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biomechZoo: An open-source toolbox for the processing, analysis, and visualization of biomechanical movement data

Philippe C. Dixon[a,b,*], Jonathan J. Loh[c], Yannick Michaud-Paquette[d], David J. Pearsall[d]

[a] *Department of Environmental Health, Harvard T.H. Chan School of Public Health, 677 Huntington Avenue, Boston, MA 02215, + 1 (617) 495-1000, USA*
[b] *Liberty Mutual Research Institute for Safety, Hopkinton, MA, USA*
[c] *Medicus Corda, Montreal, Canada*
[d] *Department of Kinesiology and Physical Education and McGill Research Centre for Physical Activity and Health, McGill University, Montreal, Quebec, Canada*

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ABSTRACT

It is common for biomechanics data sets to contain numerous dependent variables recorded over time, for many subjects, groups, and/or conditions. These data often require standard sorting, processing, and analysis operations to be performed in order to answer research questions. Visualization of these data is also crucial. This manuscript presents biomechZoo, an open-source toolbox that provides tools and graphical user interfaces to help users achieve these goals. The aims of this manuscript are to (1) introduce the main features of the toolbox, including a virtual three-dimensional environment to animate motion data (Director), a data plotting suite (Ensembler), and functions for the computation of three-dimensional lower-limb joint angles, moments, and power and (2) compare these computations to those of an existing validated system. To these ends, the steps required to process and analyze a sample data set via the toolbox are outlined. The data set comprises three-dimensional marker, ground reaction force (GRF), joint kinematic, and joint kinetic data of subjects performing straight walking and 90° turning manoeuvres. Joint kinematics and kinetics processed within the toolbox were found to be similar to outputs from a commercial system. The biomechZoo toolbox represents the work of several years and multiple contributors to provide a flexible platform to examine time-series data sets typical in the movement sciences. The toolbox has previously been used to process and analyse walking, running, and ice hockey data sets, and can integrate existing routines, such as the KineMat toolbox, for additional analyses. The toolbox can help researchers and clinicians new to programming or biomechanics to process and analyze their data through a customizable workflow, while advanced users are encouraged to contribute additional functionality to the project. Students may benefit from using biomechZoo as a learning and research tool. It is hoped that the toolbox can play a role in advancing research in the movement sciences. The biomechZoo m-files, sample data, and help repositories are available online (http://www.biomechzoo.com) under the Apache 2.0 License. The toolbox is supported for Matlab (r2014b or newer, The Mathworks Inc., Natick, USA) for Windows (Microsoft Corp., Redmond, USA) and Mac OS (Apple Inc., Cupertino, USA).

1. Introduction

The field of movement science has a long history [2], with the advent of the modern computer arguably providing the latest impetus for advances in our understanding of movement. Today, commercial motion capture data collection systems abound and are often packaged with software capable of computing standard biomechanical variables such as joint kinematics and kinetics. Popular examples are the Vicon (Vicon Motion Systems Ltd., Oxford, UK), Qualisys (Qualisys AB, Gotebörg, Sweden), and Motion Analysis (Motion Analysis Corp., Santa Rose, USA) systems. Unfortunately, these software are inflexible, costly, and opaque, making it difficult to adapt the software to the needs of a particular research project or to examine the underlying code. Visual3D (C-Motion, Inc., Germantown, USA) is a popular alternative, allowing users to develop bespoke pipelines; however, the platform is costly and advanced processing can be difficult to implement.

Many scientists instead choose to use platforms such as Matlab (The Mathworks Inc., Natick, USA) to develop and share cus-

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[*] Corresponding author.
E-mail addresses: pdixon@hsph.harvard.edu, philippe.dixon@gmail.com (P.C. Dixon).
URL: http://www.biomechzoo.com (P.C. Dixon)

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tom toolboxes given the simplicity, flexibility, and robustness of the platform. There are many such toolboxes available to address specific needs of the movement science community. An early example is the KineMat toolbox [24] which provides routines for three-dimensional kinematic analyses. Other notable examples are the MoCap [5], MOtoNMS [22], and ADAT [16] toolboxes which provide specialized analyses for music related movement, neurmuscular simulation, or sport, respectively. It is also important to highlight the BTK project [4] which contains functions to read, edit, and visualize motion capture data. This project is active and aims to expand to include greater analysis capabilities [3]. Finally, the International Society of Biomechanics maintains a repository of numerous user-generated software applications on their website (http://isbweb.org/software/). These toolboxes play crucial roles in the advancement of the movement sciences; however, what is lacking is a comprehensive framework from which to implement these various projects.

Although the research interests of the movement science community are varied, data sets are often remarkably similar. In many cases, data sets comprise numerous variables recorded over time from one or more data acquisition systems for many subjects, groups, and/or conditions. These data sets can therefore rely on a similar framework to perform sorting, processing, analysis, and visualization operations. The biomechZoo toolbox is an open-source project that provides such a framework. We strive to highlight the importance of systematic data processing and analysis procedures in improving research. Thus, the analogy of a Zoo, where the animal kingdom phyla are neatly organized, is the inspiration and guiding principle behind biomechZoo.

The aims of this manuscript are to present biomechZoo through the processing, analysis, and visualization of a sample data set and to compare biomechZoo's kinematic and kinetic computations against existing software. The toolbox can help researchers, clinicians, and students new to programming or movement science to process their data through a customizable work-flow, while advanced users are encouraged to contribute additional functionality.

2. Program description

The biomechZoo framework and features, including the web resources and graphical user interfaces (GUIs) are now described. The biomechZoo project contains two separate GitHub repositories: "biomechZoo" contains the toolbox code (m-files), while "biomechZoo-help" contains the sample data described in this manuscript, example scripts demonstrating the toolbox functions, and supplemental help materials. These repositories are all forkable and can be accessed through GitHub or the project website (www.biomechzoo.com).

In this manuscript, file names are typeset in `typewriter` font while commands, GUI headings, extensions, and file components are *italicized*.

2.1. General framework

The biomechZoo framework is set-up to allow users to process, analyze, and visualize motion capture data or data from any other field in which multiple time-dependant variables are collected. Reliance on this framework itself, rather than particular functions, allows biomechZoo to incorporate functionality from existing software and toolboxes (see Section 3.3 for how processes from the KineMat toolbox [24] and Vicon (Vicon Motion Systems Ltd., Oxford, UK) modeller were incorporated into biomechZoo). For each research project, a processing "pipeline" can be designed using blocks of biomechZoo functions, i.e., code cells defined by double comment characters (%%). This allows the user to focus on a particular process and to iteratively update the pipeline in preparation for the final analysis.

2.2. File structure and format

BiomechZoo files (zoo files) are standard Matlab MAT-files (*.mat*) saved with the extension *.zoo*. The use of this novel extension helps ensure that the appropriate files in a folder are loaded by biomechZoo functions. Each zoo file is a structured array with $n+1$ branches, where n represents the total number of video and analog variables (channels) recorded by the data acquisition system (Fig. 1). An additional *zoosystem* branch, contains meta-information related to the trial (e.g. sampling frequency). Each video or analog data channel branch is further divided into *line* and *event* sub branches. The *line* sub branch contains the time series data as a $m \times 1$ or $m \times 3$ matrix for one-dimensional or three-dimensional data, respectively, where m represents the number of data frames. The *event* sub branch is a 1×3 vector ([frame number, line value, 0]) that stores discrete information computed for a given channel. For example, if the maximum value $y_{\max}$ of a channel occurs at frame x, then the event will read $[x, y_{\max}, 0]$. The third entry is currently unused and is set to 0 by default. Many t events can be added to a given channel's event branch.

2.3. Batch processing functions

The biomechZoo toolbox is powered by functions that perform specific roles. Functions are stored within ten sub folders (Biomech Ops, Gait, KineMat, Mac Fixes, PiG Ops, Statistics, Support Functions, Visualization, Zoo Conversions, and Zoo Processing). The biomechZoo framework allows processes to be repeated automatically across the entire data set using batch processing algorithms. These functions are identifiable via the prefix `bmech_`. Related functions acting on a zoo file or line data contain the suffix `_data` or `_line`, respectively. For example, `bmech_normalize`, `normalize_data`, and `normalize_line`, time normalizes a set of files in a folder, a single loaded zoo file, or a single channel from a loaded zoo file, respectively. Main functions used in the current study are described in Table 1. See Appendix A for sample code to build a generic batch processing function. A log of the processing steps performed can be found in the *data.zoosystem.Processing* field of each zoo file.

2.4. Graphical user interfaces

The biomechZoo toolbox contains two GUIs: Director and Ensembler (Fig. 2), accessed by typing `director` or `ensembler`, respectively, in the Matlab command window. Director is a virtual three-dimensional environment used to animate motion capture data. Quantities such as joint angles can be graphed alongside the animations for enhanced data visualization. Force plates and accompanying ground reaction forces (GRFs) as well as custom objects (props) can also be added by the user (see `sample_prop_example`). The Ensembler GUI plots average time series data or bar graphs sorted by group or condition. Additionally, Ensembler can help users visually identify outliers and can perform data processing and analysis procedures via the *Processing* and *Analysis* menu options, respectively. Users can add functionality by editing the code that controls the elements of the menu bar or apply bespoke processes to a data set by typing a function name into the *custom* section of the *Processing* menu item.

3. Sample data set

This section demonstrates how to process, analyse, and visualize data to answer typical research questions in the study of gait.