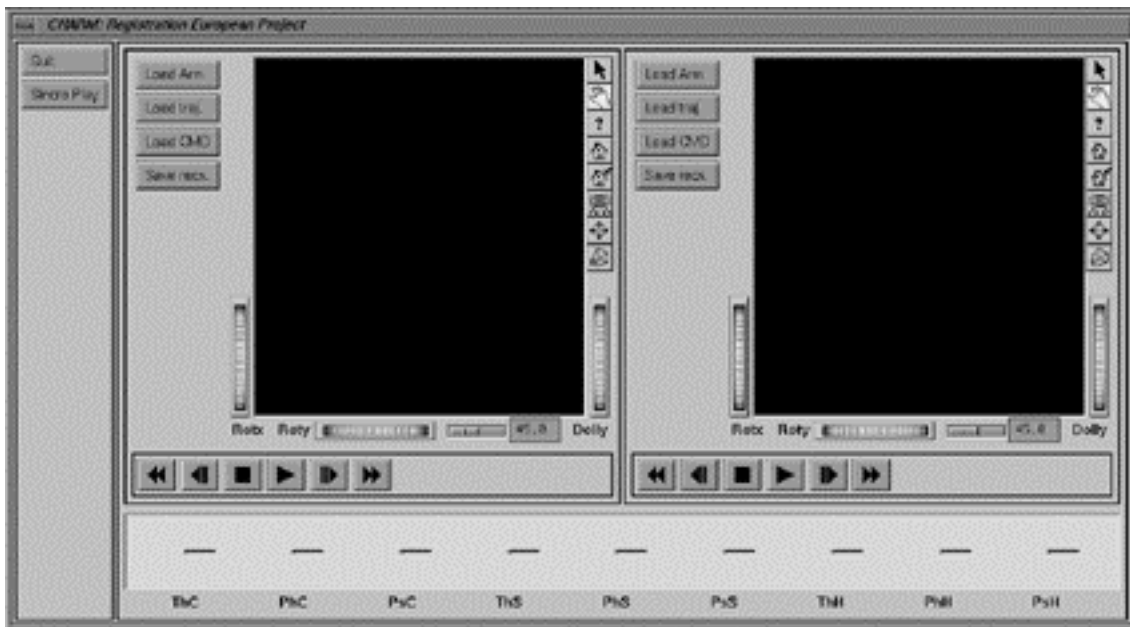
have 4 windows showing different planes and a view of the 3D object. In our case, the user has some windows showing different perspectives (albeit real) of the same object and then the 3D reconstruction. This approach gets very positively striking results when using fluoroscopies, where the images shown are images taken at orthogonal perspective planes, which is the standard for modelling packages. Although the module has four subwindows, three for the perspective images and one (the upper-right one) for the reconstructed object, it is currently able to handle up to five different perspectives.

A global view of the module interface is the following one:



The validation module looks a bit differently. It is divided into three distinct areas, two of them are viewers of the different animations of the shoulder-arm in a similar way as the subwindows of the reconstruction module, while the third area shows some angles corresponding to the two trajectories, which are shown as nine clocks for comparison. The validation module is linked to the reconstruction module, its objects being accessible by the reconstruction module. As indicated earlier, limiting to two windows this module has been an *ad hoc* solution for improving memory and loading management.

The following picture gives an indication of the validation module interface:



3.3 File formats of the reconstruction module

The input formats for the reconstruction modules are, classified according to extensions, the following ones:

*.iv	<p>File in Inventor format. The format has to be appropriate for the internal structures of the module, otherwise it will be rejected. There are three types of suitable formats:</p> <p>1) Representing vertices and faces of a bone:</p> <pre>SoSeparator { SoCoordinate3{ point[... } SoIndexedFaceSet{ coorIndex[... } ... }</pre>
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	<p>2) Representing one frame with n bones:</p> <pre>SoSeparator {SoCoordinate3{} SoIndexedFaceSet{} ... } SoSeparator {SoCoordinate3{} SoIndexedFaceSet{} ... } ... SoSeparator {SoCoordinate3{} SoIndexedFaceSet{} ... }</pre> <p>3) Representing a sequence of frames:</p> <pre>SoBlinker { SoSeparator {#Frame 1 SoSeparator {#bone 1} ... SoSeparator {#bone n} } ... SoSeparator {#Frame n SoSeparator {#bone 1} ... SoSeparator {#bone n} } }</pre>
*.cal	<p>Representing a camera calibration, by means of a list of points whose number is multiple of five and each tuple is given by:</p> <pre>coordinate pixel x coordinate pixel y coordinate 3D x coordinate 3D y coordinate 3D z</pre>
*.rgb	<p>Representing a 2D image in RGB format</p>

*.rgbs	Representing a sequence of 2D images in RGB format. This file is edited with the help of a text editor, and each row is the path to the file with the 2D image and the order is the order of the frames for visualisation or processing.
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The output file formats are:

*.iv	as described in input
*.cal	as described in input
*.cmd	File composed of centres of masses and directions with the following format: number of frames, number of bones, and for each line, the coordinates of the centre of mass and inertia axes.

The reconstruction module uses two other types of files for communicating internally with the triangularisation functions (qhull), but these formats are temporarily and invisible to the users.

3.4 File formats of the validation module

The validation module uses the following file formats as input:

*.iv	<p>Inventor file format verifying that the last son hanging from the main node is a Separator with the following structure:</p> <pre>SoSeparator { SoUnits{ } SoRatationXYZ{ } #initial positioning rotation SoMatrixTransform{ } SoRatationXYZ{axis Z angle 0} SoRatationXYZ{axis Y angle 0} SoRatationXYZ{axis X angle 0} SoMatrixTransform{ } SoFile{#Clavicle} SoMatrixTransform{ }</pre>
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	<pre> SoRatationXYZ{axis Z angle 0} SoRatationXYZ{axis Y angle 0} SoRatationXYZ{axis X angle 0} SoMatrixTransform{} SoFile{#Ulna} SoMatrixTransform{} SoRatationXYZ{axis Z angle 0} SoRatationXYZ{axis Y angle 0} SoRatationXYZ{axis X angle 0} SoMatrixTransform{} SoFile{#Humerus} } </pre>
*.trj	Trajectory file with number of frames, number of degrees of freedom and trajectories

The output files for the validation module are inventor files of any of the input formats specified above for the reconstruction module for a bone or a frame.

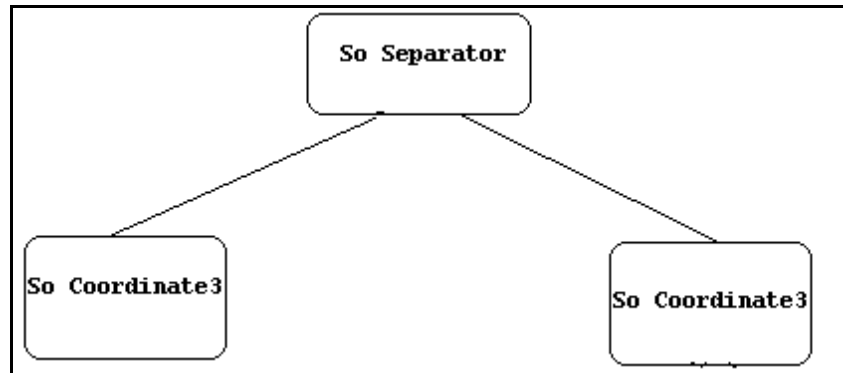
One must remark that all the *.iv files are in Inventor format and consequently can be visualised with the command ivview.

3.5 Data structure

The internal data structure corresponds to the file format described above, eventually with some added sofistications. As an example, the internal bone data structure includes a SoSeparator which allows to encapsulate deeper structure, in other terms, it is the node father of a subtree; SoCoordinate3 which is a set of 3D points and SoIndexedFaceSet, which is a set of indexed fases.

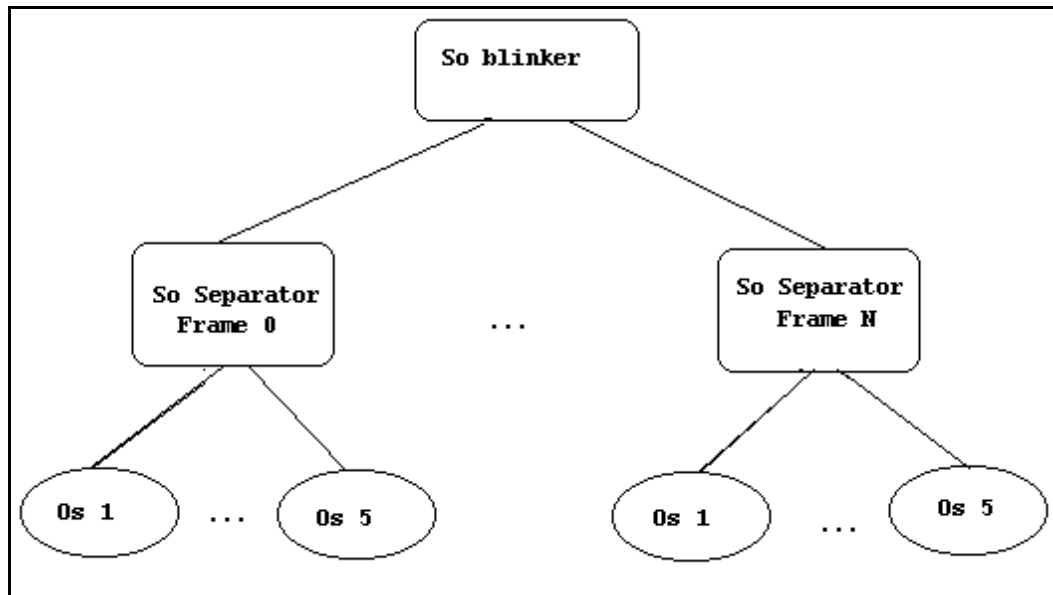
The scheme for the isolated bone is as follows:

Bone



The internal organisation of the bones structure is made of a SoBlinker which allows to group subtrees but with the characteristic that only one is selected at the time and which is used to simulate a sequence or film frame by frame.

Full Structure of a set of bones



The number of five has been chosen to manage more efficiently the memory and loading, otherwise, the environment gets very heavily loaded.

3.6 Visualisation controllers

3.6.1 Video controllers

The four subwindows of the reconstruction module and two subwindows of the validation module use several buttons to control the display frame by frame, both of 2D and 3D

sequences. The functionalities are inspired by the standard commercial video players as were designed in the deliverable D8. The meaning is:

- All Backwards or rewind: defines the first frame in the sequence as the current (and visualized) one.
- All Forward: sets the last frame as the current frame.
- Step Backwards: sets the previous frame as the current frame.
- Step Forward: the following frame becomes the current one.
- Play: a non-stop cycling display of the full sequence.
- Stop: Interrupt the cycling display.
- Selection: sets directly wich frame as current one. It is only enabled when the number of frames is bigger than one.

Currently, the speed for Play visualisation is set to one frame per second and it is not user modifiable. The video controllers are not enabled when only one image or reconstructed frame is loaded in the corresponding subwindow.

They appear as:



The video functionalities in the video controller for the validation module include the same as in the reconstruction module, with the added option for synchronising the views in the different subwindows. This option is activated through a button.

3.6.2 Zoom controllers

The three reconstruction subwindows have several buttons for image control, as follows

- Home: to take a point of view such that the whole object can be seen in the window; this function is automatically performed any time a new file is loaded.
- Point=Pixel: In order to get that a pixel image has the dimension of a pixel screen. This is the minimum zooming suggested for reconstruction tasks.
- Zoom: This is another facility essential for the reconstruction tasks. Magnifying helps the precision of the task.

- Unzoom: reverses zoom operation.
- Left: the camera view is moved to the left.
- Right: the camera view is moved to the right.
- Up: the camera view is moved upwards.
- Down: the camera view is moved downwards.



The zoom control buttons

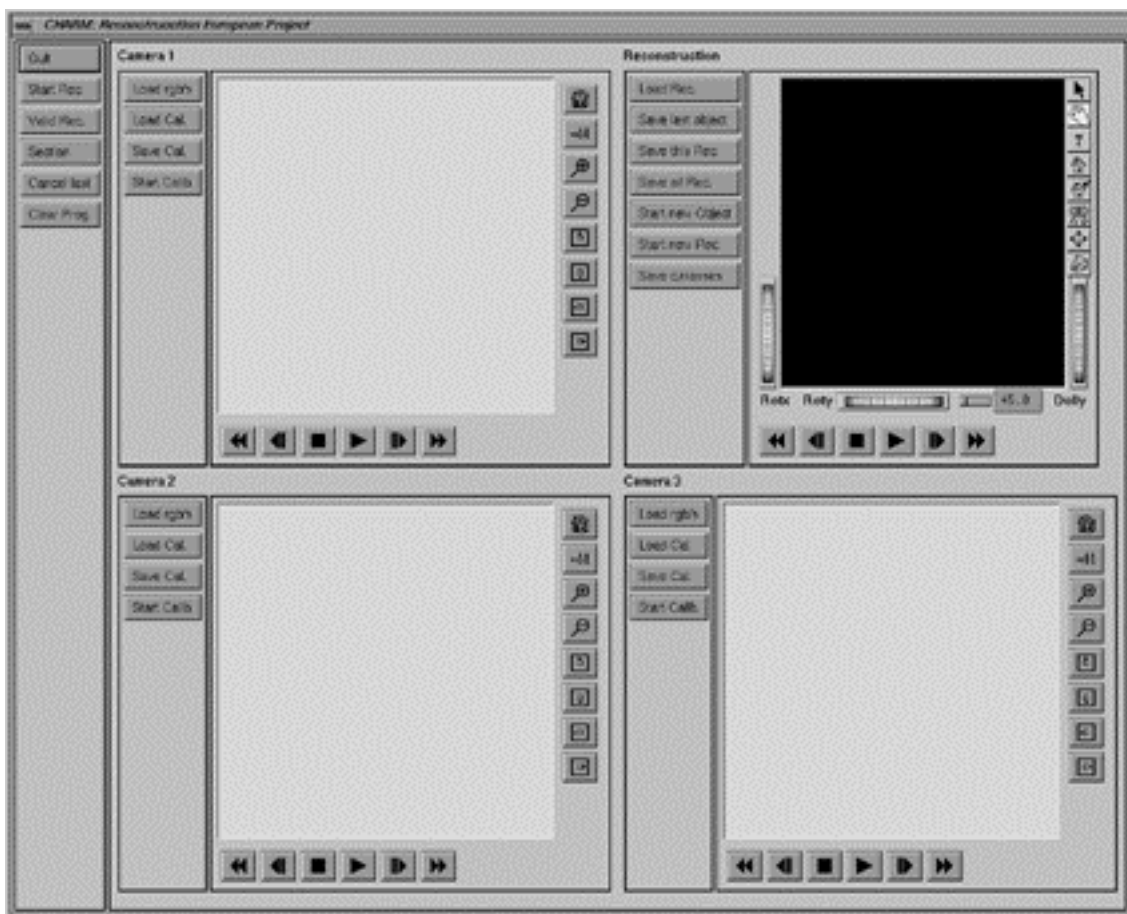
4. User manual

The modules have been developed to run on a Silicon Graphics Unix environment.

4.1 Reconstruction module

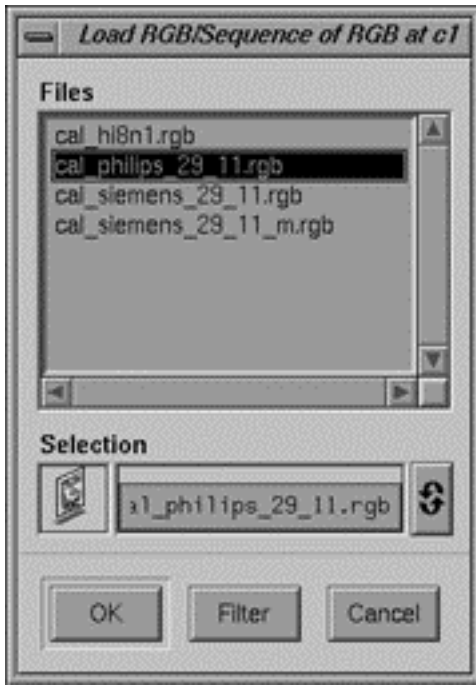
To launch the program use the command **recons** and the execution is validated. The programs **recons** and **qhull** should be inside the same directory for the correct execution.

A four window environment appears:



4.1.1 Loading files

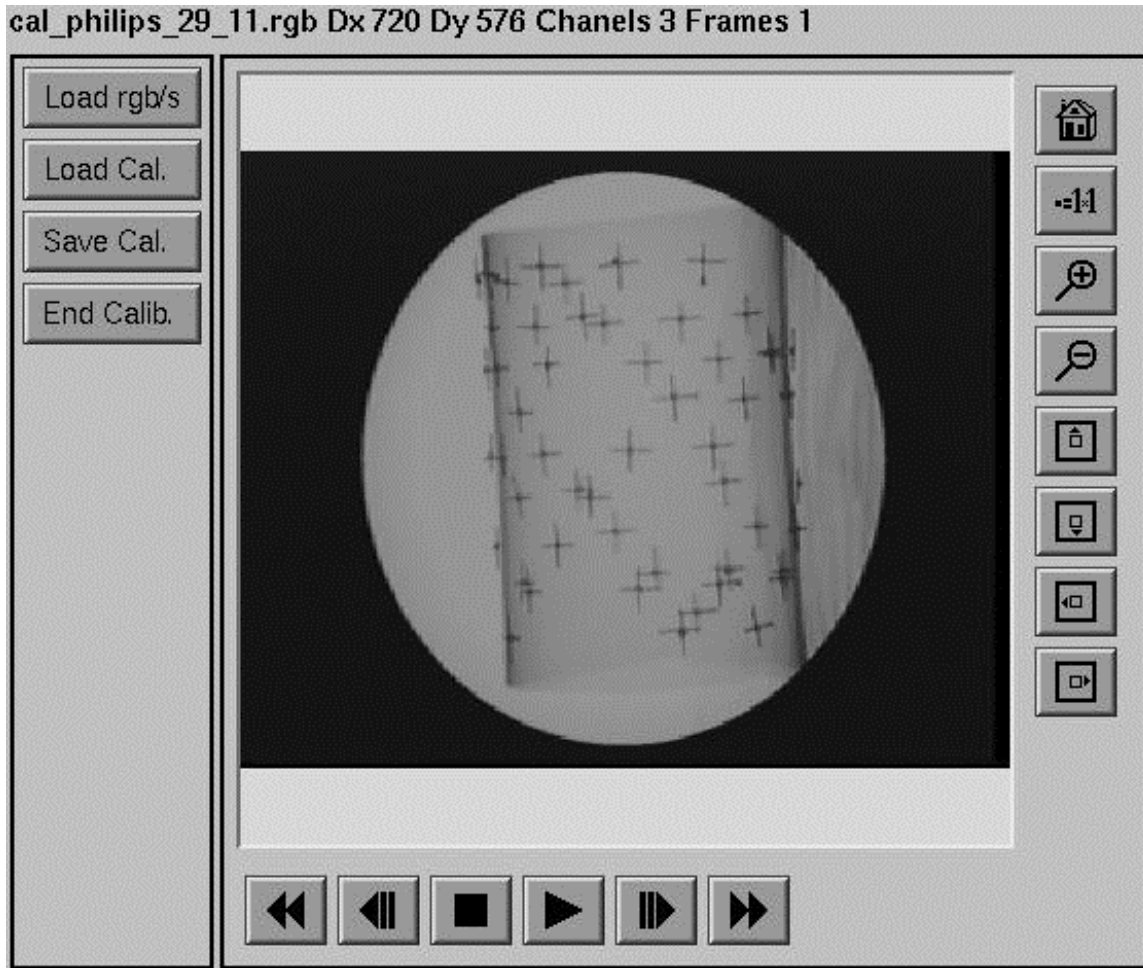
The loading files of images or sequences of formats such as described earlier can be performed in three of the subwindows (the one for the results of the 3D reconstruction is excluded). It is done by clicking on the button **Load rgb/s** of the corresponding subwindow; then a window opens for file selection.



The images are loaded in the corresponding subwindow, and if there was another image or sequence loaded, it is replaced by the newer one. Apart from the **OK** and **Cancel** typical dialog, the option **Filter** allows for choosing only some type of files to display as for loading; the default are the files with extension .rgb and .rgbs.

Once a file is loaded, its name, its dimensions and the number of frames loaded appear. For a .rgbs format file, the slider for choosing directly a specific frame is enabled; otherwise it is not visible.

Again, the object appears initially set to the subwindow size as indicated in the following picture:



The video controller with the direct to frame option enabled appears as:



4.1.2 Camera calibration

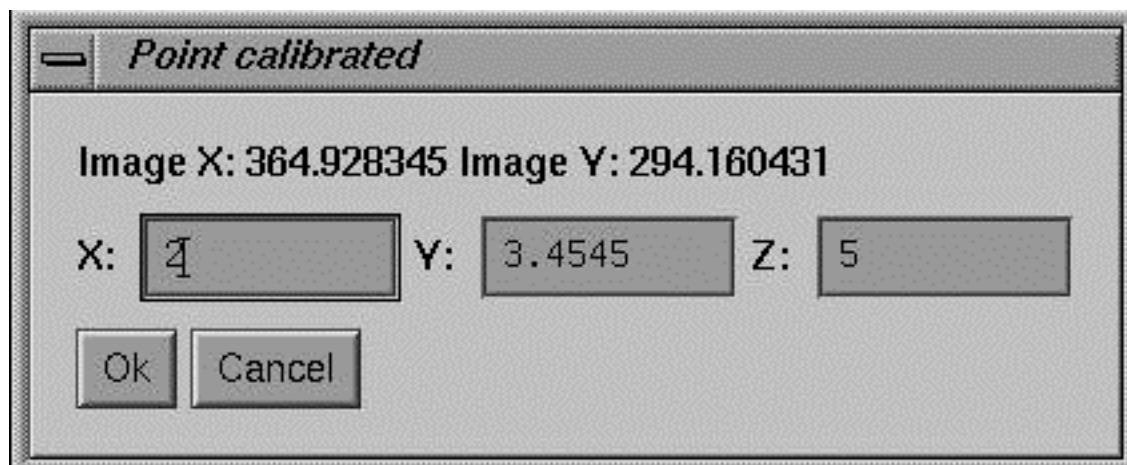
Camera calibration (obtaining the parameters corresponding to a viewpoint) can be done in two ways: manually (to obtain the first calibration) or loading it from a file (after the calibration has been performed and then it is loaded when required, or for simulations).

In order to load a calibration the user clicks on the button **Load Cal** in the corresponding subwindow and a window for choosing the calibration and loading it appears as follows:

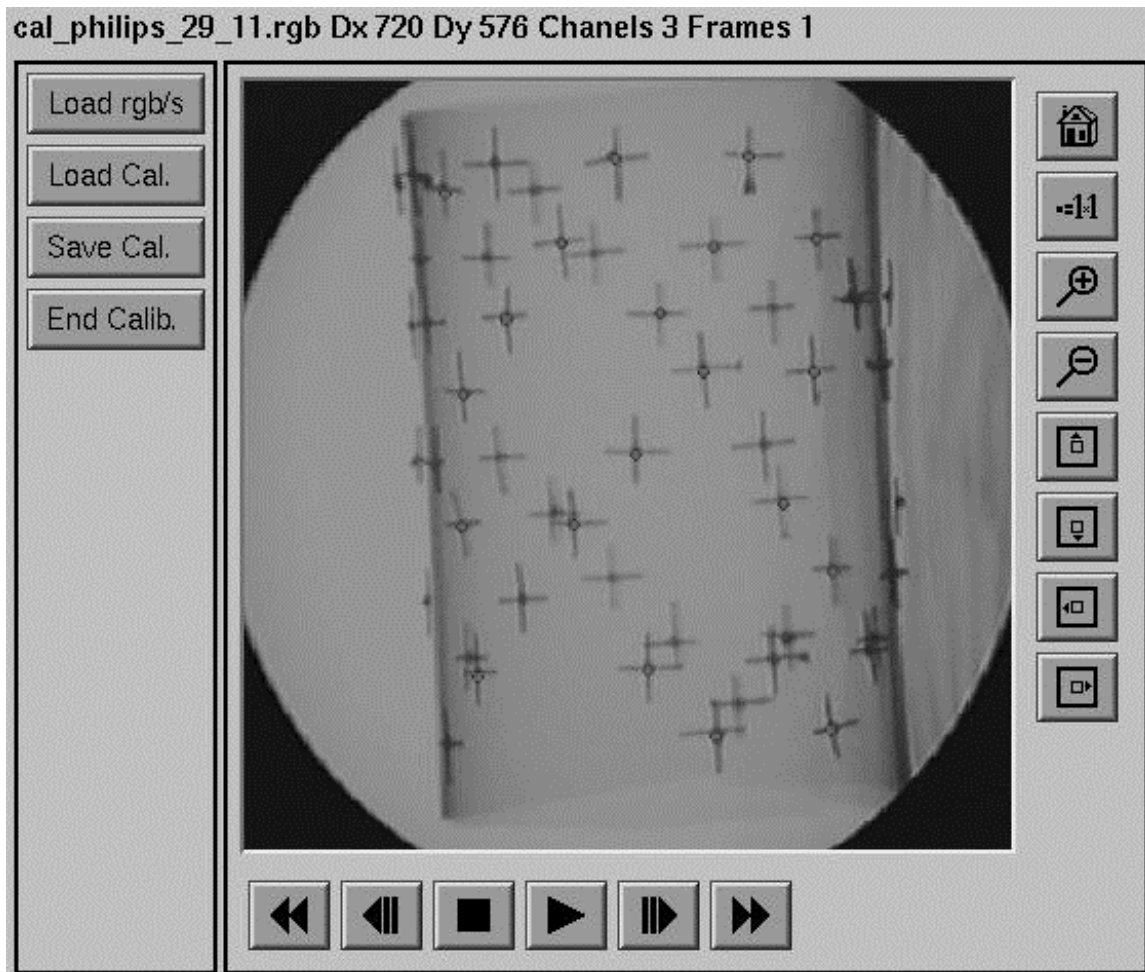


In order to perform a manual calibration the user has to perform the following steps:

- Click on the button **Start Calib** at the corresponding subwindow. The button changes to **End Calib**.
- Then select a point in the image; a window appears with the screen coordinates corresponding to this point requesting to introduce the 3D coordinates and to validate them.



- Once the calibrated point is calibrated, it appears in red to avoid re-using it. Calibration requires a minimum of 6 points and an upper limit of 20 points has been set. The following picture shows that feature:



- Once chosen all the calibration points required, the user executes the calibration by clicking on the button **End Calib** which now turns to **Start Calib**.
- Finally it is recommended to save the calibration by clicking on the button **Save Cal** which opens the appropriate selection window.

4.1.3 Reconstruction

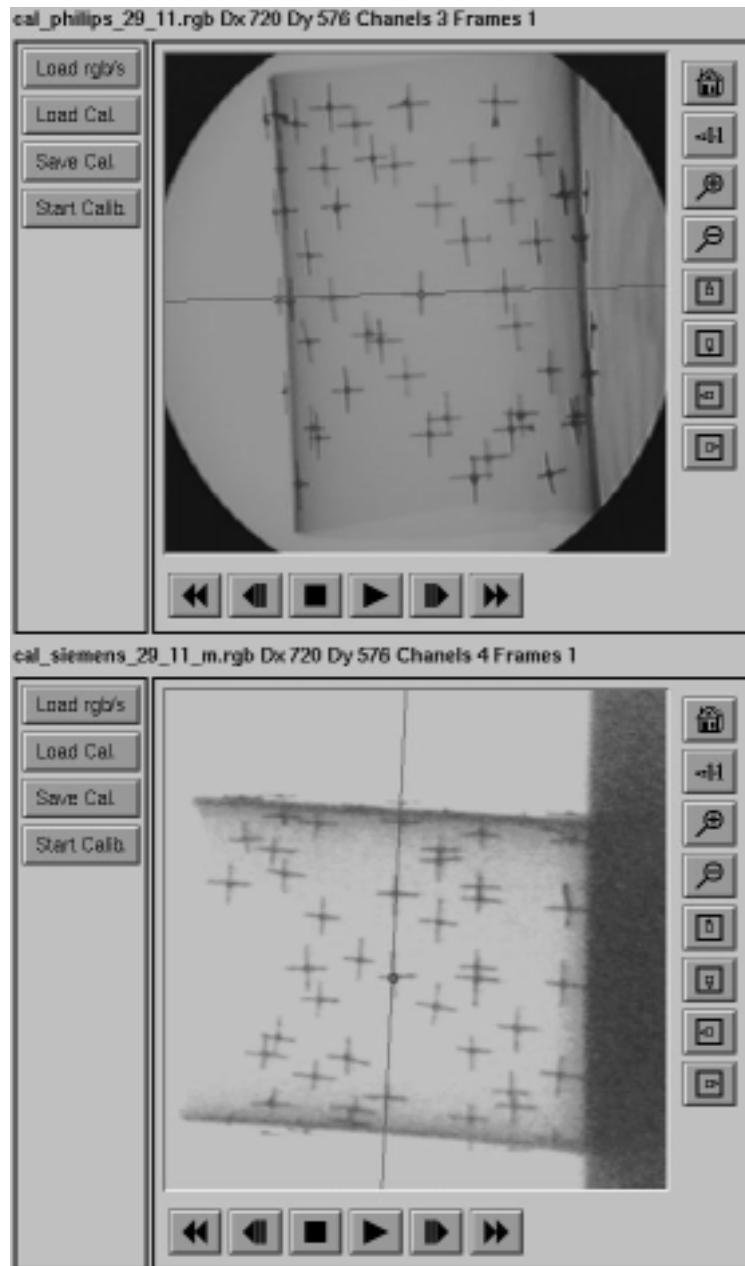
In order to start the reconstruction, the points of view corresponding to the images of the object to be reconstructed should have been calibrated previously, and a minimum of two points of view is necessary.

In order to start the reconstruction the user clicks the button **Start Rec**.

Two ways of reconstruction have been implemented, point by point and by sections. Both of them can be used simultaneously for the same object reconstruction.

Point by point reconstruction:

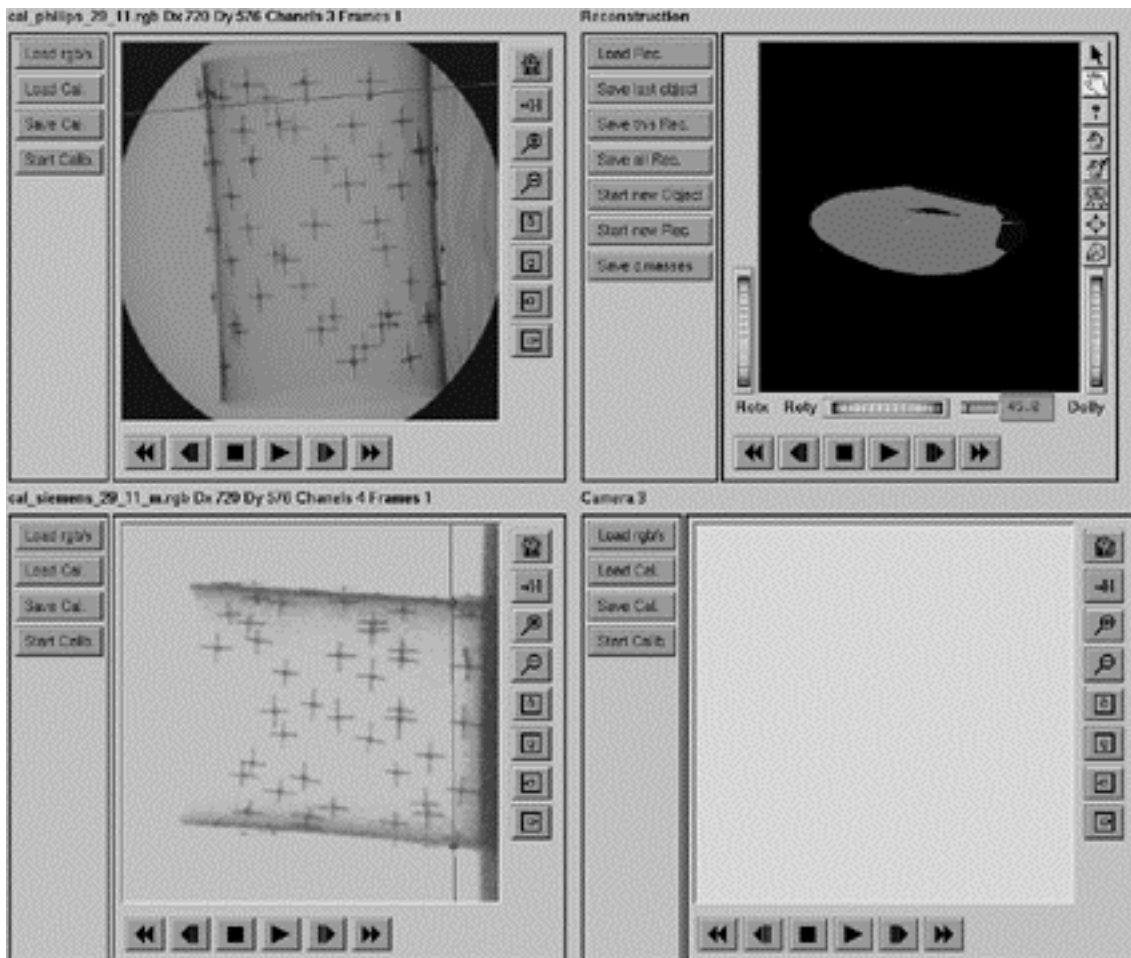
- We select the conjugate points corresponding to different calibrated cameras. The epipolar lines are drawn to help in this selection. When a point is clicked at a viewpoint it turns to red and the epipolar lines are drawn at the other viewpoints. The following figure shows it:



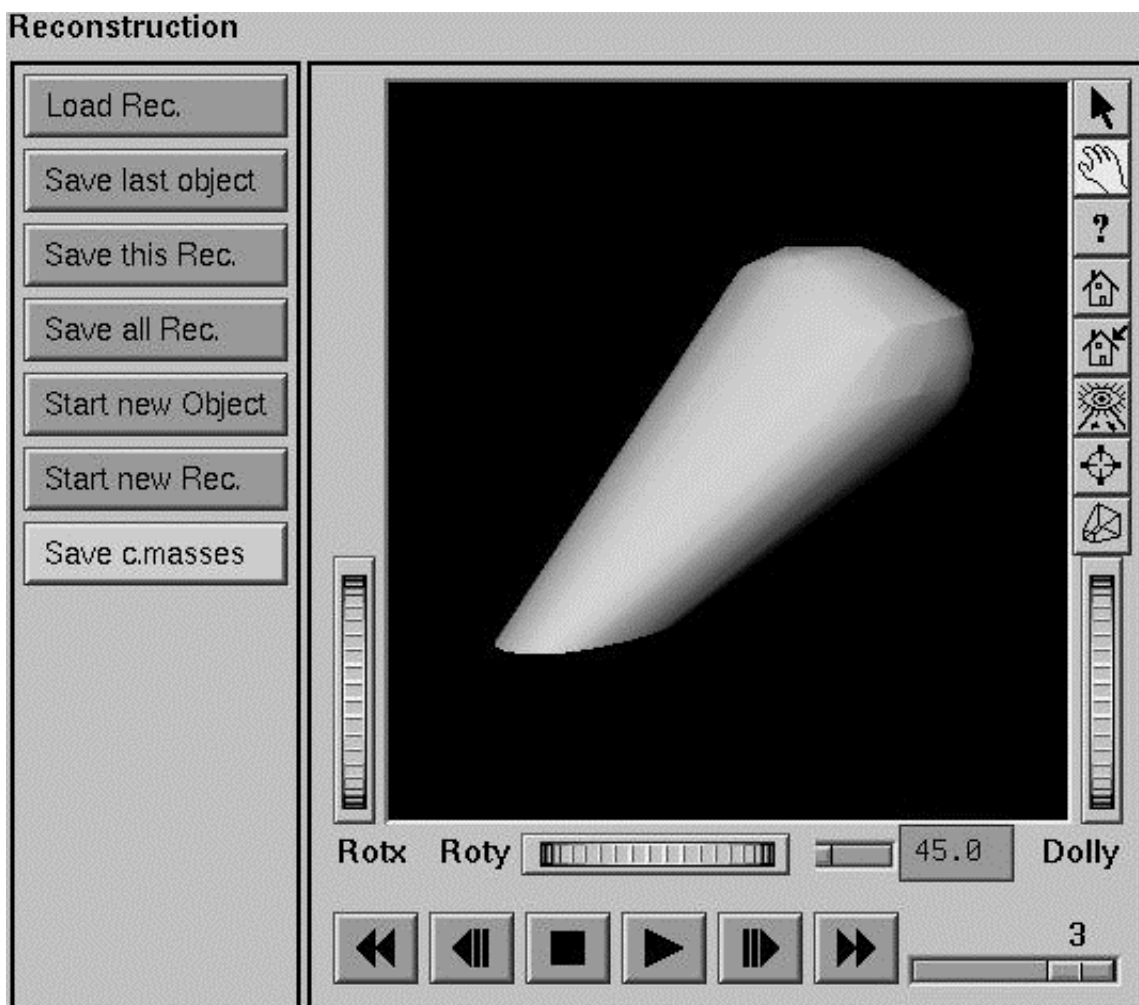
- After several groups of conjugate points have been determined the object can be reconstructed by clicking on the **Valid Rec** button. A minimum of four groups is required for the visualisation in the reconstruction subwindow

Section based reconstruction:

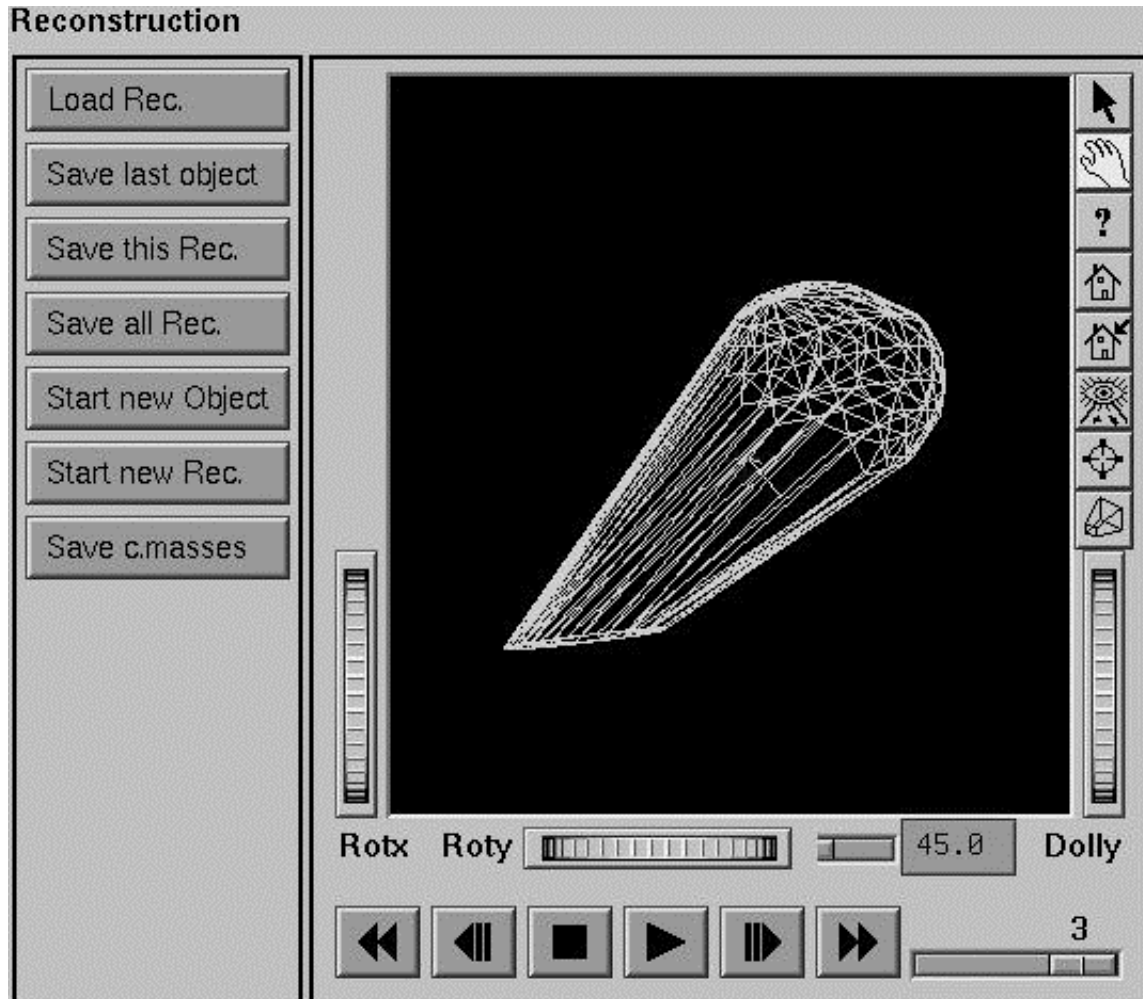
- Only two points of view (orthogonal) in the left subwindows can be used. Then we select a couple of conjugate points and click on the button **Section**, which turns to an **End Sec** button.
- Another couple of conjugate points is selected and then by clicking on the **End Sec** button the section is computed and is represented in the up left subwindow, as appears next:



The reconstructed object appears in the following way:

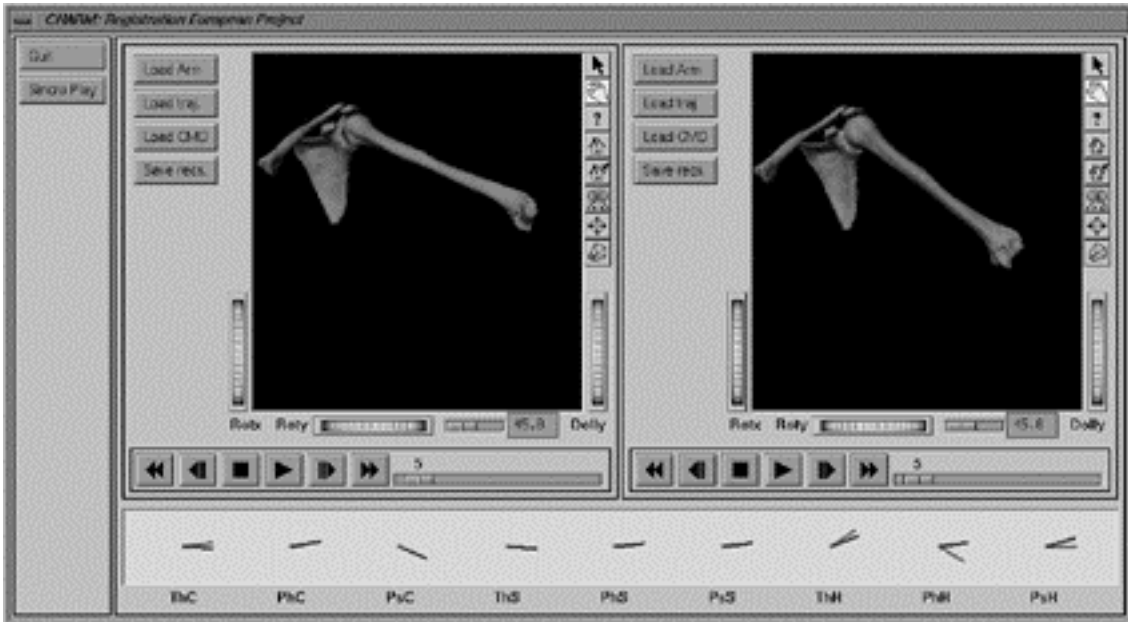


A wireframe representation allows for easier viewing of the centre of masses and principal inertia axes of the object as shown next:



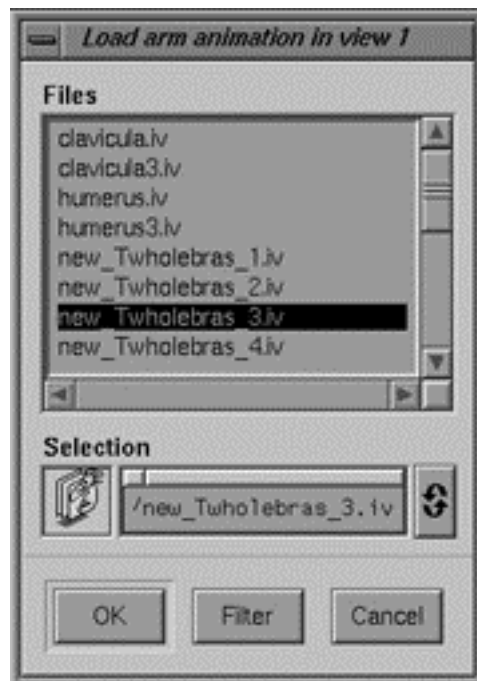
4.2. Registration/validation module

Type the command **regist** and then execution is started. The following image gives a view of the module's interface:



4.2.1. Loading an arm

At any of the views, click the button **Load Arm** in order to start loading a model arm in the file format described earlier. Then a dialog opens:



Similar functionalities as previously are available. The default extension is .iv.

4.2.2. Trajectory loading

At any of the views, click the button **Load traj** in order to start loading a trajectory file. Then a dialog opens with similar functionalities as earlier although the default file format is with extension .traj.



4.2.3. Centre of masses and principal directions loading

The button **Load CMD** is used with default file format .cmd.



4.2.4. Saving reconstructions

This functionality saves the current frame, which can be loaded into the reconstruction module for computation of centres of masses and principal directions. It is activated by clicking the button **Save recs**.

4.2.5. Play synchronising

This functionality allows for activating and deactivating the temporal synchronisation (by the frame number) of the movements in the two subwindows. Only the **Play** and **Stop** buttons are synchronised, not the other video controllers. In the future the synchronisation will take into account the possibility that the number of frames is different in the two sequences.

This functionality is activated by clicking on the **Sincro Play** button. Messages ask for confirmation of the activation or deactivation:



4.2.6. Video controllers

They have been already described.

4.2.7. Quitting

For both modules clicking on the **Quit** button opens a confirmation dialog:



4.3 Error messages

During the execution, errors of the user can be corrected. Error message windows are of the following type:



5. Spatial registration and validation results

As indicated in the deliverable D11, temporal registration of the movements is manually obtained by having a synchronising event in the real sequences, through which static reconstruction can be performed, and the simulation can be synchronised, which can be then played visually in a synchronised way, as described above.

Spatial registration of the objects is quite a complex issue, with a lot of biomedical literature. In the framework of the CHARM project we have studied several methods and implemented an easy and significant one to enable initial validation with the modes of images we deal with in this CHARM phase.

We have chosen to register the images based on two simple physical characteristics of the bones: the centre of masses - giving the position - and the principal inertia axes - giving the orientation -. They are computed from the reconstructed surface coming both from the bones reconstructed from fluoroscopies and from the VHD based models.

As we want to compare trajectories, the inertia axes are the really significant characteristics which allow us to compute the evolution of some angles which show the evolution of some joints.

So far, we have not achieved a good automatic registration based on these parameters which could be used for better visual registration and matching including skin surface. The movements used for the validation are so different that the validation shows them as different with very little problems.

APPENDIX 1: Validation through EMG

Another resource for validation which was preliminary explored by UIB, through the Physiology Professor Ruben Rial, was to check the results obtained in the CHARM project through optimisation techniques about the activation levels of the actuators against actual measurements. Two techniques are available in practice to estimate the activation level of a muscle actuator: the electromyographic measurements (EMG) and the intramuscular pressure measurements (IMP). Both methods provide complementary informations on the muscle activation state. However, as they provide more accurate data than IMP measurements, EMG measurements have been more commonly used.

Preliminary work was developed: bibliographical survey was conducted, experiences were designed to get EMG recordings, and first trials performed. Surface EMGs were recorded in these first trials using conventional adhesive surface electrodes (paper and magnetic FM tape were used), while the subject performed movements of abduction and adduction of about 30° , with and without loading (in this case, against a 10 kg load applied to the elbow); six simultaneous channels were used for the main muscles.

APPENDIX 2: Some moving images tools

Although the more advanced image analysis tools are not fully integrated in the validation environment, due to the late integration of this part, the methods for allowing the tracking of the objects and computing the kinematics parameters have been developed. We enclose two reports: Segmentation of 3D images and video sequences (V Caselles and J L Lisani) and Snakes in movement (V Caselles and B Coll).