
qpretrieve Documentation

Release 0.1.0

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Feb 13, 2022

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The qpretrieve Python library provides algorithms for the retrieval of quantitative phase information from experimental data, based on Fourier analysis (peak detection in Fourier space and filtering). Currently, qpretrieve only supports the analysis of holograms (with the characteristic fringe patterns). If you are looking for a library to load quantitative phase data from disk, please have a look at [qpformat](#). The [qpimage](#) library can be used for further processing (e.g. background correction). This is the documentation of qpretrieve version 0.1.0.

INTRODUCTION

1.1 Citing qpretrieve

If you are using qpretrieve in a scientific publication, please cite it with:

```
(...) using qpretrieve version X.X.X (available at  
https://pypi.python.org/pypi/qpretrieve).
```

or in a bibliography

```
Paul Müller (2022), qpretrieve version X.X.X: Phase image analysis  
[Software]. Available at https://pypi.python.org/pypi/qpretrieve.
```

and replace X.X.X with the version of qpretrieve that you used.

Furthermore, several ideas implemented in qpretrieve have been described and published in scientific journals:

- Phase retrieval from holographic images with a gaussian filter is implemented according to [SSM+15].

GETTING STARTED

2.1 Installing qpretrieve

qpretrieve is written in pure Python and supports Python version 3.6 and higher. qpretrieve depends on several other scientific Python packages, including:

- `numpy`,
- `scipy`,
- `h5py` (caching),
- `lmfit` (background estimation),
- `nrefocus` (numerical focusing), and
- `scikit-image` (phase unwrapping using `skimage.restoration.unwrap_phase()`).

To install qpretrieve, use one of the following methods (package dependencies will be installed automatically):

- **from PyPI:** `pip install qpretrieve`
- **from sources:** `pip install -e .` or

2.2 User API

TODO

EXAMPLES

3.1 Digital hologram of a single cell

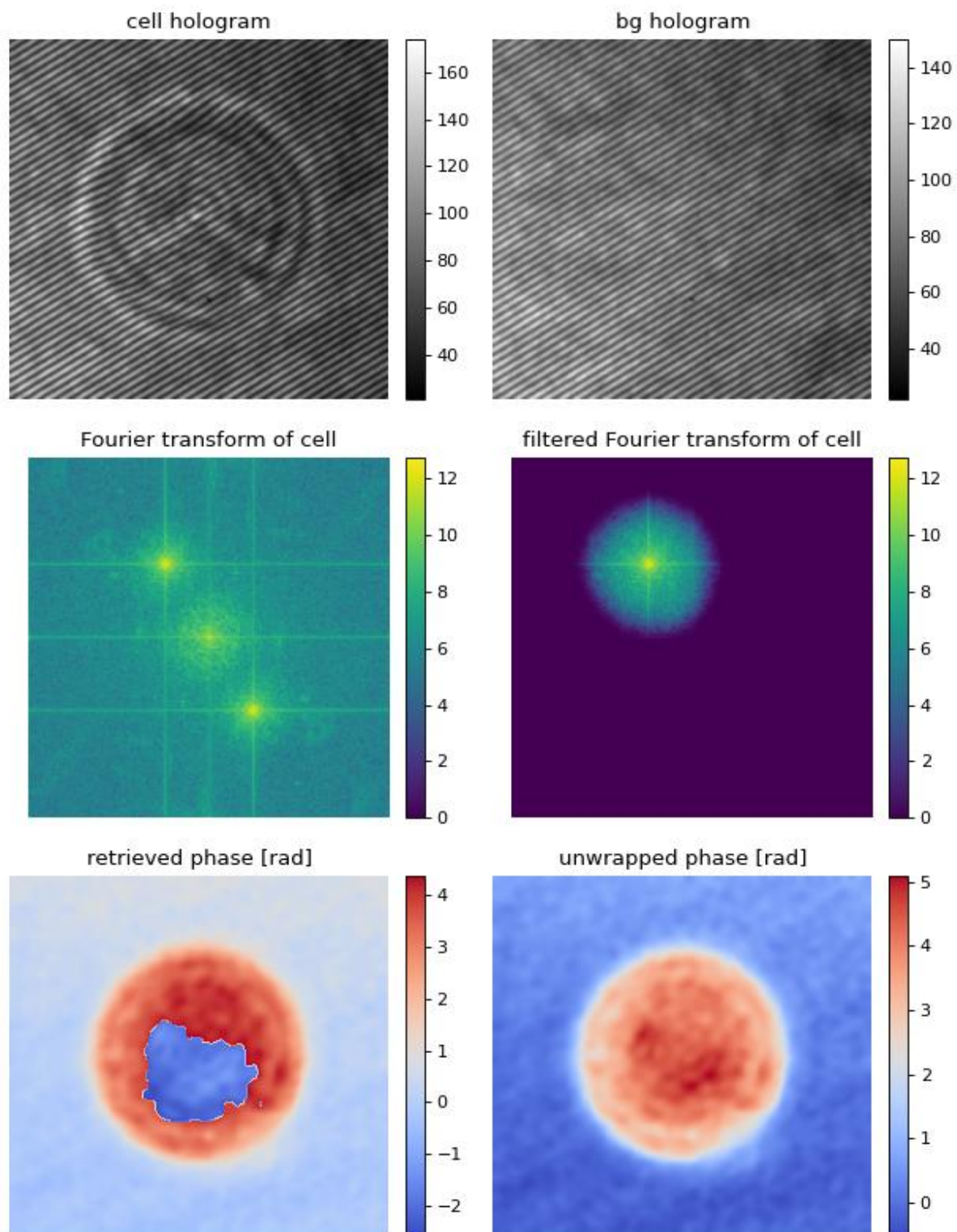
This example illustrates how `qpretrieve` can be used to analyze digital holograms. The hologram of a single myeloid leukemia cell (HL60) was recorded using off-axis digital holographic microscopy (DHM). Because the phase-retrieval method used in DHM is based on the *discrete* Fourier transform, there always is a residual background phase tilt which must be removed for further image analysis. The setup used for recording these data is described in reference [SSM+15].

Note that the fringe pattern in this particular example is over-sampled in real space, which is why the sidebands are not properly separated in Fourier space. Thus, the filter in Fourier space is very small which results in a very low effective resolution in the reconstructed phase.

`hologram_cell.py`

```
1 import matplotlib.pyplot as plt
2 import numpy as np
3 import qpretrieve
4 from skimage.restoration import unwrap_phase
5
6 # load the experimental data
7 edata = np.load("./data/hologram_cell.npz")
8
9 holo = qpretrieve.OffAxisHologram(data=edata["data"])
10 holo.run_pipeline(
11     # For this hologram, the "smooth disk"
12     # filter yields the best trade-off
13     # between interference from the central
14     # band and image resolution.
15     filter_name="smooth disk",
16     # Set the filter size to half the distance
17     # between the central band and the sideband.
18     filter_size=1/2)
19 bg = qpretrieve.OffAxisHologram(data=edata["bg_data"])
20 bg.process_like(holo)
21
22 phase = holo.phase - bg.phase
23
24 # plot the properties of `qpi`
25 fig = plt.figure(figsize=(8, 10))
26
27 ax1 = plt.subplot(321, title="cell hologram")
```

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```

28 map1 = ax1.imshow(edata["data"], interpolation="bicubic", cmap="gray")
29 plt.colorbar(map1, ax=ax1, fraction=.046, pad=0.04)
30
31 ax2 = plt.subplot(322, title="bg hologram")
32 map2 = ax2.imshow(edata["bg_data"], interpolation="bicubic", cmap="gray")
33 plt.colorbar(map2, ax=ax2, fraction=.046, pad=0.04)
34
35 ax3 = plt.subplot(323, title="Fourier transform of cell")
36 map3 = ax3.imshow(np.log(1 + np.abs(holo.fft_origin)), cmap="viridis")
37 plt.colorbar(map3, ax=ax3, fraction=.046, pad=0.04)
38
39 ax4 = plt.subplot(324, title="filtered Fourier transform of cell")
40 map4 = ax4.imshow(np.log(1 + np.abs(holo.fft_filtered)), cmap="viridis")
41 plt.colorbar(map4, ax=ax4, fraction=.046, pad=0.04)
42
43 ax5 = plt.subplot(325, title="retrieved phase [rad]")
44 map5 = ax5.imshow(phase, cmap="coolwarm")
45 plt.colorbar(map5, ax=ax5, fraction=.046, pad=0.04)
46
47 ax6 = plt.subplot(326, title="unwrapped phase [rad]")
48 map6 = ax6.imshow(unwrap_phase(phase), cmap="coolwarm")
49 plt.colorbar(map6, ax=ax6, fraction=.046, pad=0.04)
50
51 # disable axes
52 [ax.axis("off") for ax in [ax1, ax2, ax3, ax4, ax5, ax6]]
53
54 plt.tight_layout()
55 plt.show()

```


CODE REFERENCE

CHANGELOG

List of changes in-between qpretrieve releases.

5.1 version 0.1.0

- initial release

BILBLIOGRAPHY

INDICES AND TABLES

- `genindex`
- `modindex`
- `search`

BIBLIOGRAPHY

- [SSM+15] M. Schürmann, J. Scholze, P. Müller, C. J. Chan, A. E. Ekpenyong, K. J. Chalut, and J. Guck. Chapter 9 - Refractive index measurements of single, spherical cells using digital holographic microscopy. In Ewa K Paluch, editor, *Biophysical Methods in Cell Biology*, volume 125 of *Methods in Cell Biology*, pages 143–159. Academic Press, 2015. doi:[10.1016/bs.mcb.2014.10.016](https://doi.org/10.1016/bs.mcb.2014.10.016).