

pyomeca: An Open-Source Framework for Biomechanical Analysis

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Statement of Need

Biomechanics is defined as the study of the structure and function of biological systems by means of the methods of mechanics (Hatze, 1974). While musculoskeletal biomechanics branches into several subfields, the data used are remarkably similar. The processing, analysis and visualization of these data could therefore be unified in a software package. Most biomechanical data characterizing human and animal movement appear as temporal waveforms representing specific measures such as muscle activity or joint angles. These data are typically multidimensional arrays structured around labels with arbitrary metadata ([Figure 1](#)). Existing software solutions share some limitations. Some of them are proprietary (Damsgaard, Rasmussen, Christensen, Surma, & Zee, 2006) or based on closed-source programming language (Dixon, Loh, Michaud-Paquette, & Pearsall, 2017; Muller, Pontonnier, Puchaud, & Dumont, 2019). Others do not leverage labels and metadata (Hachaj & Ogiela, 2019; Virtanen et al., 2020; Walt, Colbert, & Varoquaux, 2011). *pyomeca* is a Python package designed to address these limitations. It provides basic operations useful in the daily workflow of a biomechanical researcher such as reading, writing, filtering and plotting, but also more advanced biomechanical routines geared towards rigid body mechanics and signal processing. By offering a single, efficient and flexible implementation, *pyomeca* standardizes these procedures, freeing up valuable research time, thereby allowing researchers to focus on the scientific research questions at hand.

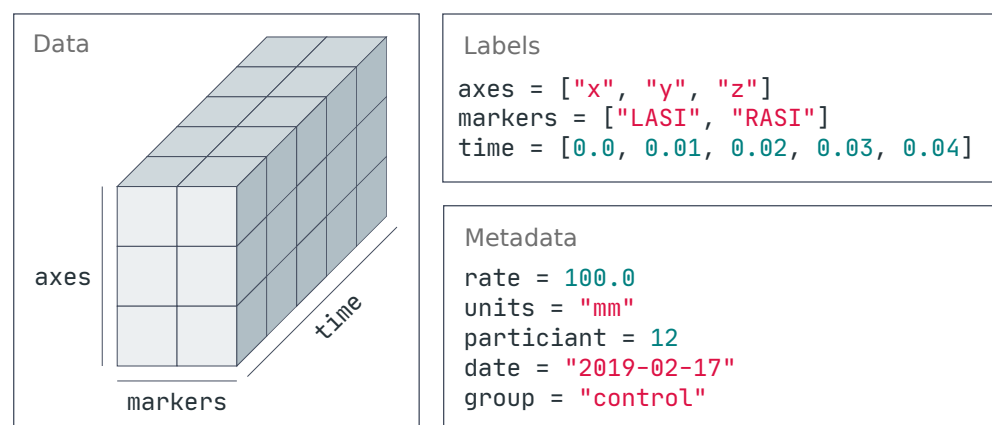


Figure 1: An example of musculoskeletal biomechanical data with skin marker positions. These data are inherently multidimensional and structured around labels. Metadata are also needed to inform about important features of the experiment.

Summary

As a Python library, `pyomeca` enables extraction, processing and visualization of biomechanical data for use in research and education. It is motivated by the need for simpler tools and more reproducible workflows allowing practitioners to focus on their specific interests and leaving `pyomeca` to handle the computational details for them. `pyomeca` builds on the core scientific Python packages, in particular `numpy` (Walt et al., 2011), `scipy` (Virtanen et al., 2020), `matplotlib` (Hunter, 2007) and `xarray` (Hoyer & Hamman, 2017). By providing labeled querying and computation, efficient algorithms and persistent metadata, the integration of `xarray` facilitates usability, which seems to be relevant in a context where scientists do not always receive extensive training in programming. `xarray` is designed as a general-purpose library and tries to avoid including domain specific functionalities — but inevitably, the need for more domain specific logic arises. `pyomeca` provides a biomechanics layer that supports specialized file formats (`c3d`, `mat`, `trc`, `sto`, `mot`, `csv` and `xlsx`) and implements signal processing and matrix manipulation routines commonly used in musculoskeletal biomechanics. We believe `pyomeca` is a solid foundation for more advanced research implementations and could, in the future, provide functions for processing and extracting meaningful clinical outputs from the raw data. `pyomeca` was written with the Unix philosophy in mind, that is to design each program to do one thing well and expect the output of every program to become the input to another, as yet unknown, program. As such, it is written in a modular, object-oriented way — which makes it extensible and easy to develop — and it interacts well with other projects under the `pyomeca umbrella`, namely `ezc3d`, `pyosim` or `biorbd-viz`. `pyomeca` follows software best practices by being fully tested, linted and type annotated — ensuring that the package is easily distributable and modifiable. In addition to the [static documentation and API reference](#), `pyomeca` includes a set of Jupyter Notebooks with examples. These notebooks can be read and executed by anyone with only a web browser through [binder](#).

Features

`pyomeca` inherits from the `xarray` feature set, which includes label-based indexing, arithmetic, aggregation and alignment, resampling and rolling window operations, plotting, missing data handling and out-of-core computation. In addition, `pyomeca` has four data structures built upon `xarray`. Each structure is associated with a specific biomechanical data type:

- `Angles`: joint angles,
- `Rototrans`: rototranslation matrix,
- `Analogs`: generic signals such as electromyographic (EMG) and force signals or any other analog signals,
- `Markers`: skin markers positions.

While there are technically dozens of functions implemented in `pyomeca`, one can generally group them into two distinct categories: object creation and data processing.

Object Creation

The starting point for working with `pyomeca` is to create an object with one of the specific methods associated with the different classes available. `pyomeca` offers several ways to create these objects: by directly specifying the data, by sampling random data from distributions, by converting other data structures or by reading files ([Figure 2](#)).

Angles	from_random_data	From scratch		
	from_rototrans		From data structures	
Rototrans	from_random_data	From scratch		
	from_averaged_rototrans		From data structures	
	from_euler_angles			
	from_markers			
	from_transposed_rototrans			
from_files				
Analog	from_random_data	From scratch		
	from_c3d		From files	
	from_csv			
	from_excel			
	from_mot			
	from_sto			
Markers	from_random_data	From scratch		
	from_rototrans		From data structures	
	from_c3d			From files
	from_csv			
	from_excel			
	from_trc			

Figure 2: *pyomeca* offers several ways to create specialized data structures: from scratch (orange), from random data (red), from other data structures (blue) or from files (green).

Data Processing

pyomeca's main functionality is to offer dedicated biomechanical routines. These features can be broadly grouped into different categories: filtering, signal processing, normalization, matrix manipulation and file output functions (Figure 3).

DataArrayAccessor	band_pass	Filters
	band_stop	Filters
	high_pass	Filters
	low_pass	Filters
	detect_onset	Signal processing
	detect_outliers	Signal processing
	fft	Signal processing
	normalize	Normalization
	time_normalize	Normalization
	abs	Matrix manipulation
	center	Matrix manipulation
	matmul	Matrix manipulation
	norm	Matrix manipulation
	rms	Matrix manipulation
	sqrt	Matrix manipulation
	square	Matrix manipulation
	to_csv	File output
	to_matlab	File output
	to_wide_dataframe	File output

Figure 3: pyomeca data processing capabilities are available through the meca DataArrayAccessor (e.g. array.meca) that allow implementing domain specific methods on xarray data objects. These methods can be categorized into filters (orange), signal processing (red), normalization (blue), matrix manipulation (green) and file output (purple) routines.

A Biomechanical Example: Electromyographic Pipeline

pyomeca has documented examples for different biomechanical tasks such as getting Euler angles from a rototranslation matrix, creating a system of axes from skin markers positions or setting a rotation or a translation. Another typical task concerns EMG data processing. Using pyomeca, one can easily extract (Figure 4), process (Figure 5) and visualize (Figure 6, Figure 7 and Figure 8) such data.

```
from pyomeca import Analogs

emg = Analogs.from_c3d("data.c3d")
emg.plot(x="time", hue="channel")
```

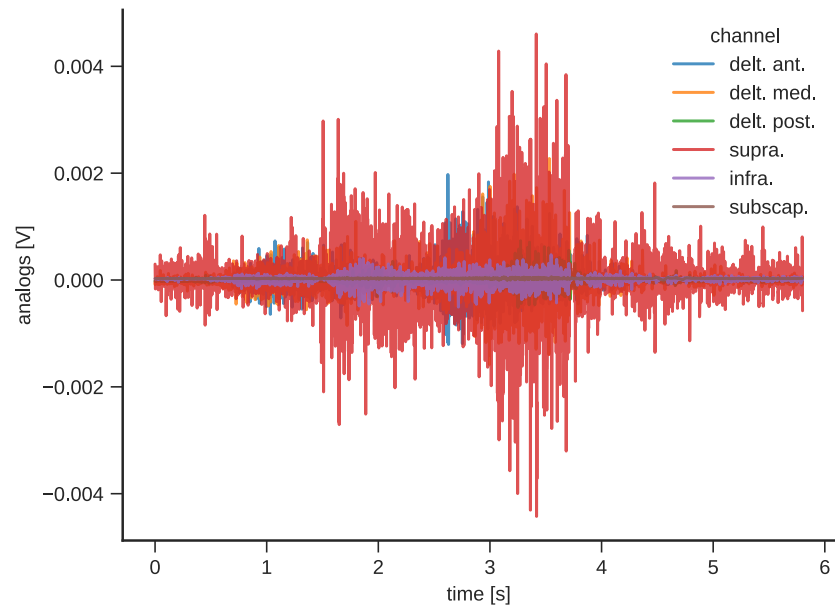


Figure 4: Biomechanical data are often stored in the c3d binary file format. Thanks to the ezc3d library (Michaud & Begon, 2020), pyomeca can easily read these files and visualize them with the matplotlib interface provided by xarray.

```
emg_processed = (  
    emg.meca.band_pass(order=2, cutoff=[10, 425])  
    .meca.center()  
    .meca.abs()  
    .meca.low_pass(order=4, cutoff=5)  
    .meca.normalize()  
)  
emg_processed.plot(x="time", col="channel", col_wrap=3)
```

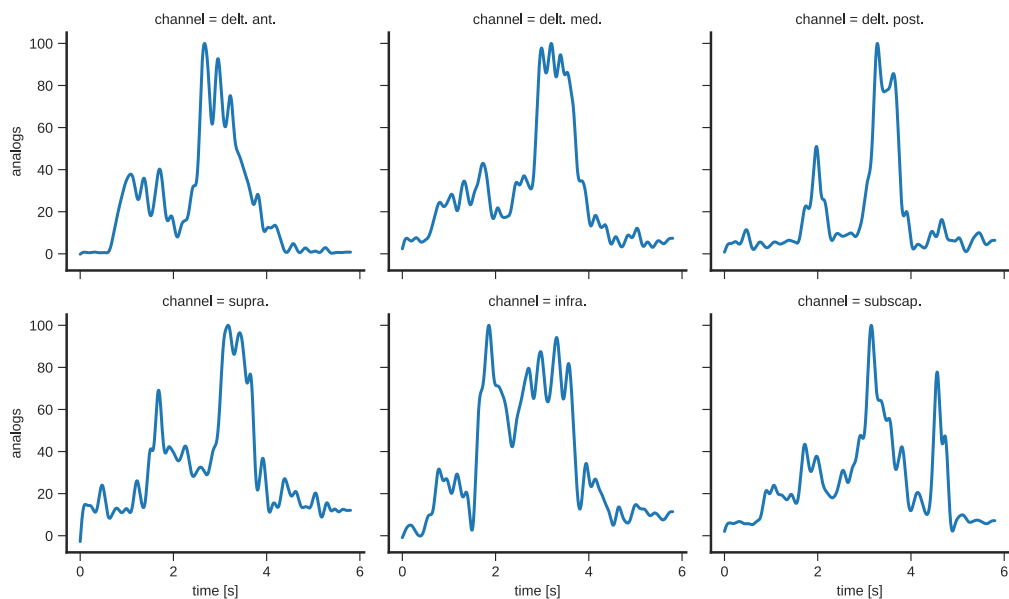


Figure 5: EMG data analysis consists of a series of signal processing steps that can be carried out by `pyomeca` in a clear and modular way.

```
import matplotlib.pyplot as plt

_, axes = plt.subplots(ncols=2)

emg_processed.mean("channel").plot(ax=axes[0])
emg_processed.plot.hist(ax=axes[1], bins=50)
```

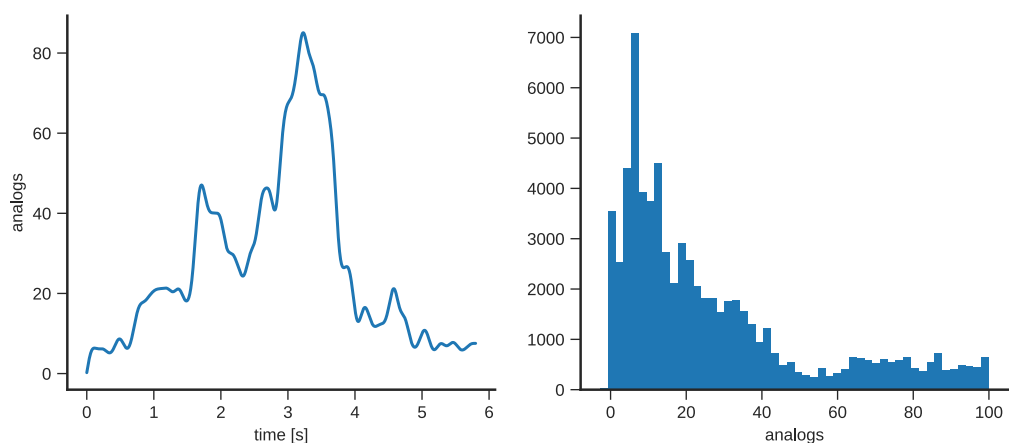


Figure 6: It is straightforward to represent the average profile of the EMG signal (left) or the distribution of EMG activations (right) thanks to `xarray`.

```
emg_dataframe = emg_processed.meca.to_wide_dataframe()
emg_dataframe.plot.box(showfliers=False)
```

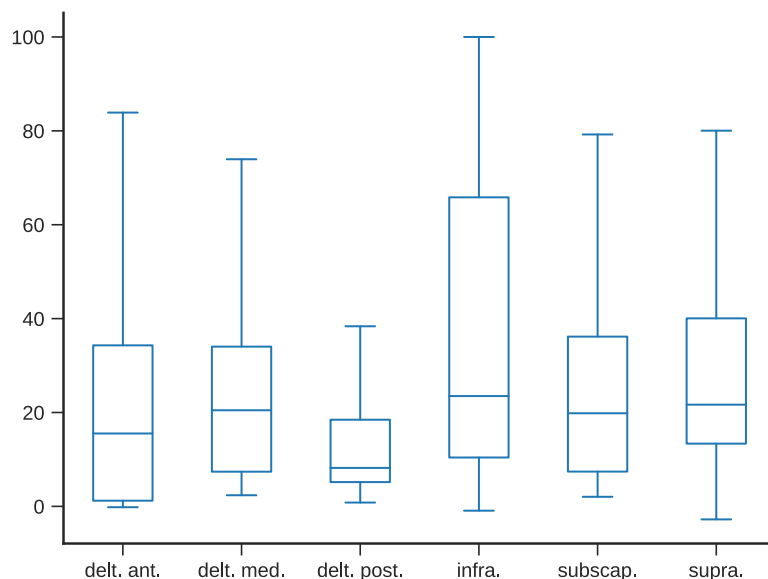


Figure 7: `pyomeca` offers a method to convert the data structure into a pandas dataframe (McKinney, 2010). This allows users to further extend the plot possibilities using the visualization built into pandas itself, such as boxplot.

```
emg_dataframe.corr().style.background_gradient().set_precision(2)
```

	delt. ant.	delt. med.	delt. post.	infra.	subscap.	supra.
delt. ant.	1.0	0.78	0.38	0.74	0.6	0.6
delt. med.	0.78	1.0	0.77	0.74	0.76	0.9
delt. post.	0.38	0.77	1.0	0.62	0.67	0.84
infra.	0.74	0.74	0.62	1.0	0.61	0.75
subscap.	0.6	0.76	0.67	0.61	1.0	0.78
supra.	0.6	0.9	0.84	0.75	0.78	1.0

Figure 8: By using a pandas dataframe, users also benefit from its broad range of IO tools and statistical methods, such as computing the correlation matrix between the different muscles.

Research Projects Using `pyomeca`

You can find an [up-to-date list of research projects using `pyomeca`](#) on the static documentation.

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