# bmlab Documentation

*Release v0.8.0*

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This is bmlab, a Python library for Brillouin microscopy data analysis. This is the documentation of bmlab version v0.8.0.

CHAPTER

ONE

# GETTING STARTED

## 1.1 Installation

To install bmlab, use one of the following methods:

- **from PyPI:** `pip install bmlab`
- **from sources:** `pip install .`

## 1.2 Basic usage

```
import pathlib

from bmlab.controllers import Controller
from bmlab.models import Orientation
from bmlab.models.setup import AVAILABLE_SETUPS

filepath = pathlib.Path(__file__).parent.parent / 'tests' / 'data' / 'Water.h5'
setup = AVAILABLE_SETUPS[0]
orientation = Orientation(rotation=1, reflection={
        'vertically': False, 'horizontally': False
    })

# Frequency ranges to evaluate in Hz
brillouin_regions = [(4.0e9, 6.0e9), (9.0e9, 11.0e9)]
rayleigh_regions = [(-2.0e9, 2.0e9), (13.0e9, 17.0e9)]

# The number of Brillouin peaks to fit. Can be set to 2
# for samples where contributions to the Brillouin shift
# from different materials are expected in the same focal
# volume, e.g. droplets.
nr_brillouin_peaks = 1

# Bounds for the multi-peak fit, only considered for nr_brillouin_peaks = 2.
# Possible options: 'min', 'max', '-inf', 'inf' or number in GHz.
multi_peak_bounds = [
    ['min', 5.0],
    [5.5, 'inf']
]
```

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```
# This condition is necessary due to
# bmlab using multiprocessing!
if __name__ == '__main__':
    session = Controller().evaluate(
        filepath,
        setup,
        orientation,
        brillouin_regions,
        rayleigh_regions,
        nr_brillouin_peaks,
        multi_peak_bounds
    )
    session.save()
```

## 1.3 Citing bmlab

If you use bmlab in a scientific publication, please cite it with:

> bmlab developers (2022), bmlab version X.X.X: Python library for the post-measurement analysis of Brillouin microscopy data sets [Software]. Available at https://github.com/BrillouinMicroscopy/bmlab.

CHAPTER

TWO

# CODE REFERENCE

**class** bmlab.file.**BrillouinFile**(*path*)

Load a HDF file with Brillouin microscopy data.

**Parameters** **path** (*Path*) – path of the file to load

**Raises** **OSError** – when trying to open non-existing or bad file

**get_repetition**(*repetition_key*, *mode='Brillouin'*)

Get a repetition from the data file based on given key.

**Parameters**

- **repetition_key** (*str*) – key to identify the repetition in the Brillouin group
- **mode** (*str*) – the mode to look at

**Returns** **out** – the repetition

**Return type** *Repetition*

**repetition_count**(*mode='Brillouin'*)

Get the number of repetitions in the data file.

**Returns** **out** – Number of repetitions in the data file

**Return type** int

**repetition_keys**(*mode='Brillouin'*)

Returns list of keys for the various repetitions in the file.

**Returns** **out**

**Return type** list of str

**class** bmlab.file.**Repetition**(*repetition_group*, *file*)

Creates a repetition from the corresponding group of a HDF file.

**Parameters** **repetition_group** (*HDF group*) – The HDF group representing a Repetition. Consists of payload, calibration and background.

**class** bmlab.file.**Payload**(*payload_group*, *repetition*)

Creates a payload representation from the corresponding group of a HDF file.

**Parameters** **payload_group** (*HDF group*) – The payload of a repetition, basically a set of images

**class** bmlab.file.**Calibration**(*payload_group*, *repetition*)

Creates a calibration representation from the corresponding group of a HDF file.

**Parameters** **payload_group** (*HDF group*) – Calibration data of a repetition from an HDF file.

Module for interacting with files containing Brillouin microscopy data.

NOTE: Ideally, the users of bmlab should not have to know about the file format in which the data are stored. So, if possible, do not expose HDF objects to the outside (like BMicro).

**exception** `bmlab.file.`**`BadFileException`**

CHAPTER

THREE

# DEVELOPMENT

For the general workflow, please refer to the BMicro docs.

## 3.1 Tests

We try to adhere to test-driven development. Please always write test functions for your code. Please make sure the *pytest* package is installed:

```
pip install pytest
```

You can run all tests via:

```
py.test tests
```

## 3.2 Making a new release

The release process of bmlab is completely automated. All you need to know is that you have to create an incremental tag on the main branch:

```
git tag -a "0.1.3"
# or (if you have set up PGP)
git tag -s "0.1.3"
# and finally
git push --tags
```

For more information on how automatic deployment to PyPI works, please read on.

## 3.3 Continuous integration

The following things are automated:

- pytest and flake8 on Linux, macOS, and Windows via GitHub Actions: https://github.com/BrillouinMicroscopy/bmlab/actions?query=workflow%3AChecks

  You should always check that all checks pass before you merge a pull request (A green state on your local machine does not mean a global green state).

- automatic deployment to PyPI on tag creation via GitHub Actions: https://github.com/BrillouinMicroscopy/bmlab/actions?query=workflow%3A%22Release+to+PyPI%22

  Paul Müller created the bmlab package on PyPI and gave the user `ci_bm` permission to upload new releases. The password for this user is an organization secret.

- documentation is built automatically (for all tags and for the latest commit to the main branch) on readthedocs: https://readthedocs.org/projects/bmlab/builds/

- coverage statistics are done with codecov: https://codecov.io/gh/BrillouinMicroscopy/bmlab

  Please try stay above 90% coverage.

Badges for all of these CI tasks are in the main `README.rst` file.

CHAPTER

FOUR

# CHANGELOG

List of changes in-between bmlab releases.

## 4.1 version ## 0.7.0 - 2022-09-28

## 4.2 version

## 4.3 version ### Added

## 4.4 version - Implement 4-peak fitting #167

## 4.5 version

## 4.6 version ## 0.6.1 - 2022-09-16

## 4.7 version

## 4.8 version ### Fixed

## 4.9 version - Fix get_frequencies_by_time #165

## 4.10 version - Fix evaluating files without calibration #166

## 4.11 version

## 4.12 version ## 0.6.0 - 2022-09-14

## 4.13 version

## 4.14 version ### Added

## 4.15 version - Implement exporting 3D data #162

## 4.16 version

## 4.17 version ### Changed

## 4.18 version - Fit Brillouin spectrum on frequency axis #158

## 4.19 version

## 4.20 version ### Fixed



## 4.21 version - Fix parameter label in csv files #163

## 4.22 version

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