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# **Xfluo Documentation**

*Release 0.0.1*

**Argonne National Laboratory**

**May 04, 2019**



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## Contents

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This is a template to add sphinx / Read The Docs documentation to any python project to generate this Xfluo Docs.

These pages are written using reStructuredText that allows *emphasis*, **strong**, `literal` and many more styles.

You can add a reference [A1], include equations like:

$$V(x) = \left( \frac{1-\eta}{\sigma\sqrt{2\pi}} \right) \cdot \exp\left(\frac{x^2}{2\sigma^2}\right) + \eta \cdot \frac{\sigma}{2\pi} \cdot \frac{1}{x^2 + \left(\frac{\sigma}{2}\right)^2}$$

or

$$I_{white} = \int_{E_1}^{E_2} I(\theta, E) \cdot F(E) dE.$$

and tables:

Member	Type	Example
first	ordinal	1st
second	ordinal	2nd
third	ordinal	3rd

More examples:

$$X(e^{j\omega}) = x(n)e^{-j\omega n}$$

**Warning:** Warning text.

---

**Note:** Note text.

---



# CHAPTER 1

---

## Features

---

- List here
- the module features





## CHAPTER 2

---

### Contribute

---

- Documentation: <https://github.com/tomography/xfluo/tree/master/doc>
- Issue Tracker: <https://github.com/tomography/xfluo/docs/issues>
- Source Code: <https://github.com/tomography/xfluo/xfluo>



### 3.1 About

This section describes what the [Xfluo](#) is about.

### 3.2 Install

This section covers the basics of how to download and install [Xfluo](#). We recommend you to install the [Anaconda Python](#) distribution.

#### Contents:

- *Installing from source*

#### 3.2.1 Installing from source

Clone the [Xfluo](#) from [GitHub](#) repository:

```
git clone https://github.com/tomography/xfluo.git xfluo
```

then:

```
cd xfluo
python setup.py install
```

## 3.3 Development

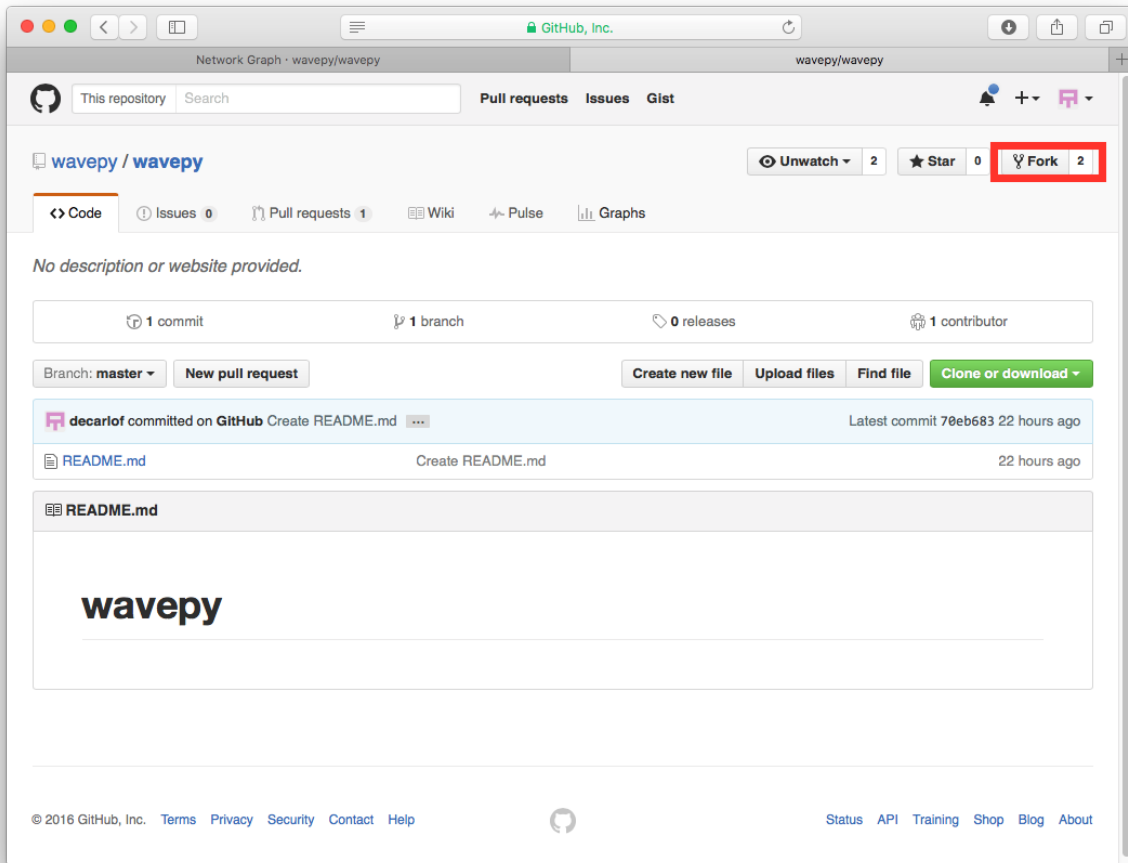
This section explains the basics for developers who wish to contribute to a project maintained on GitHub and using the fork / pull request mechanism for accepting developer contributions.

### Contents:

- *Fork the repository*
- *Clone the repository*
- *Coding conventions*
- *Package versioning*
- *Committing changes*
- *Contributing back*

### 3.3.1 Fork the repository

The project is maintained on GitHub, which is a version control and a collaboration platform for software developers. To start first register on [GitHub](#) and fork the [Xfluo repository](#) by clicking the **Fork** button in the header of the [Xfluo repository](#):

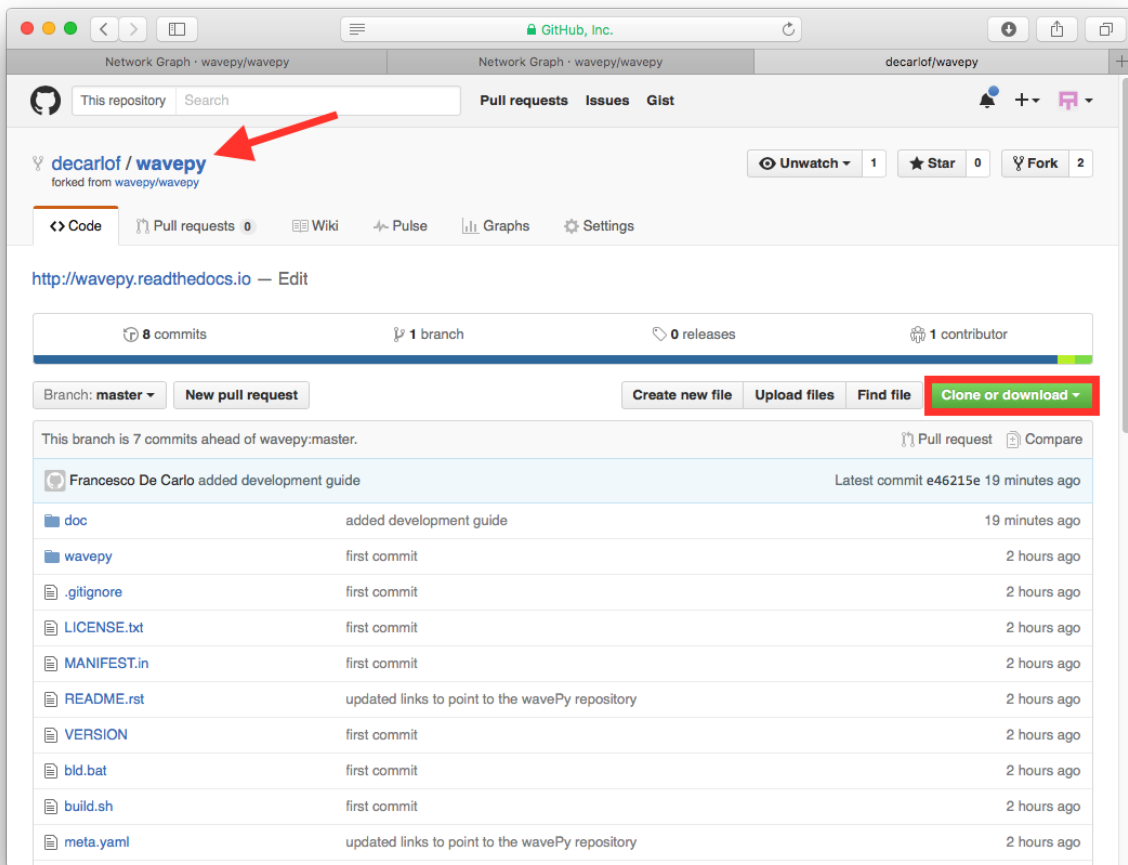


This successfully creates a copy of the project in your personal GitHub space.

### 3.3.2 Clone the repository

The next thing you want to do is to clone the repository you just created in your personal GitHub space to your local machine.

You can do this by clicking the **Clone in Desktop** button in the bottom of the right hand side bar:



This will launch the GitHub desktop application (available for both [Mac](#) and [Win](#)) and ask you where you want to save it. Select a location in your computer and feel comfortable with making modifications in the code.

### 3.3.3 Coding conventions

We try to keep a consistent and readable code. So, please keep in mind the following style and syntax guidance before you start coding.

First of all the code should be well documented, easy to understand, and integrate well into the rest of the project. For example, when you are writing a new function always describe the purpose and the parameters:

```
def my_awesome_func(a, b):
    """
    Adds two numbers.

    Parameters
    -----
    a : scalar (float)
        First number to add

    b : scalar (float)
        Second number to add
```

(continues on next page)

(continued from previous page)

```

Returns
-----
output : scalar (float)
        Added value
"""
return a+b

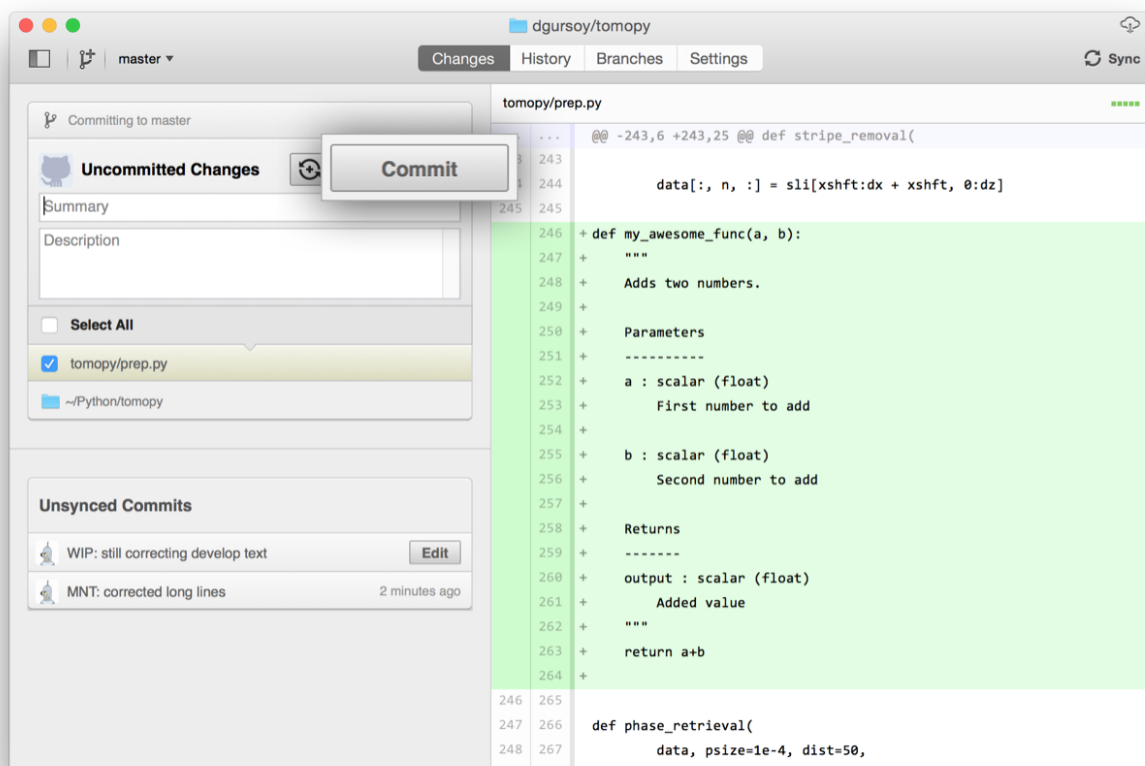
```

### 3.3.4 Package versioning

We follow the X.Y.Z (Major.Minor.Patch) semantic for package versioning. The version should be updated before each pull request accordingly. The patch number is incremented for minor changes and bug fixes which do not change the software's API. The minor version is incremented for releases which add new, but backward-compatible, API features, and the major version is incremented for API changes which are not backward-compatible. For example, software which relies on version 2.1.5 of an API is compatible with version 2.2.3, but not necessarily with 3.2.4.

### 3.3.5 Committing changes

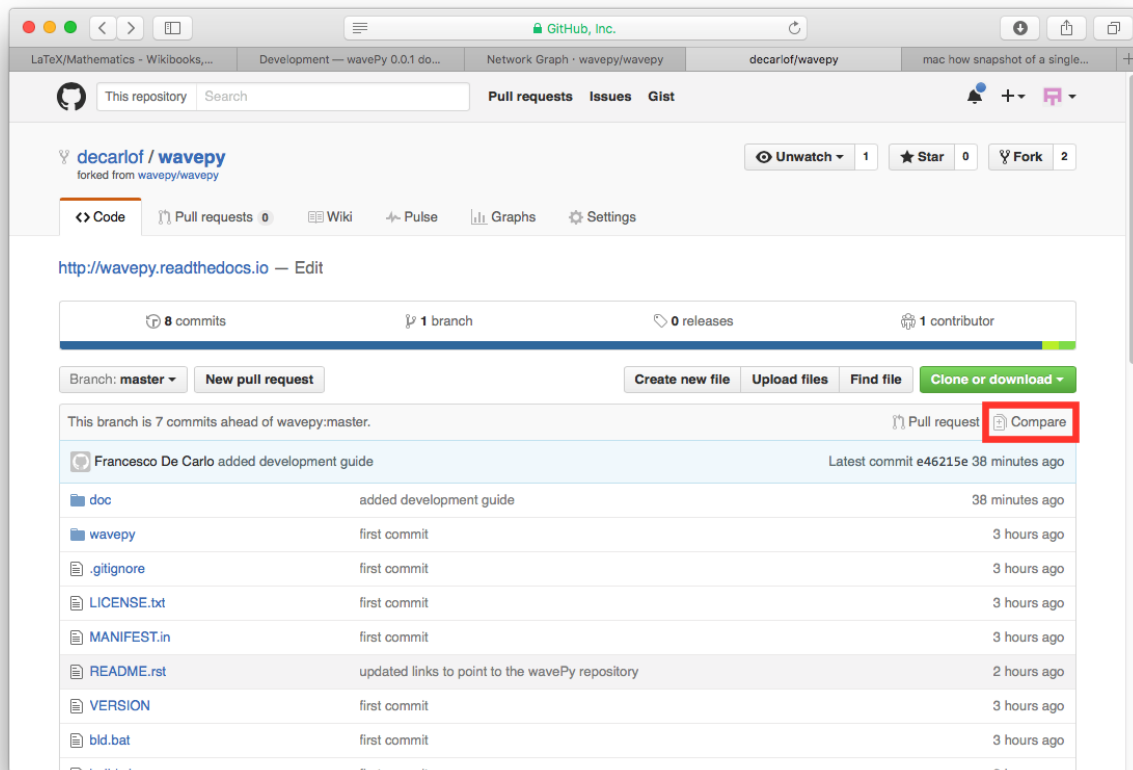
After making some changes in the code, you may want to take a *snapshot* of the edits you made. That's when you make a *commit*. To do this, launch the GitHub desktop application and it should provide you all the changes in your code since your last commit. Write a brief *Summary* and *Description* about the changes you made and click the **Commit** button:



You can continue to make changes, add modules, write your own functions, and take more *Commit snapshots* of your code writing process.

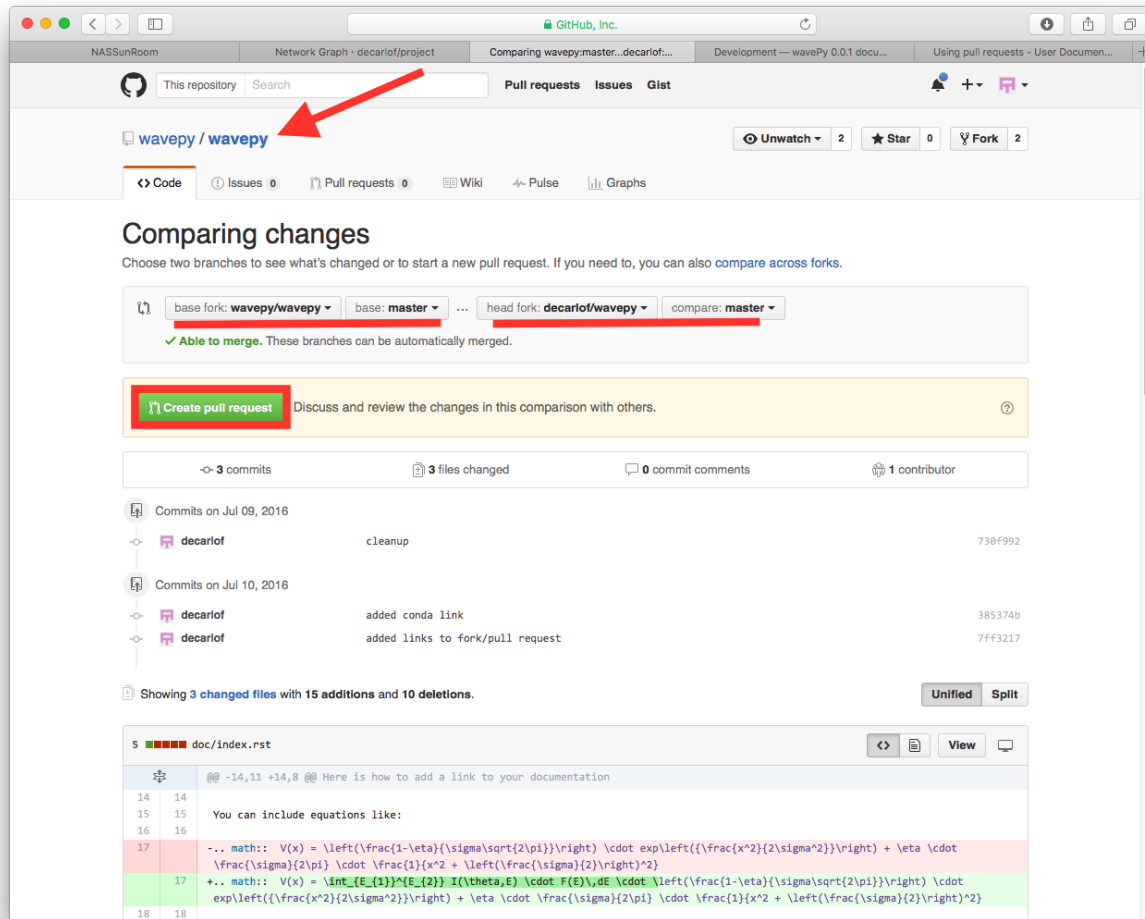
### 3.3.6 Contributing back

Once you feel that the functionality you added would benefit the community, then you should consider contributing back to the project. For this, go to your online GitHub repository of the project and click on the *compare* button to compare, review and create a pull request.



After clicking on this button, you are presented with a review page where you can get a high-level overview of what exactly has changed between your forked branch and the original project repository. When you're ready to submit your pull request, click **Create pull request**:





Clicking on **Create pull request** sends you to a discussion page, where you can enter a title and optional description. It's important to provide as much useful information and a rationale for why you're making this Pull Request in the first place.

When you're ready typing out your heartfelt argument, click on **Send pull request**.

You're done!

## 3.4 API reference

Xfluo Modules:

### 3.4.1 xfluo.reco

Functions:

---

`tomo(params)`

---

`xfluo.reco.tomo(params)`

## 3.4.2 xfluo.elements

Properties of the chemical elements.

Each chemical element is represented as an object instance. Physicochemical and descriptive properties of the elements are stored as instance attributes.

**Author** Christoph Gohlke

**Version** 2019.1.1

### Requirements

- CPython 2.7 or 3.5+

### Revisions

**2019.1.1** Update copyright year.

**2018.8.15** Move modules into molmass package.

**2018.5.25** Style and docstring fixes.

**2016.2.25** Fixed some ionization energies.

### References

- (1) <http://physics.nist.gov/PhysRefData/Compositions/>
- (2) <http://physics.nist.gov/PhysRefData/IonEnergy/tblNew.html>
- (3) [http://en.wikipedia.org/wiki/%\(element.name\)s](http://en.wikipedia.org/wiki/%(element.name)s)
- (4) <http://www.miranda.org/~jkominek/elements/elements.db>

### Examples

```
>>> from elements import ELEMENTS
>>> len(ELEMENTS)
109
>>> str(ELEMENTS[109])
'Meitnerium'
>>> ele = ELEMENTS['C']
>>> ele.number, ele.symbol, ele.name, ele.eleconfig
(6, 'C', 'Carbon', '[He] 2s2 2p2')
>>> from pprint import pprint
>>> pprint(ele.eleconfig_dict)
{(1, 's'): 2, (2, 'p'): 2, (2, 's'): 2}
>>> sum(ele.mass for ele in ELEMENTS)
14659.1115599
>>> for ele in ELEMENTS:
...     ele.validate()
...     ele = eval(repr(ele))
```

**Functions:**


---

ELEMENTS	Ordered dict of Elements with lookup by number, symbol, and name.
<i>Element</i> (number, symbol, name, **kwargs)	Chemical element.
<i>Isotope</i> ([mass, abundance, massnumber])	Isotope massnumber, relative atomic mass, and abundance.

---

**class** xfluo.elements.**Element** (*number, symbol, name, \*\*kwargs*)

Bases: object

Chemical element.

**number**

Atomic number

**Type** int

**symbol**

Chemical symbol

**Type** str of length 1 or 2

**name**

Name in english

**Type** str

**group**

Group in periodic table

**Type** int

**period**

Period in periodic table

**Type** int

**block**

Block in periodic table

**Type** int

**series**

Index to chemical series

**Type** int

**protons**

Number of protons

**Type** int

**neutrons**

Number of neutrons in the most abundant naturally occurring stable isotope

**Type** int

**nominalmass**

Mass number of the most abundant naturally occurring stable isotope

**Type** int

**electrons**

Number of electrons

**Type** int

**mass**

Relative atomic mass. Ratio of the average mass of atoms of the element to 1/12 of the mass of an atom of <sup>12</sup>C

**Type** float

**exactmass**

Relative atomic mass calculated from the isotopic composition

**Type** float

**eleneg**

Electronegativity (Pauling scale)

**Type** float

**covrad**

Covalent radius in Angstrom

**Type** float

**atmrad**

Atomic radius in Angstrom

**vdwrad**

Van der Waals radius in Angstrom

**Type** float

**tboil**

Boiling temperature in K

**Type** float

**tmelt**

Melting temperature in K

**Type** float

**density**

Density at 295K in g/cm<sup>3</sup> respectively g/L

**Type** float

**oxistates**

Oxidation states

**Type** str

**eleaffin**

Electron affinity in eV

**Type** float

**eleconfig**

Ground state electron configuration

**Type** str

**eleconfig\_dict**

Ground state electron configuration (shell, subshell): electrons

**Type** dict

**elshells**

Number of electrons per shell

**Type** int

**ionenergy**

Ionization energies in eV

**Type** tuple

**isotopes**

Isotopic composition. keys: isotope mass number values: Isotope(relative atomic mass, abundance)

**Type** dict

**description**

Lazy object attribute whose value is computed on first access.

**eleconfig\_dict**

Lazy object attribute whose value is computed on first access.

**elshells**

Lazy object attribute whose value is computed on first access.

**exactmass**

Lazy object attribute whose value is computed on first access.

**neutrons**

Lazy object attribute whose value is computed on first access.

**nominalmass**

Lazy object attribute whose value is computed on first access.

**validate ()**

Check consistency of data. Raise Error on failure.

**class** xfluo.elements.Isotope (*mass=0.0, abundance=1.0, massnumber=0*)

Bases: object

Isotope massnumber, relative atomic mass, and abundance.

**abundance**

**mass**

**massnumber**

### 3.4.3 xfluo.file\_io.reader

Module for importing raw data files.

#### Functions:

<i>find_elements(channel_names)</i>	Extract a sorted element list from a channel list
<i>read_theta(path_files, theta_index, hdf_tag)</i>	Reads hdf file and returns theta
<i>read_projection(fname, element, hdf_tag, ...)</i>	Reads a projection for a given element from a single xrf hdf file

Continued on next page

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<code>read_channel_names(fname, hdf_tag, channel_tag, nel_tag)</code>	Read the channel names
<code>read_mic_xrf(path_files, element_index, ...)</code>	Converts hdf files to numpy arrays for plotting and manipulation

`xfluo.file_io.reader.find_elements(channel_names)`

Extract a sorted element list from a channel list

**Parameters** `channel_names` (*list*) – List of channel names

**Returns** `elements` (*list*) – Sorted list of elements

`xfluo.file_io.reader.read_theta(path_files, theta_index, hdf_tag)`

Reads hdf file and returns theta

**Parameters**

- `path_files` (*list*) – List of path+filenames
- `theta_index` (*int*) – Index where theta is saved under in the hdf MAPS/extra\_pvs\_as\_csv tag  
This is: 2-ID-E: 663; 2-ID-E (prior 2017): 657; BNP: 8
- `hdf_tag` (*str*) – String defining the hdf5 data\_tag name (ex. MAPS)

**Returns** `ndarray` (*ndarray*) – 1D array [theta]

`xfluo.file_io.reader.read_projection(fname, element, hdf_tag, roi_tag, channel_tag)`

Reads a projection for a given element from a single xrf hdf file

**Parameters**

- `fname` (*str*) – String defining the file name
- `element` (*str*) – String defining the element to select
- `hdf_tag` (*str*) – String defining the hdf5 data\_tag name (ex. MAPS)
- `roi_tag` (*str*) – data tag for corresponding roi\_tag (ex. XRF\_roi)
- `channel_tag` (*str*) – String defining the hdf5 channel tag name (ex. channel\_names)

**Returns** `ndarray` (*ndarray*) – projection

`xfluo.file_io.reader.read_channel_names(fname, hdf_tag, channel_tag)`

Read the channel names

**Parameters**

- `fname` (*str*) – String defining the file name
- `hdf_tag` (*str*) – String defining the hdf5 data\_tag name (ex. MAPS)
- `channel_tag` (*str*) – String defining the hdf5 channel tag name (ex. channel\_names)

**Returns** `channel_names` (*list*) – List of channel names

`xfluo.file_io.reader.read_mic_xrf(path_files, element_index, hdf_tag, roi_tag, channel_tag)`

Converts hdf files to numpy arrays for plotting and manipulation

**Parameters**

- `path_files` (*list*) – List of (path + filenames)
- `theta_index` (*int*) – Index where theta is saved under in the hdf MAPS/extra\_pvs\_as\_csv tag  
This is: 2-ID-E: 663; 2-ID-E (prior 2017): 657; BNP: 8

- **hdf\_tag** (*str*) – String defining the hdf5 data\_tag name (ex. MAPS)
- **roi\_tag** (*str*) – data tag for corresponding roi\_tag (ex. XRF\_roi)
- **channel\_tag** (*str*) – String defining the hdf5 channel tag name (ex. channel\_names)

**Returns** `ndarray` (*ndarray*) – 4D array [elements, projection, y, x]

### 3.4.4 `xfluo.models.file_table`

Subclasses the `h5py` module for interacting with Data Exchange files.

#### Functions:

<code>FileTableModel([parent])</code>	Interact with Data Exchange files.
<code>TableArrayItem(fname)</code>	

**class** `xfluo.models.file_table.TableArrayItem` (*fname*)

**class** `xfluo.models.file_table.FileTableModel` (*parent=None, \*args*)

Bases: `sphinx.ext.autodoc.importer._MockObject`

Interact with Data Exchange files.

**data** (*self, index, role*)

Helper function for ...

**loadDirectory** (*self, directoryName, ext='\*.h5\*'*)

This method is used to ...

**columnCount** (*parent*)

**data** (*index, role*)

**flags** (*index*)

**getFirstCheckedFilePath** ()

**loadDirectory** (*directoryName, ext='\*.h5\*'*)

**loadThetas** (*img\_tag*)

**loadThetasLegacy** (*thetaPV*)

**rowCount** (*parent*)

**setAllChecked** (*value*)

**setChecked** (*rows, value*)

**setData** (*index, value, role=<sphinx.ext.autodoc.importer.\_MockObject object>*)

**sort** (*col, order*)

Sort table by given column number.

### 3.4.5 `xfluo.models.element_table`

#### Functions:

---

*ElementTableModel*([parent])
 

---

```

class xfluo.models.element_table.ElementTableModel (parent=None, *args)
    Bases: sphinx.ext.autodoc.importer._MockObject

    columnCount (parent)

    data (index, role)

    flags (index)

    loadElementNames (filePath, image_tag, element_tag)

    rowCount (parent)

    setAllChecked (value)

    setChecked (rows, value)

    setData (index, value, role=<sphinx.ext.autodoc.importer._MockObject object>)
  
```

## 3.5 Examples

Here we describe what the examples are doing. You can cite with [B1].

### 3.5.1 HDF reader

This section contains an example of how to read a projection from an hdf file for a given element.

Download file: `example_01.py`

```

1  #!/usr/bin/env python
2  # -*- coding: utf-8 -*-
3
4  # #####
5  # Copyright (c) 2018, UChicago Argonne, LLC. All rights reserved.
6  #
7  # Copyright 2018. UChicago Argonne, LLC. This software was produced
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```

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```

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44 # LIABILITY, OR TORT (INCLUDING NEGLIGENCE OR OTHERWISE) ARISING IN #
45 # ANY WAY OUT OF THE USE OF THIS SOFTWARE, EVEN IF ADVISED OF THE #
46 # POSSIBILITY OF SUCH DAMAGE. #
47 # #####
48
49 """
50 Example script
51 """
52
53 from __future__ import print_function
54
55 import os
56 import sys
57 import argparse
58
59 import xfluo
60
61 def main(arg):
62
63     parser = argparse.ArgumentParser()
64     parser.add_argument("fname", help="Directory containing multiple datasets or file_
↳name of a single dataset: /data/ or /data/sample.h5")
65     parser.add_argument("--start", nargs='?', type=float, default=0.0, help="Angle_
↳first projection (default 0.0)")
66     parser.add_argument("--end", nargs='?', type=float, default=180.0, help="Angle_
↳last projection (default 180.0)")
67     parser.add_argument("--element", nargs='?', type=str, default="Si", help="Select_
↳the element to reconstruct (default Si)")
68
69     args = parser.parse_args()
70
71     # Set path to the micro-CT data to reconstruct.
72     fname = args.fname
73     angle_start = float(args.start)
74     angle_end = float(args.end)
75     element = args.element
76
77     if os.path.isfile(fname):
78

```

(continues on next page)

```
79     elements = xfluo.read_elements(fname)
80     for i, e in enumerate(elements):
81         print ('%d: %s' % (i, e))
82
83     proj, theta = xfluo.read_projection(fname, element, 663)
84     print ("theta:", theta)
85     # print (theta.shape)
86     print ("proj:", proj)
87     print (proj.shape)
88
89     elif os.path.isdir(fname):
90         # Add a trailing slash if missing
91         top = os.path.join(fname, '')
92
93         h5_file_list = list(filter(lambda x: x.endswith('.h5', '.hdf'), os.
↪listdir(top)))
94
95         for i, fname in enumerate(h5_file_list):
96             proj, theta = xfluo.file_io.read_projection(top+fname, element, 663) #
↪#657
97             print(i, theta, fname)
98
99     else:
100         print("Directory or File Name does not exist: ", fname)
101
102 if __name__ == "__main__":
103     main(sys.argv[1:])
```

## 3.6 Credits

### 3.6.1 Citations

We kindly request that you cite the following article [A1] if you use project.

### 3.6.2 References

---

## Bibliography

---

- [A1] Gürsoy D, De Carlo F, Xiao X, and Jacobsen C. Tomopy: a framework for the analysis of synchrotron tomographic data. *Journal of Synchrotron Radiation*, 21(5):1188–1193, 2014.
- [B1] De Carlo F, Gürsoy D, Marone F, Rivers M, Parkinson YD, Khan F, Schwarz N, Vine DJ, Vogt S, Gleber SC, Narayanan S, Newville M, Lanzirotti T, Sun Y, Hong YP, and Jacobsen C. Scientific data exchange: a schema for hdf5-based storage of raw and analyzed data. *Journal of Synchrotron Radiation*, 21(6):1224–1230, 2014.



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