Modern Visualisation Tools for Research and Education in Biomechanics

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Abstract

The DataManager presented in this paper allows the multimodal visualisation of heterogeneous data originating from the biomedical field and, more particularly, Biomechanics. In the latter, the aim is to increase our understanding of the musculo-skeletal system, and to achieve this, numerous disparate data must be collected and combined. Previously, no software tool fully allowed such integration, but the DataManager and its development environment (the MAF) now provide an answer to that problem.

This paper presents the current visualisation and data processing tools available from the DataManager. Its usefulness for research, educational and clinical activities will be demonstrated.

The system developers hope that the data management mechanisms available within the software will stimulate data sharing between scientists and will encourage them to participate in enhancing the system by integrating their own software tools.

Keywords--- **Multimod project, MAF, DataManager, Biomechanics, biomedical visualisation, education, anatomy, multimodality**.

1. Introduction

There is a continuing demand for more effective visualisation tools from many biomedical applications due to the complexity and heterogeneity of the data that must be considered.

Typically, data collected for biomechanical applications are extremely disparate:

- limb motion data from video (*stereophotogrammetry*);
- muscle activity (*electromyography*);
- joint kinematics data (*electrogoniometry*);
- medical imaging (*magnetic resonance imaging, MRI*, and *computerised tomography, CT*);
- three-dimensional reconstruction of anatomical structures;
- etc.

Traditionally, such data are visualised individually using specialised tools. It is up to the observer mentally to synthesise the information available from the various data sources. Such an operation demands a high level of skill and training and is prone to errors of judgment in some conditions (e.g., junior or tired observer). In clinical practice, such problems are crucial.

Though less dramatic, interpretation of heterogeneous data is even more complicated for students that must study the various aspects of the Human Anatomy using the above sources of information. Medical students are usually poorly trained mentally to combine information; full interpretation of the content is therefore often not optimal [1].

The availability of efficient software tools for the combination of heterogeneous data is critical to improve the interpretation and increase the understanding of the available information. To answer these needs, the EC-funded MULTIMOD project has developed an architecture (called the *Multimod Application Framework*, or *MAF*) and a set of visualisation tools (Fig. 1).

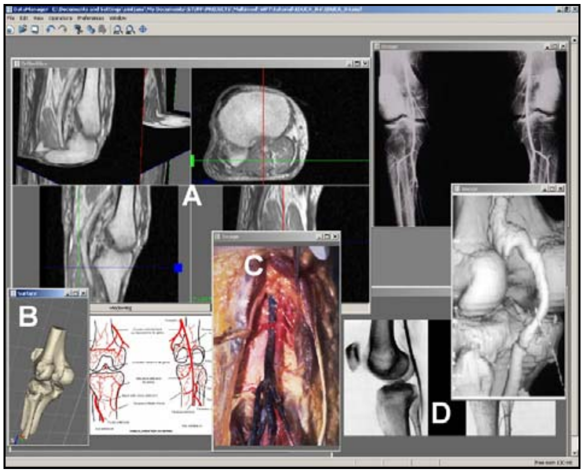


Figure 1. Example of heterogeneous data visualised within the DataManager. A: MRI data, B: 3D bone modelling, C: multimedia class showing a dissection, D: arteriography.

The MAF architecture and visualisation tools are presented in other papers, including the concepts behind the data combination and registration [2, 3]. This paper describes a typical application, called the DataManager, developed from the MAF architecture, and its use in both research and pedagogical contexts.

2. Data Management and Data Visualisation

Conceptually, two kinds of end-users can be considered when using vertical applications like the DataManager implemented from the MAF: management users (***MNG***) and visualisation users (***VIZ***). These will use the interface for different purposes, so it must answer the expectations of both sides.

2.1. MNG approach

MNG users are typically individuals who need to organise their data hierarchically either for research purposes or to prepare data distribution to third parties (e.g. students) who will adopt the VIZ approach.

The interface must address data management issues related to organising large disparate data stored on the user system. An important MAF feature is the ability to allow the MNG user to sort the available data within a multiple-level hierarchy. The data is organised into a tree-like structure, called the VME tree, in which nodes and branches represent the available information as organised by the MNG user (Fig. 2).

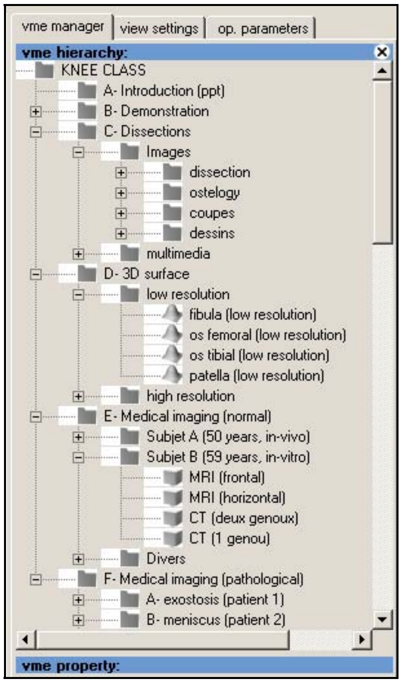


Figure 2. Example of VME tree. The VME tree illustrated here is related to heterogeneous data used to describe various aspects of the knee anatomy (e.g. Powerpoint presentation, multimedia files, medical imaging, 3D modelling). In this particular example, more than 1 Gb of data is available from the VME tree, which runs on standard PCs.

It must be emphasised that the data available from each VME node is stored separately on the hard disk, while the description of the VME tree is stored in a independent file (with extension MSF). This allows large amounts of data to be combined without the sacrifice of flexibility and interactivity.

2.2. VIZ approach

Some users do not need to organise data but, rather, need to visualise them (for example, a medical professional who consults a patient report, or a student studying the content of a tutorial). The above VME tree can become extremely large and complex and thus tend to confuse for a VIZ user. The MAF architecture, therefore, allows the creation of so-called *layouts*, which are shortcuts that will automatically display pre-selected data from the VME tree. The data pre-selection is typically performed by MNG users, and stored into labelled layouts within the MSF file. VIZ users load available layouts from the *layout dialog box* (Fig. 3). This feature is a key-element for allowing non-technical users to access large amount of heterogeneous data swiftly with just a few mouse clicks.

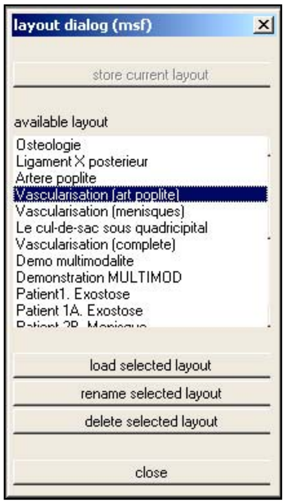


Figure 3. Layout dialog box. The list displays all available pre-selected data. Loading the unlighted layout will pop up the user screen visible at Fig. 1.

A user can easily switch between MNG and VIZ modes according its current needs.

3. Using the DataManager interface

One of the aims of the MAF architecture is to offer the possibility of creating an environment for simultaneous visualisation of heterogeneous data. An environment such as the DataManager offers both import and export facilities, combined with various kinds of visualisation windows and data processing tools.

3.1. Data import/export

Heterogeneous data currently accepted by the DataManager includes standards from various data collection procedures (Table 1). Non-standard data can be imported using raw formats.

Table 1. Standard formats available within MAF

DATA TYPE	***FORMATS***
Property format	MSF
Exchange format	VTK
Motion data	C3D, PGD
3D modelling	STL, VRML
Medical imaging	DICOM
Images	BMP, JPG, PNG, TIF

Once a dataset has been imported it becomes a member of the current VME tree (see Fig. 2). Its position in the VME hierarchy can be altered using copy/paste operations.

3.2. Data viewers

Once data of a particular type is imported into a VME tree, it can be visualised by the system viewers. Each viewer is able to detect automatically compatible data from the VME tree (Fig. 4).

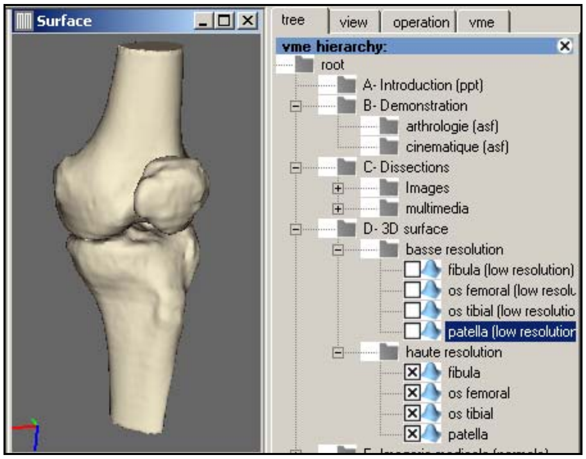


Figure 4. Automatic detection of "visualisable" VME elements. The current viewer (here a "surface viewer") indicates which data can be displayed by the presence of empty clickable boxes next to the compatible VME data. Crossed boxes indicate the data that is currently displayed in the window. All viewers in the DataManager are based on the same principle.

3.2.1. Surface viewer (Fig. 4)

This allows visualisation of any data (geometry, motion, medical imaging) spatially defined according to some technical frames. The technical frame of each dataset available in the VME tree can be modified either by associating it with a VME element located higher up in the VME tree hierarchy, or by performing registration. The latter is the key-feature allowing heterogeneous data combination (see Section 3.3).

3.2.2. Single Slice and Orthoslice viewers (Fig. 5)

Both of these deal with medical imaging datasets. The Single Slice viewer displays a single slice along one of the original dataset axes, while the Orthoslice viewer shows four images – a slice along each axis and a 3D viewer (top-left window in Fig. 5). Displaying a 3D model, with or without transparency, in such window allows the visualisation of particular anatomical structures (e.g. bones, as in the illustrated example) with the surrounding environment (e.g. soft tissue).

Such a feature is of interest when estimating the extension of a structure within the subject's anatomy or when learning how to recognise anatomical features within medical imaging datasets.

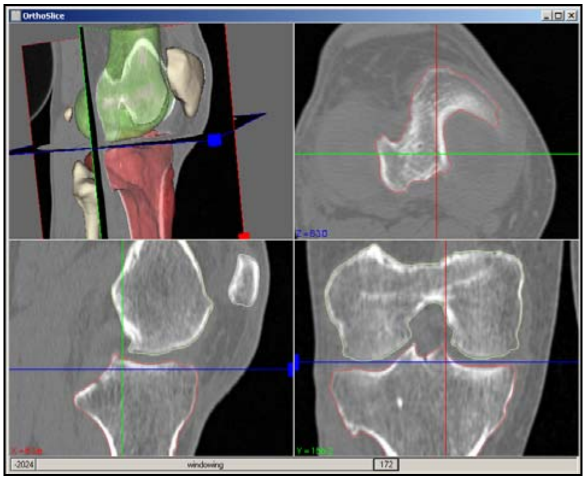


Figure 5. Orthoslice viewer. A CT dataset of a knee is displayed together with the 3D bone models of the joint.

3.2.3. RX-CT viewer (Fig. 6)

This presents several slices in a slightly different way from the previous viewers. The main difference is the ability to interpolate X-ray-like images from a CT dataset. This is useful when digital X-ray images are not available. Displaying 3D models is also possible (see Fig. 6, femoral bone in red, patella in blue) and allows a better understanding of the available information.

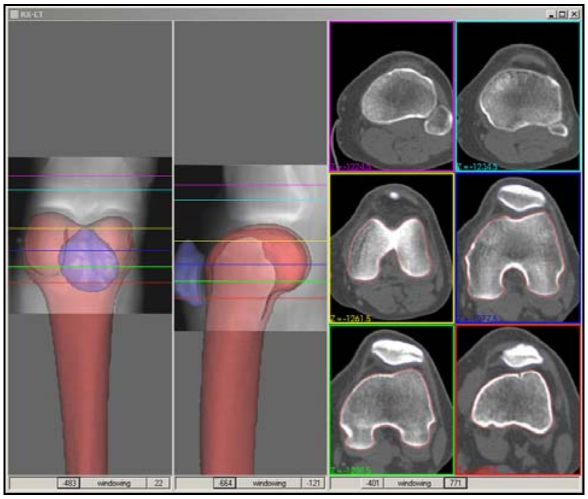


Figure 6. RX-CT viewer. The left half of the screen shows the X-ray interpolation obtained from the CT-Scan. The levels of the slices on the right are selected by dragging coloured bars in the X-Ray viewer. Contrast windowing is also available.

3.2.4. Arbitrary slice viewer

This allows a user to interpolate slices through a medical imaging dataset. The difference from the previous slice viewers is that the arbitrary slicer is able to perform the interpolation along any orientation (the previous slicers were limited to the orthogonal planes of the dataset). This allows images to be provided according to the orientation of particular anatomical structures, rather than the way in which the imaging equipment captured the data. This reduces the need to perform further real (and costly) medical imaging sequences to align the data captured with the particular orientation of each of the anatomical structures of interest in the patient.

3.2.5. The isosurface viewer (Fig. 7)

This is based on a novel and extremely fast algorithm that allows the generation of 3D isosurfaces in real time on standard PCs. Surfaces are generated at speeds of 10-100 times faster than the standard Marching Cubes algorithm. This allows modification of the threshold levels (i.e. the Houndsfield Unit, or HU) , characterising the structure of interest in the dataset, to take place interactively – a dramatic improvement on standard procedures. Fine-tuning of the final results is improved compared to standard isosurface algorithms.

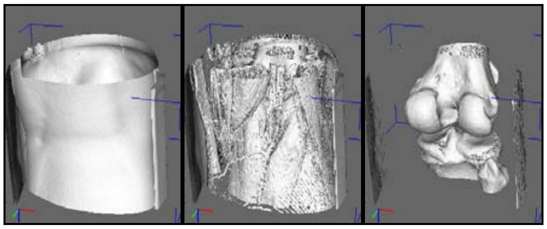
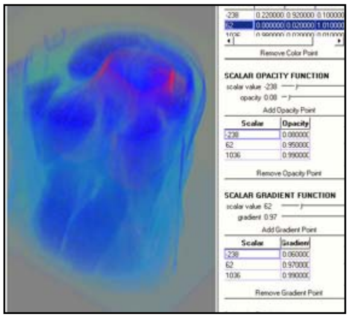


Figure 7. Isosurface generation has been performed using a CT dataset of a knee joint. Results of three different thresholds are shown (left: skin = -220 HU; centre: muscles and veins = 40 HU; right : bone = 180 HU). Results are displayed instantaneously when modifying the threshold.

3.2.6. Volume rendering (Fig. 8)

This use more complex algorithms that process the projection of rays through the dataset according to several properties (colour, opacity, gradient) given to particular HU values found in the dataset [3]. Anatomical structures can be simultaneously distinguished according their intensity properties.



-238	0.220000	0.920000	0.100000
62	0.000000	0.020000	1.010000

scalar value -238

opacity 0.08

Scalar	Opacity
-238	0.00000C
62	0.95000C
1036	0.99000C

scalar value 62

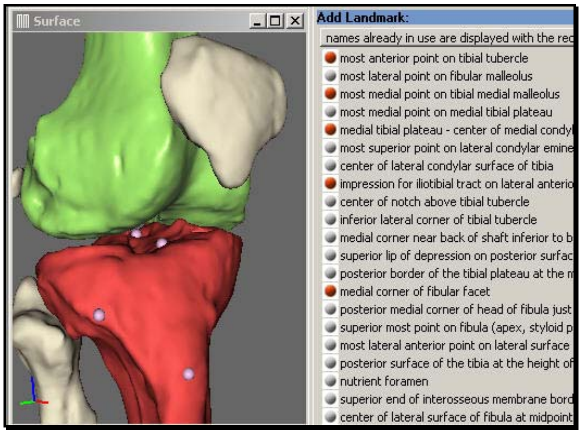
gradient 0.97

Scalar	Gradien
-238	0.06000C
62	0.97000C
1036	0.99000C

Figure 8. Volume rendering of a CT dataset (same dataset & orientation as Fig. 7). Three different materials are shown (skin = -238 HU, in green; muscles = 62 HU, in blue; bone = 1036 HU, in red).

3.3. Data registration and landmark setting

Data registration is the basis for combining heterogeneous data. Most suchprocedures are based on registering the coordinates of particular landmarks that are located within the datasets [4]. Spatial setting and location are available from the DataManager in a convenient way: the user has the possibility to create a personalised *landmark dictionary*.



names already in use are displayed with the rec

- ● most anterior point on tibial tubercle
- ○ most lateral point on fibular malleolus
- ● most medial point on tibial medial malleolus
- ○ most medial point on medial tibial plateau
- ● medial tibial plateau - center of medial condyl
- ○ most superior point on lateral condylar emine
- ○ center of lateral condylar surface of tibia
- ● impression for iliotibial tract on lateral anterio
- ○ center of notch above tibial tubercle
- ○ inferior lateral corner of tibial tubercle
- ○ medial corner near back of shaft inferior to b
- ○ superior lip of depression on posterior surfac
- ○ posterior border of the tibial plateau at the m
- ● medial corner of fibular facet
- ○ posterior medial corner of head of fibula just
- ○ superior most point on fibula (apex, styloid p
- ○ most lateral anterior point on lateral surface
- ○ posterior surface of the tibia at the height of
- ○ nutrient foramen
- ○ superior end of interosseous membrane bord
- ○ center of lateral surface of fibula at midpoint

Figure 9. Setting of anatomical landmarks (ALs). ALs are first selected in the dictionary list on the right, then set on the 3D surface by clicking on the area of interest. A sphere located on the selected area is displayed, and the selected AL string is flagged with a coloured bullet in the list (this avoids selecting the same AL twice). Spatial AL coordinates are stored into the VME tree.

Once loaded, the dictionary allows a landmark name to be chosen from the dictionary, and the corresponding point to be identified on the surface of 3D models (Fig. 9). This operation is called *virtual palpation*.

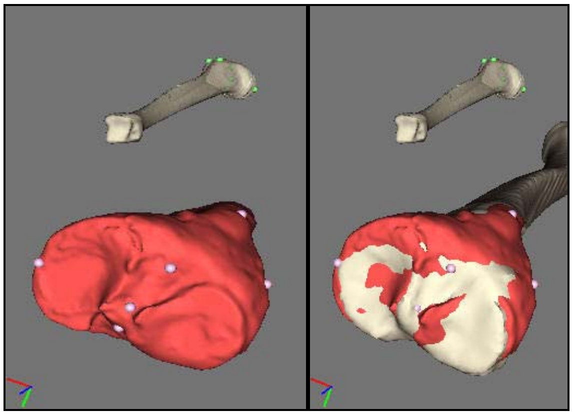


Figure 10. Registration of two tibial bones. Left: before registration. Right: after registration (using *similarity* mode). At first, each 3D model is associated with an AL cloud (pink spheres for red tibial bone, green spheres for yellow tibial bone). Then, registration takes place based on the transformation interpolated between the spatial attitudes of both AL clouds. The same transformation is applied on the 3D bone model (here the yellow bone). In this particular case, scaling has been performed as well.

All selected ALs for a particular 3D model are grouped in an *AL cloud*. In order to be registered, two datasets must each have their own AL cloud including landmarks located on the same anatomical spots. Once several clouds of landmarks are available, registration can take place. Registration processes the relevant spatial location and orientation of AL clouds in the dataset, and determines a spatial transformation matrix that will align them (Fig. 10). Because anatomical structures rarely have the same sizes and proportions, several registration procedures are implemented into the DataManager (*rigid* if the datasets have the same sizes and proportions; *similarity* if sizes are different but not the proportions; *affine* is both sizes and proportions are different).

3.4. Registration of motion data and 3D bone modelling

Simultaneous observation of motion data and the underlying joint anatomy is of great assistance in increasing our understanding of motion mechanisms and joint pathology [5]. Thanks to the operations described above, such real-time motion simulation is straightforward within the DataManager (Fig. 11).

At first, the motion data and 3D bone models are imported according to the above-mentioned formats. The motion data file usually includes spatial trajectories of particular ALs recorded by some motion analysis system. Each AL is associated with a particular limb segment (e.g. thigh, shank, or foot). The DataManager is able to sort ALs into segmental clouds automatically based on user-defined dictionaries (Fig. 11A).

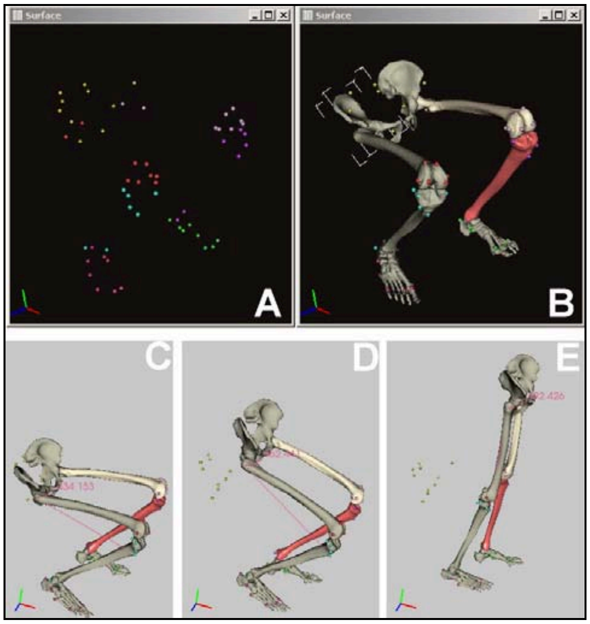


Figure 11. Real time motion data registered to 3D bone model obtained from CT-Scan (see text for explanations).

The same AL clouds are attached to the imported 3D bone models using virtual palpation. Registration is then performed in order to transform the models to the attitude of the limb segments at the beginning of the analyzed motion (Fig. 11B).

Once registration is satisfactory, motion data are used to transform the 3D bone models (Fig. 11C,D,E). The quality of the visualisation strongly depends upon the quality of both the virtual palpation and the motion data collection.

3.5. Data processing operations

The DataManager does not only provide visualisation of imported data, it also supports processing of the data and storing of the results.

Several useful operations are already included in the interface, besides the above registration procedures: generation of finite element properties, on-line distance determination between 2 ALs (Fig. 12), volume sampling, volume cropping, mapping, surface filtering (decimation, smoothing), etc.

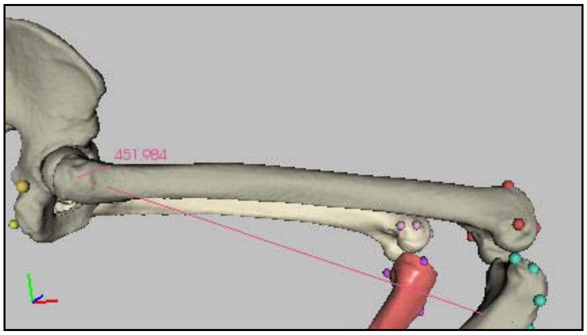


Figure 12. The variation of the distance between 2 particular landmarks is processed on-line during a motion simulation. This allows the study of, for example, muscle excursion or tendon lengthening during particular tasks.

4. Conclusions

This paper has presented a vertical application, the DataManager, built from the MAF architecture. Although more features will be added in the future, the DataManager has already shown itself useful for extensive registration of heterogeneous data. Such an interface is very promising to facilitate more extensive analysis of the various disparate datasets generated within the biomedical fields.

It is also a compact way of exchanging data between locations that usually use different standards. This is important in a field, such as Biomechanics, that deals with numerous data obtained from a variety of sources.

No individual department has convenient access to all the data collection tools that are needed to obtain the wide range of quality data essential for making significant progress towards more realistic and more anatomically correct musculo-skeletal models. Such tools include medical imaging for morphological data, motion analysis for limb motion, electrogoniometry for joint kinematics, electromyography for muscle activity, constraint gauges, body donation for cadaver dissection, 3D modelling software, histological properties of bone and soft tissue, advanced registration algorithms, finite element modelling, etc.

An environment like the DataManager, including many attractive tools for both visualisation and data processing, should motivate teams, worldwide, to translate their data into a MAF-compatible format. Such standardisation should help to increase data sharing and international collaboration.

The ability of the DataManager to allow the visualisation of multimodal data is also interesting to produce simultaneous visualisation of anatomical (see Fig. 1) or clinical information (Fig. 13). In the latter case, this should help to improve the diagnosis of musculo-skeletal disorders, for which the etiology is usually very complex, and difficult to interpret even for well trained and highly experienced clinicians.

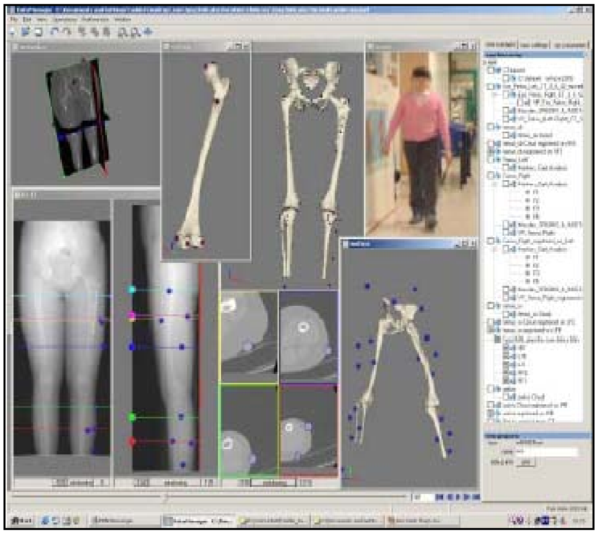


Figure 13. Multimodality analysis of heterogeneous data collected as part of a diagnosis protocol of a 5-year old child suffering of bone cancer. Displayed data include: CT data, interpolated X-ray, 3D bone models, video of gait, motion analysis data, landmark location, motion simulation.

Besides encouraging data sharing, the DataManager has a structure that will allow continuous improvement by the integration of new software tools developed by third-party programmers willing to share their work. Such participation will certainly help to maintain the improvement to our understanding of the human musculo-skeletal system that developments of recent years have furnished. Medical education and research, both fundamental and clinical, can only benefit from such progress.

Acknowledgements

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