BIOMECHANICAL TOOLKIT: A STEP TOWARD INDEPENDENCY BETWEEN MOTION CAPTURE DATA AND BIOMECHANICAL ANALYSIS

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The goal of this workshop is to present the usage of the Biomechanical ToolKit library in a context of gait analysis and bicycle pedaling analysis. Firstly, a brief history of the project will be presented. Then, an interactive demonstration of the software Mokka (MOtion Analysis Kinematic and Kinetic Analysis) will be realized. The second part will be on the next major evolution of the project that is currently in progress. Indeed, this project wants to go forward by proposing a generic architecture for all types of measurements but also by introducing biomechanical models. Thus, it will improve and help exchanges and collaborations between laboratories. The behaviour of the proposed architecture will be presented, including the comparison of models results. Finally, the last part will be an open questions session regarding the usage of BTK/Mokka by the auditory.

KEY WORDS: Biomechanics, user-computer interface, motion capture systems, joint kinematics, data processing, open-source.

INTRODUCTION: Since 2009, the project Biomechanical-Toolkit (Barré and Armand, 2014) proposes tools to help scientists to deal with motion capture data. These tools proposed firstly in a C++ library were ported to Matlab (Mathworks, USA) and Python due to their large usage in the scientific community. Moreover, a standalone software application named MOKKA (MOtion Kinematics and Kinetics Analyzer) was developed to visualize the content of a biomechanical trial (Figure 1). These tools are now used around the world for research purposes, for example to convert data between two capture systems (Bley et al., 2014), or used directly in data processing workflow (Laroche et al., 2014; Sarcher et al., 2015). They are also used in the academic domain where no dedicated software application exists to learn some fields of the biomechanics. With the release of BTKCore 0.3 in January 2014, more than 20 data file formats were readable and others were already in development for the next release. However, several limitations emerged when the project wanted to pass to a major enhancement: the integration of biomechanical models and all associated computations and analyses. Indeed, to go further in laboratories sharing and exchange, the use of common tools is largely required to work on advanced analyses like for joint kinematics and kinetics. However, a lack of end-user tools in this domain was noticed. Except the use of costly third-party software applications like Visual3D (C-Motion, Germantown, USA), there is no simple way to perform such operations. Moreover, each motion capture system embeds its own biomechanical model to compute joint kinematics and kinetics parameters, (e.g. PlugIn Gait (PiG) provided by Vicon (Oxford, UK) or Helen Hayes (HH) provided by Motion Analysis Corporation (Santa Rosa, USA)). Thus, most of the scientists and clinicians are limited to the usage of the models proposed with their motion capture system. This limits considerably multi-centric studies or collaboration. Some published models like the Calibration of Anatomical System Technique (CAST) (Cappozzo, Catani, Della Croce, & Leardini, 1995) or the International Society of Biomechanics (ISB) proposition (Wu et al., 2002, 2005) would be preferred, but this would require implementing them. Unfortunately, a large number of laboratories might not have required skills to do this. This is also without counting on the debugging steps, cases management, etc. The Biomechanical-ToolKit project wants to fill this gap by offering new tools containing reverse-engineered commercial models and published models.
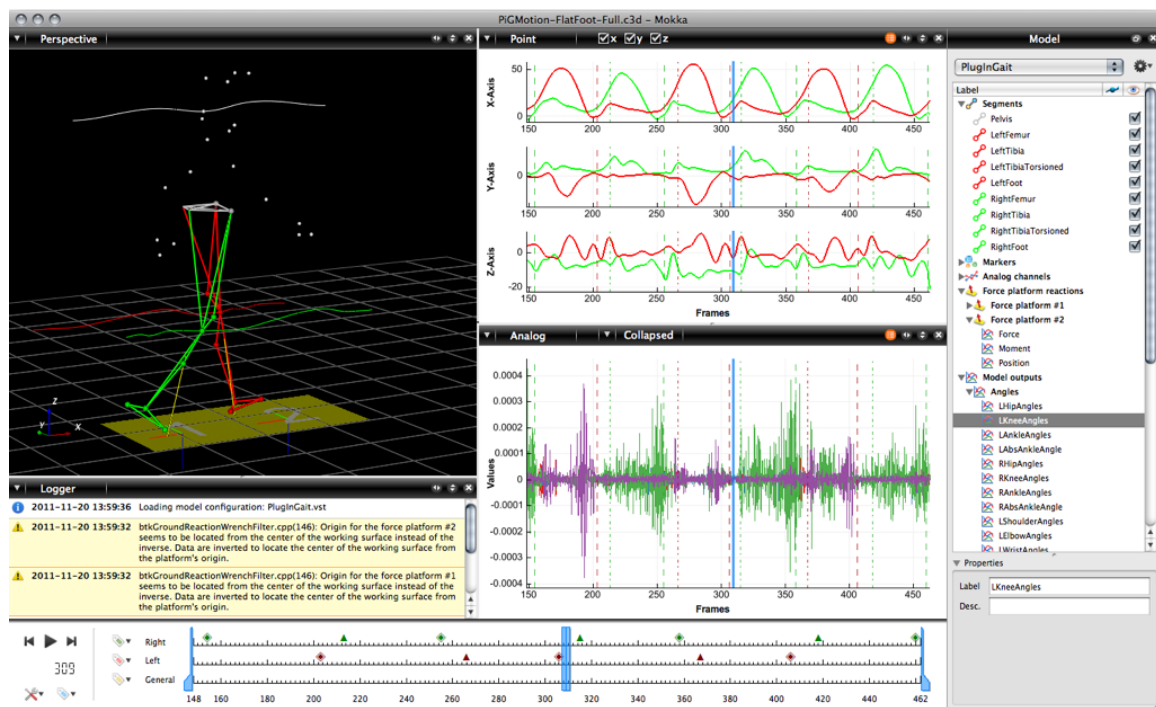
Figure 1: Screenshot of MOKKA (version 0.6.2) under MacOS X configured to visualize motion capture data (top left), joint angles (top middle), and EMG signals (center middle), time bar with events (bottom).

DEVELOPMENT: The integration of the concepts behind biomechanical modelling and post-processing computation shown several limitations in the original code architecture of BTK. Indeed, the project was firstly intended to convert motion capture file formats to the C3D file format (http://www.c3d.org). Thus, several concepts were renewed and others extended. The most important modification visible by the users would be the new generic storage architecture designed as a dynamic tree (Figure 2). Previously, a monolithic storage was implemented to store metadata, events, 1D, and 3D data. Instead of distinguishing data series as in the C3D file format (3D data with residuals or 1D analog data), those are now conceptualized behind time sequences with any number of dimensions and components. Thus a time sequence can store for example one trajectory, analog channel, segment's motion, pressure insole data, or inertial measurement data. The addition of the biomechanical modelling is also stored in a tree. Mainly, a model is composed of segments and joints. For predefined model (like PiG, HH, CAST, and ISB) a rig is happened. The later will manage the setup of the model, its configuration, the generation of segments' motion and if necessary the finalization of joint parameters (i.e. adapt left and right parameters for clinical interpretation). All these steps can be realized for one or several trials. The other major modification will reside in the simplification of the design of a pipeline (i.e. a set of filters – or blocks of data processing – linked together to transform data). Indeed, with the development of new filters used to process model's data, new kind of inputs and outputs would be expected. This would largely complicate the task of the developer and even worse break the internal update mechanism of the pipeline (i.e. only filters associated with modified filters will be processed at the next update) as inputs might not be compatible between them. Instead, a generic node is now passed to each filter. Before processing data, each filter checks the given input(s) and verifies if their content is adapted. Thus, most of the filters would be able to manage transparently the processing of one trial / model as well as several ones. This would simplify the development of custom filters or batch processing.
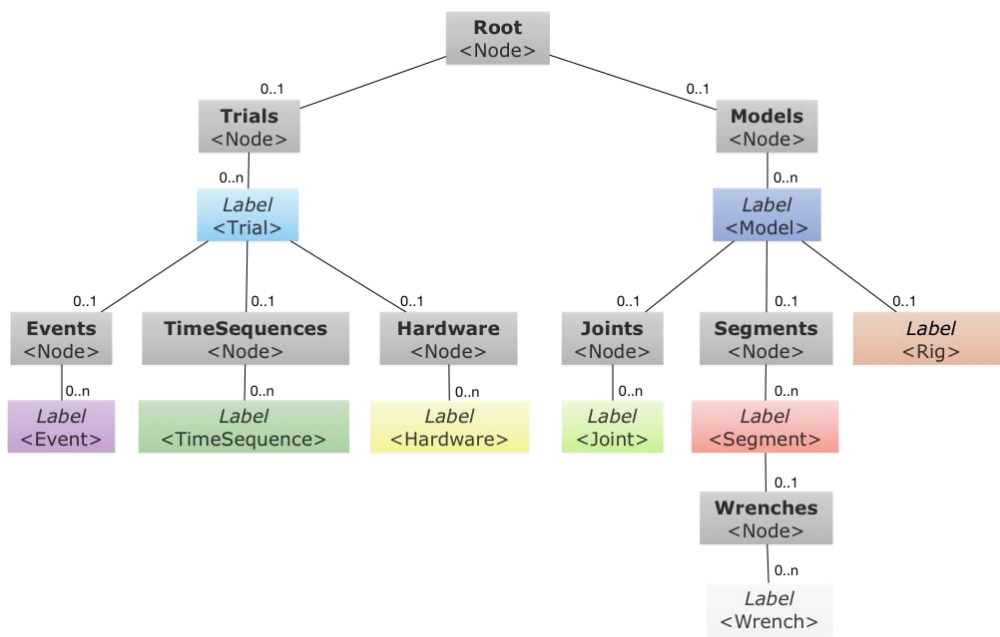
Figure 2: Details of the internal structure proposed in the development version of BTK to store trial data and model setup. Each rectangle's colour indicates a node. The numbers on top of each rectangle means the minimum and maximum number of storable nodes.

PRACTICAL EXAMPLE: The current development will give the possibility to execute powerful pipeline to compute joint kinematics and kinetics and export the results in a file (Figure 3) or compute outcome parameters. At the end, the user would need to give only filenames to load subject's information, calibrate model, generate segments motion, and export results. Several filters will be customizable by proposing different techniques (e.g. event detection algorithms). The user would have then the possibility to compare efficiently different techniques for the same dataset.
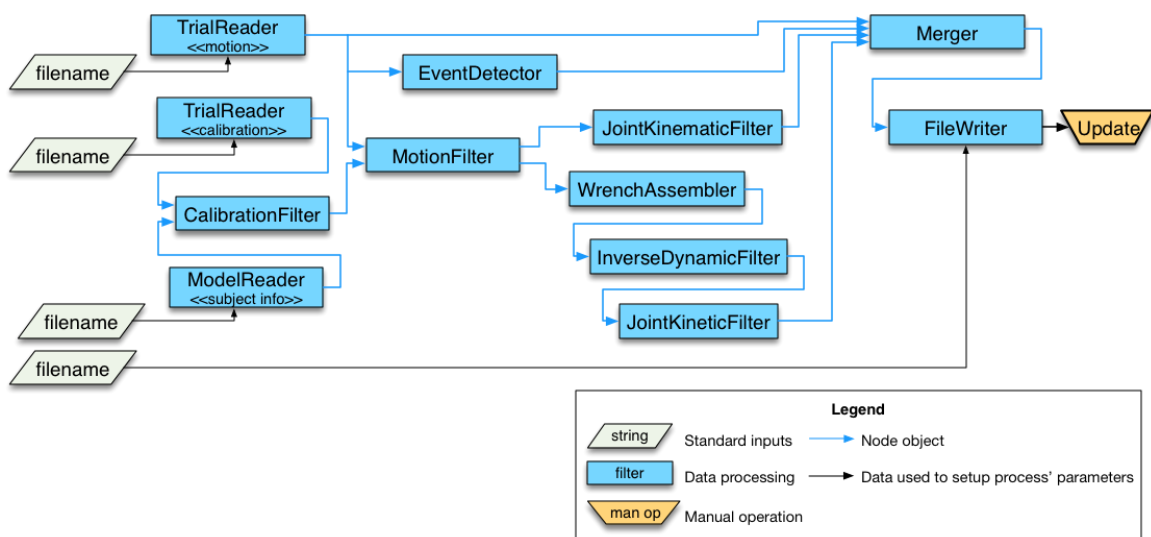

Figure 3: Example of a pipeline to compute joint kinematics and kinetics with the development version of BTK.

Considering results using similar pipelines as illustrated in Figure 3, it comes easier to compare outcomes between different models. For example, the same data collection can be used to compare joint kinematics parameter computed by different models, like PiG, HH and ISB (Barré, Turcot, Bonnefoy-Mazure, & Armand, 2014).

DISCUSSION / CONCLUSION: Thus, most of the technical difficulties are tackled to consider large-scale collaboration in an effort to (1) improve movement analysis and (2) focus on next generation of parameter outcomes. How would you use the next version of BTK to improve your researches?

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