

STUDYJOINT

An Intuitive Software for Diarthrodial Joint Analysis

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Abstract—The presented software provides a set of elaboration functions to investigate the diarthrodial joint kinematics (helical axes, instantaneous rotations, instantaneous displacements), bone anatomy (contact points, 2D bone sections, profile fittings) and ligament-tendon properties (elongations, orientations, fibre strain). Moreover, an user-friendly graphical interface allows the end user to manage time-space data obtained from medical images, navigation systems, spatial linkages or digitalizers, and to generate printable reports as well as multiple graphs.

Joint; kinematics; anatomy; joint model; software; StudyJoint

I. INTRODUCTION

The recent development of navigation systems for surgery and orthopaedic treatment and the increased interest in biomechanical modeling are requiring more accurate tools in order to have a more precise knowledge of joint functions and have a correct evaluation of reconstruction surgery [1-6].

This growing interest in the investigation of human joints, and in particular of the knee [7], led us to extend the primitive separate MATLAB (The MathWorks Inc.) functions and develop a general-purpose environment for standard biomechanical analysis. Therefore this study presents a novel software tool, called **StudyJoint**, specifically developed for an easy and extensive analysis of diarthrodial joints (e.g. human knee, hip, shoulder or elbow), considering both the joint motions and relative anatomical structures. Specifically this tool allows the user to interact with the acquired data through 3D and 2D visualizations, providing moreover all standard methods for specific investigations on joints.

II. PROGRAM DESCRIPTION

The aim of our project is to provide physicians, medical experts or researchers involved in clinical or medical applications with a free software for Windows (Microsoft Corporation) PC with all the classical computations usually performed. For this reason **StudyJoint** was developed (1) with a user-friendly and easy-to-use interface, (2) with intuitive display of surface data of anatomical structures, (3) with computational methods classified according to the standard use on the different anatomical structures or motion data. As said before, **StudyJoint** was developed in MATLAB, a mathematic-oriented language and high-level development environment, in order to focus primarily on the necessary

definition of data structures and validate rapidly computational algorithms.

A. Input and Output Data

StudyJoint motion and anatomical data can be obtained from many different devices with a simple conversion phase. Data about motion and surfaces can be acquired, for example, with navigation or tracking systems (e.g. optoelectronic systems, electrogoniometers, spatial linkages or digitalizers) and then converted in the MATLAB environment, obtaining motion homogeneous matrices and 3D spatial data vectors in *mat* format. In particular we have successfully implemented conversion functions for FlashPoint (Image Guided Surgery Technology Inc.) and Polaris (Northern Digital Inc.) optoelectronic systems, and for the FaroArm (FARO Technologies Inc.) digitizer. Similarly also typical medical images (such as DICOM images from magnetic resonance or computer tomography) can provide anatomical data useful for biomechanical investigations and become a valid input for **StudyJoint**. Standard input data are classified and described according to the following typology: *bones*, *ligaments*, *axes* and *motions*.

In particular:

- bone data are stored as a set of scattered surface points;
- ligament data are stored as a couple of insertion area boundaries and may include an arbitrary number of fibers;
- axes are stored as a couple of two points, identifying the relative directions;
- motion files are stored as a list of 4×4 homogeneous matrices, representing the instantaneous rigid transformation matrices between the mobile segment of the diarthroid joint and the fixed one.

The input data framework is defined in a description file that contains the features and the relationships between the different anatomical structures. The details of this file are described in Table I. Computational outputs and results are displayed in 3D or 2D graphics windows or plotting areas. The data can be saved by the user as images (*bmp*, *jpg*, *tiff* formats) or as numeric output files in ASCII or Excel (Microsoft Corporation) format.

TABLE I. DESCRIPTION FILE CONTENT

NAME	STRUCTURED VARIABLES	FIELD	DESCRIPTION
description.mat	bonedesc(i)	name	name of the i^{th} bone
		status	(0 = fixed bone / 1 = mobile bone)
	axisdesc(i)	name	name of the i^{th} axis
		start	number of bone, axis starts from
		end	number of bone, axis ends on
	ligdesc(i)	name	name of the i^{th} ligament
		start	number of bone, ligament starts from
		end	number of bone, ligament ends on
		fibername	description of possible fibers
	motiondesc(i)	name	name of the i^{th} bone
label		labels on specific frame	

B. User Interface

The **StudyJoint** user interface was designed to allow an intuitive interactive display, a simple manipulation of the 3D window, and the possibility of a quantitative elaboration of surface and motion data. For these reasons the main window was divided into four different panels (Fig. 1).

- The *upper middle panel*: the 3D display window represents the digitized objects as clouds of scattered points and allows the frame-by-frame or continuous display of the relative position of the bones and their subsets (e.g. the ligaments insertion areas) during the recorded movements. Standard 3D view manipulation (zoom in, zoom out, pan and rotate 3D), display saving, and printing are available through contextual menus;
- The *right panel* (loaded data display management): lists the loaded objects and their relative status through pop-up menus, and additional information is available for motion and ligament data (such as fibers number and names);
- The *left panel*: a list of available computational methods and algorithms and data analysis functions are available. In particular, it offers evaluations feasible on bone sections, ligament orientation or elongation, and instantaneous or mean helical axis due to the relative motion of the reference systems
- The *lower middle panel* (computation-specific interface): this area is activated to help the end user to introduce input data for specific evaluations (such as

the thickness, the position and orientation of the slide in the bone section).

C. Computational methods and algorithms

StudyJoint permits a complete management of 3D image display, including standard features, such as 3D rotations along the three coordinate axes, roll along the camera axis, pan of camera position, and zoom out and zoom in on 3D data.

In bone section management, surface scattered 3D points are projected onto user-defined planes (considering planes in fixed or mobile reference systems, planes perpendicular to axes, or arbitrary oriented planes). The obtained profiles can be fitted by lines, circles or ellipses, through standard least-square optimization (Fig. 2). Contact points can be defined by mouse clicking and are evaluated as the nearest point on bone projection to the current identified area. Both the fittings and the contact points are tracked in the slides through the motion.

Two functions are available for the ligaments: (1) the ligament or fiber elongations (absolute or percentage), evaluated through the tracking of the Euler distance of insertions; and (2) the ligament or fiber orientations, evaluated as the angle between the vector identifying ligament direction and a specific plane (coordinate plane or also the plane fitting ligament insertions).

The computation on motion data includes the decomposition of the relative motion between fixed and mobile reference systems by Euler algorithm and display or the instantaneous helical axis frame-by-frame or the mean helical axis of the whole movement.

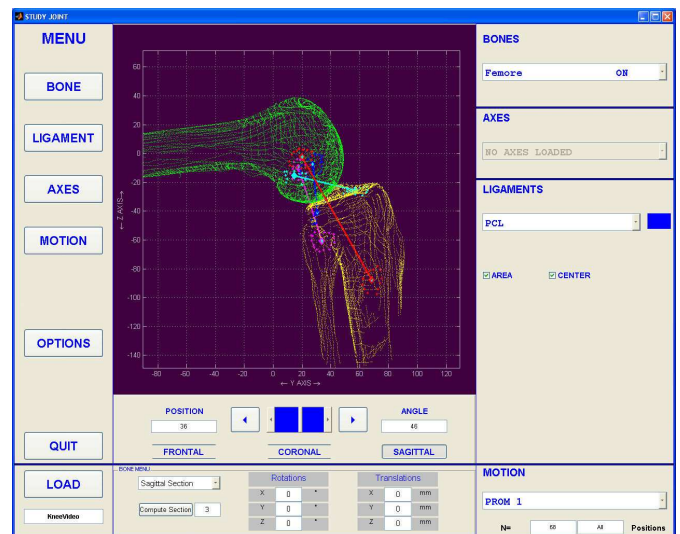


Figure 1. Example of **StudyJoint** Main Interface

III. HARDWARE AND SOFTWARE SPECIFICATIONS

StudyJoint was entirely developed using MATLAB 7.0.4 with Service Pack 2 (Release 14). The final version of the package was compiled as a standalone Microsoft Windows application (with the MATLAB Compiler), run and tested on a

32-bit Microsoft Windows operating systems (Windows 98/Me/NT/2000/XP). In this way the program is now independent from MATLAB's complete installation and no additional licences are required to use **StudyJoint** package, as the necessary libraries (Matlab Runtime Environment) are included in the program distribution.

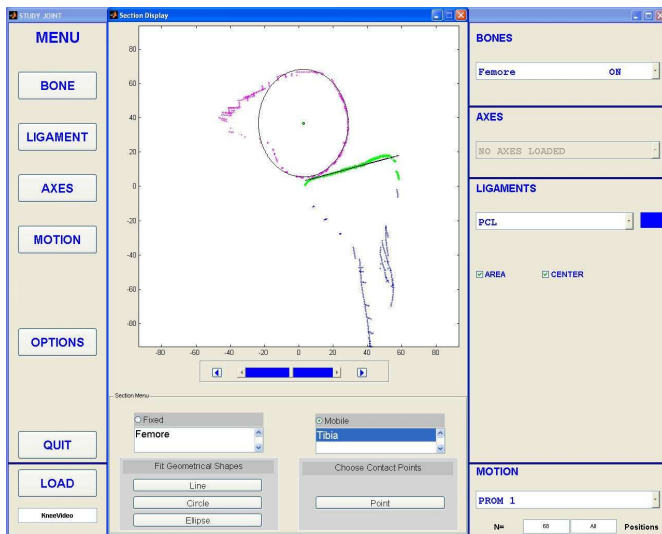


Figure 2. Bone Section Interface (with fittings)

IV. CONCLUSIONS

We have presented a software tool implementing a rather complete analysis of a joint in an easy interface. **StudyJoint** was successfully used with data about ligaments or axes, for investigations into knee joint rotations and laxities [8-10]. **StudyJoint** is able to calculate most of the classical anatomical measurements performed on 3D medical images (computer tomography or magnetic resonance), such as conformity of bone surfaces in the articulating areas, bone morphology and ligament insertions. Moreover, it also includes all standard elaborations for the analysis both of joint kinematics and of soft-tissue behaviour, such as ligament elongation or strain, helical axes and angles evaluation, instantaneous rotations and displacements in a user-chosen reference frame, centres of rotation.

Furthermore, it can be used to process in-vivo data from computer-assisted procedures and elaborate laboratory tests, thanks to its user-friendly interface and implemented analysis functions. The adjustable input management can help to work also on specific data subsets and investigate a precise structure behaviour or on standard medial images [11]

This tool is aimed at physicians and medical experts to be used research settings, or on clinical data, and scientists for laboratory tests and fast joint behaviour evaluation.

Further development of the present release will include the extension of input data format, the implementation of non-standard computational methods for joint kinematics. Moreover, the further step will be the migration from MATLAB environment (mainly useful for the definition of

algorithm and data structures) to the JAVA environment, that permits an extended compatibility, with a simple management of graphics.

V. AVAILABILITY

StudyJoint package is available free of charge upon request. A version updated in summer 2005 is available for download at <http://www.StudyJoint.org>. Input data transformation or plug-ins for specific acquisition devices can be obtained from the authors within the frame of a research agreement.

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REFERENCES

- [1] M. Sati, H. Staubli, Y. Bourquin, M. Kunz, L.P. Nolte, "Real-time computerized in situ guidance system for ACL graft placement", in *Computer Aided Surgery*, 2002, 7(1), pp. 25-40.
- [2] M. Degenhart, "Computer-navigated ACL reconstruction with the OrthoPilot(R)", in *Surgical Technology International XII*, Universal Medical Press, Inc., San Francisco, California, USA, 2004, pp. 245-51.
- [3] R. Lattanzi, M. Viceconti, C. Zannoni, P. Quadrani, A. Toni, "Hip-Op: an innovative software to plan total hip replacement surgery", in *Medical Informatics and the Internet in Medicine*, 2002, 27(2), pp. 71-83.
- [4] S. Martelli, F. Acquaroli, V. Pinskerova, A. Spettoli, A. Visani, "An anatomical model of the knee joint obtained by computer dissection", in *Lecture Notes in Computer Science n. 2489*, Proceedings of 5th MICCAI, eds. T. Dohi and R. Kikinis, Springer Verlag, London, UK, 2002, pp. 308-314.
- [5] S. Zaffagnini, S. Martelli, F. Acquaroli, "Computer investigation of ACL orientation during passive range of motion", in *Computers in Biology and Medicine*, 2004, 34(2), pp. 153-163.
- [6] S. Martelli, V. Pinskerova, "The shapes of the tibial and femoral articular surfaces in relation to tibiofemoral movement", in *Journal of Bone and Joint Surgery [BR]*, 2002, 84-B(4), pp. 607-613.
- [7] S. Martelli, S. Zaffagnini, R. Minola, P. Golano, D. Giovannucci, "Computerized kinematic analysis of rotator cuff behaviour during passive motion", in *Proceedings of 4th Annual Meeting of CAOS-International*, eds. F. Langlotz, B.L. Davies, S.D. Stulberg, Preferred Meeting Management Inc., San Diego, USA, 2004, pp. 349-350.
- [8] S. Zaffagnini, S. Martelli, L. Garcia, A. Visani, "Computer analysis of PCL fibres during range of motion, in *Knee Surgery*", *Sports Traumatology, Arthroscopy*, 2004, 12, pp. 420-428.
- [9] S. Martelli, S. Zaffagnini, B. Falcioni, M. Motta, "Determination of an optimal kinematic protocol for computer-assisted evaluation of anterior cruciate ligament deficiency", in *Annals of Biomedical Engineering*, 2001, 29, pp. 1112-1121.
- [10] S. Zaffagnini, S. Martelli, B. Falcioni, M. Motta, M. Marcacci, "Rotational laxity after anterior cruciate ligament injury by kinematic evaluation of clinical tests", in *Journal of Medical Engineering and Technology*, 2000, 24(5), pp. 230-236.
- [11] S. Martelli, A. Visani, "Computer investigation into the anatomical location of the axes of rotation in the knee", in *Journal of Mechanics in Medicine and Biology*, 2002, 2(3-4), pp. 433-447.