

# Pyto overview

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April 26, 2020

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\$Revision: 1647 \$

## 1 Summary

This document covers the installation of pyto package and gives general information about its usage.

## 2 Installation

### 2.1 Software requirements

- OS: We work under linux, but pyto should work on other platforms because it was (mostly) written to be platform independent.
- Python 3, also compatible with Python 2.7+ except that new developments might be 3 only
- Numpy, scipy packages
- Matplotlib: used for plotting graphs
- Pandas: currently used very little, but it's expected to increase in future
- Ipython, Jupyter (optional): standard interactive python shell and notebook
- All of the above can be installed using the Anaconda distribution

### 2.2 Pyto

- Pyto can be unpacked anywhere in the directory tree
- Add Pyto root directory (../..) to your PYTHONPATH
- To check the installation, start python shell (e.g. ipython) and import pyto, there should be no errors:

```
>>> import pyto
```

### 3 Pyto applications

Pyto package can be used for the following applications:

1. Detection (segmentation) and analysis of pleomorphic molecular complexes bound to larger structures (such as membranes). The detection is performed by the Hierarchical connectivity segmentation. The analysis consists of the determination of various properties of the individual segments (morphology, localization, ...), segment classification based on some of these properties and the statistical analysis between experimental groups. Examples of this application include segmentation and analysis of presynaptic cytomatrix and of synaptic adhesion complexes.
2. Correlation between various imaging modes. The goal is to determine the precise location of a structure of interest detected in one imaging mode in another mode. Current applications include correlations between light microscopy and transmission electron microscopy and between light microscopy and scanning electron or focused ion beam microscopy.
3. Tomography tools (work in progress)

### 4 Usage

Three usage types envisaged, here listed in the increasing order of difficulty:

1. The most straightforward way to perform a procedure in pyto is to execute the appropriate python scripts (located in `pyto/scripts/`).
2. The scripts can be customized by the user. This requires some understanding of Python.
3. Finally, individual tasks can be executed by using pyto classes and methods. However, this approach requires a solid understanding of Python, Numpy and Scipy packages as well as pyto.

### 5 Documentation

- Hierarchical connectivity segmentation guide: `segmentation.pdf`
- Segment analysis guide: `analysis.pdf`
- Specific segmentation and analysis workflows including parameter settings: `workflows.pdf`
- Commonly used pyto procedures are implemented in script files (`pyto/scripts/`). They contain info about the procedures as well as about parameters that need to be specified.
- Correlative microscopy guide: `correlation.pdf`
- Almost all classes and methods are documented by `__doc__` strings. This info is also available in epydoc form.

### 6 Citing

Please consider citing us if you use Pyto:

For general use, segmentation and analysis: Lučić V, Fernández-Busnadiego R, Laugks U and Baumeister W, 2016. Hierarchical detection and analysis of macromolecular complexes in cryo-electron tomograms using Pyto software. *J Struct Biol.* 196(3):503-514. <http://dx.doi.org/10.1016/j.jsb.2016.10.004>.

For 3D to 2D correlation, please cite: Arnold, J., J. Mahamid, V. Lucic, A. d. Marco, J.-J. Fernandez, Laugks, H.-A. Mayer, Tobias, W. Baumeister, and J. Plitzko, 2016. Site-specific cryo-focused ion beam sample preparation guided by 3-dimensional correlative microscopy. *Biophysical Journal* 110:860-869. <http://dx.doi.org/10.1016/j.bpj.2015.10.053>.

For all other correlative work: Fukuda, Y., N. Schrod, M. Schaffer, L. R. Feng, W. Baumeister, and V. Lucic, 2014. Coordinate transformation based cryo-correlative methods for electron tomography and focused ion beam milling. *Ultramicroscopy* 143:15– 23. <http://dx.doi.org/10.1016/j.ultramic.2013.11.008>.

Thank you.