
impose Documentation

Release 0.4.3

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Aug 25, 2023

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With impose, you can superimpose different imaging modalities (e.g. fluorescence imaging and Brillouin microscopy) and use the structural information from one modality to extract quantitative information from the other modality. This is particularly useful if you have no other means of mapping one imaging modality to the other (different stage or microscope).

GETTING STARTED

1.1 Installation

To install impose, use:

```
pip install impose
```

1.2 How to cite

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

Paul Müller and others (2020), impose version X.X.X: Graphical user interface for superimposing and quantifying data from different imaging modalities [Software]. Available at <https://github.com/GuckLab/impose>.

If the journal does not accept *and others*, you can fill in the missing names from the [credits file](#).

CHANGELOG

List of changes in-between impose releases.

2.1 version 0.4.3

- fix: only edit/display one structure when changing large composites (#59)
- enh: improved widget placement in collect and colocalize UI
- enh: always display the last dataset when switching to colocalize in UI
- setup: bump pyqtgraph from 0.12.4 to 0.13.3
- setup: require Python 3.9
- BREAKING: build recipe broken for macOS

2.2 version 0.4.2

- fix: workaround for TypeError when moving ROI with mouse
- ci: update badge and codecov

2.3 version 0.4.1

- fix: exception in Collect/Colocalize tab when using the sliders in the visualization panel (#51)

2.4 version 0.4.0

- fix: bump bmlab from 0.2.3 to 0.6.1 (file format changes) (#53)

2.5 version 0.3.1

- fix: bump bmlab from 0.1.10 to 0.2.3 (file format changes) (#49)

2.6 version 0.3.0

- feat: implement saving and loading of structure composites (#1)
- fix: visualization issue with empty data (#47)
- fix: editing layers not possible (regression from migration to PyQt6)
- fix: initial wrong scaling in colocalize when input data has different pixel sizes along the dimensions

2.7 version 0.2.4

- fix: properly handle FileNotFoundError (#44)
- fix: properly handle bmlab exceptions (#42)
- enh: reduce complexity of error message if an associated file is missing
- fix: close bmlab session after loading data (#48)
- build: add github action to create installer packages (#31)
- build: add Github deploy action
- build: pin shapely to fix macOS DMG packages

2.8 version 0.2.3

- fix: properly handle nan-valued data in colocalize (#36)
- fix: properly handle nan-valued data in collect (#36)
- setup: bump bmlab to 0.1.8 (#37)

2.9 version 0.2.2

- fix: properly handle nan-valued data (#25)
- fix: correctly open bmlab files with multiple repetitions (#26)

2.10 version 0.2.1

- enh: keep the order of data keys returned by bmlab for user convenience (#24)
- setup: migrate from PyQt5 (5.15.0) to PyQt6 (6.2.0) (#23)
- setup: bump bmlab from 0.1.1 to 0.1.2 (#24)
- setup: bump pyqtgraph from 0.12.3 to 0.12.4 (#23)

2.11 version 0.2.0

- feat: support bmlab session file format (#18)
- enh: prevent users from loading the same file twice

2.12 version 0.1.2

- fix: color of shapes in colocalize view not updated when changed in collect view
- setup: bump pyqtgraph from 0.12.1 to 0.12.3
- setup: bump required Python version to 3.7, because pyqtgraph has that dependency

2.13 version 0.1.1

- initial public release

**CHAPTER
THREE**

BILBLIOGRAPHY

**CHAPTER
FOUR**

INDICES AND TABLES

- genindex
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