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# **florin**

***Release 0.0.1a***

**Jul 10, 2019**



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FLoRIN, the Flexible Learning-free Reconstruction of Neural Volumes pipeline, is a pipeline for large-scale parallel and distributed computer vision. Offering easy setup and access to hierarchical parallelism, FLoRIN is ideal for scaling computer vision to HPC systems.

Originally, this project was our response to the question of how to segment and reconstruct neural microscopy (e.g., micro-CT tomography, low-resolution electron microscopy, fluorescence microscopy etc.) without large amounts of training data available to train a neural network. We tackled this problem by revisiting classical computer vision methods, eventually developing the N-Dimensional Neighborhood Thresholding (NDNT) algorithm as a modern update to integral image-based thresholding. FLoRIN has since been shown to be a fast, robust segmentation and reconstruction engine across different imaging modalities and datasets.

This package implements the NDNT algorithm, as well as a straightforward API for mixed serial, parallel, and distributed computer vision. These docs provide examples of how to use FLoRIN with various mixtures of serial and parallel processing and how to customize the FLoRIN pipeline with new functions and features.



# CHAPTER 1

---

## Installation

---

*pip*

```
pip install florin
```

*anaconda*

```
conda install -c jeffkinnison florin
```





1. Shahbazi, Ali, Jeffery Kinnison, Rafael Vescovi, Ming Du, Robert Hill, Maximilian Jösch, Marc Takeno et al. “Flexible Learning-Free Segmentation and Reconstruction of Neural Volumes.” Scientific reports 8, no. 1 (2018): 14247.

## 2.1 Installation

FLoRIN can be installed with all of its Python dependencies through the Python Package Index or Anaconda.

### 2.1.1 PyPI

```
pip install florin
```

### 2.1.2 Anaconda

```
conda install -c jeffkinnison florin
```

### 2.1.3 Python Dependencies

- Python 3.4+
- numpy
- scipy
- scikit-image
- pathos
- mpi4py

- h5py

## 2.2 Examples using FLoRIN

### 2.2.1 A First Example

This example will walk through basic FLoRIN usage segmenting and reconstructing a small X-Ray volume.

#### Segmenting

The following code sets up a serial pipeline to segment the image:

```
import florin
import florin.conncomp as conncomp
import florin.morphology as morphology
import florin.thresholding as thresholding

# Set up a serial pipeline
pipeline = florin.Serial(
    # Load in the volume from file
    florin.load(),

    # Tile the volume into overlapping 64 x 64 x 10 subvolumes
    florin.tile(shape=(10, 64, 64), stride=(10, 32, 32)),

    # Threshold with NDNT
    thresholding.ndnt(shape=(10, 64, 64), threshold=0.3),

    # Clean up a little bit
    morphology.binary_opening(),

    # Save the output to a TIFF stack
    florin.save('segmented.tiff')
)

# Run the pipeline
segmented = pipeline()
```

At the end of the pipeline, a TIFF stack with the binary segmentation will be output.

#### Weak Classification

After we have the binary mask, we want to determine what type of structure each object is. The previous pipeline can be extended to perform weak classification by user-defined bounds on the segmented objects:

```
import florin
import florin.conncomp as conncomp
import florin.morphology as morphology
import florin.thresholding as thresholding

# Set up a serial pipeline
pipeline = florin.Serial(
    # Load in the volume from file
```

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```

florin.load(),

# Tile the volume into overlapping 64 x 64 x 10 subvolumes
florin.tile(shape=(10, 64, 64), stride=(10, 32, 32)),

# Threshold with NDNT
thresholding.ndnt(shape=(10, 64, 64), threshold=0.3),

# Clean up a little bit
morphology.binary_opening(),

# Save the output to a TIFF stack
florin.save('segmented.tiff'),

# Find connected components
conncomp.label(),
morphology.remove_small_holes(min_size=20),
conncomp.regionprops(),

# Classify the connected components by their volume and dimensions
florin.classify(
    florin.bounds_classifier(
        'cell',
        area=(100, 300),
        depth=(10, 25),
        width=(50, 100),
        height=(50, 100)
    ),
    florin.bounds_classifier('vasculature')
),

# Reconstruct the labeled volume
florin.reconstruct(),

# Write out the labeled volume
florin.save('labeled.tiff')
)

# Run the pipeline
segmented = pipeline()

```

This pipeline save both the binary segmentation and the labeled volume where each class is represented by a different color.

## Closing Remarks

Rolling out a basic FLoRIN pipeline is relatively easy (20 lines of code without the comments and whitespace). This example runs everything on a single cores, but the next example demonstrates parallel processing, which is just as easy to set up.

## 2.2.2 Parallel Processing Pipelines

This example will show how to convert the previous example to perform multiprocessing on the tiles and connected components created during segmentation and weak classification, respectively.

## Parallelism

Parallel processing can be invoked by creating sub-pipelines around commands that will receive multiple inputs.

### Multithreading

```
import florin
import florin.conncomp as conncomp
import florin.morphology as morphology
import florin.thresholding as thresholding

# Set up a serial pipeline
pipeline = florin.Serial(
    # Load in the volume from file
    florin.load(),

    # Tile the volume into overlapping 64 x 64 x 10 subvolumes
    florin.tile(shape=(10, 64, 64), stride=(10, 32, 32)),

    florin.Multithread(
        # Threshold with NDNT
        thresholding.ndnt(shape=(10, 64, 64), threshold=0.3),

        # Clean up a little bit
        morphology.binary_opening()
    ),

    # Save the output to a TIFF stack
    florin.save('segmented.tiff'),

    # Find connected components
    conncomp.label(),
    morphology.remove_small_holes(min_size=20),
    conncomp.regionprops(),

    # Classify the connected components by their volume and dimensions
    florin.Multithread(
        florin.classify(
            florin.bounds_classifier(
                'cell',
                area=(100, 300),
                depth=(10, 25),
                width=(50, 100),
                height=(50, 100)
            ),
            florin.bounds_classifier('vasculature')
        )
    ),

    # Reconstruct the labeled volume
    florin.reconstruct(),

    # Write out the labeled volume
    florin.save('labeled.tiff')
)

# Run the pipeline
segmented = pipeline()
```

## Multiprocessing

```

import florin
import florin.conncomp as conncomp
import florin.morphology as morphology
import florin.thresholding as thresholding

# Set up a serial pipeline
pipeline = florin.Serial(
    # Load in the volume from file
    florin.load(),

    # Tile the volume into overlapping 64 x 64 x 10 subvolumes
    florin.tile(shape=(10, 64, 64), stride=(10, 32, 32)),

    florin.Multiprocess(
        # Threshold with NDNT
        thresholding.ndnt(shape=(10, 64, 64), threshold=0.3),

        # Clean up a little bit
        morphology.binary_opening()
    ),

    # Save the output to a TIFF stack
    florin.save('segmented.tiff'),

    # Find connected components
    conncomp.label(),
    morphology.remove_small_holes(min_size=20),
    conncomp.regionprops(),

    # Classify the connected components by their volume and dimensions
    florin.Multiprocess(
        florin.classify(
            florin.bounds_classifier(
                'cell',
                area=(100, 300),
                depth=(10, 25),
                width=(50, 100),
                height=(50, 100)
            ),
            florin.bounds_classifier('vasculature')
        )
    ),

    # Reconstruct the labeled volume
    florin.reconstruct(),

    # Write out the labeled volume
    florin.save('labeled.tiff')
)

# Run the pipeline
segmented = pipeline()

```

## MPI

```
import florin
```

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```

import florin.conncomp as conncomp
import florin.morphology as morphology
import florin.thresholding as thresholding

# Set up a serial pipeline
pipeline = florin.Serial(
    # Load in the volume from file
    florin.load(),

    # Tile the volume into overlapping 64 x 64 x 10 subvolumes
    florin.tile(shape=(10, 64, 64), stride=(10, 32, 32)),

    florin.MPI(
        # Threshold with NDNT
        thresholding.ndnt(shape=(10, 64, 64), threshold=0.3),

        # Clean up a little bit
        morphology.binary_opening()
    ),

    # Save the output to a TIFF stack
    florin.save('segmented.tiff'),

    # Find connected components
    conncomp.label(),
    morphology.remove_small_holes(min_size=20),
    conncomp.regionprops(),

    # Classify the connected components by their volume and dimensions
    florin.MPI(
        florin.classify(
            florin.bounds_classifier(
                'cell',
                area=(100, 300),
                depth=(10, 25),
                width=(50, 100),
                height=(50, 100)
            ),
            florin.bounds_classifier('vasculature')
        )
    ),

    # Reconstruct the labeled volume
    florin.reconstruct(),

    # Write out the labeled volume
    florin.save('labeled.tiff')
)

# Run the pipeline
segmented = pipeline()

```

All of these examples scale to the number of available cores (or MPI ranks in the MPI version), and can be parameterized to use a specific number when the sub-pipelines are created.

## Mixed Parallelism

Using the sub-pipeline model in the above example, it is possible to mix parallel processing paradigms. For example, segmenting tiles with NDNT uses vectorized operations and may be better suited to multi-node parallelism with MPI, but classification is more lightweight and can be carried out in threads. This sort of a pipeline would look like:

```
import florin
import florin.conncomp as conncomp
import florin.morphology as morphology
import florin.thresholding as thresholding

# Set up a serial pipeline
pipeline = florin.Serial(
    # Load in the volume from file
    florin.load(),

    # Tile the volume into overlapping 64 x 64 x 10 subvolumes
    florin.tile(shape=(10, 64, 64), stride=(10, 32, 32)),

    florin.MPI(
        # Threshold with NDNT
        thresholding.ndnt(shape=(10, 64, 64), threshold=0.3),

        # Clean up a little bit
        morphology.binary_opening()
    ),

    # Save the output to a TIFF stack
    florin.save('segmented.tiff'),

    # Find connected components
    conncomp.label(),
    morphology.remove_small_holes(min_size=20),
    conncomp.regionprops(),

    # Classify the connected components by their volume and dimensions
    florin.Multithread(
        florin.classify(
            florin.bounds_classifier(
                'cell',
                area=(100, 300),
                depth=(10, 25),
                width=(50, 100),
                height=(50, 100)
            ),
            florin.bounds_classifier('vasculature')
        )
    ),

    # Reconstruct the labeled volume
    florin.reconstruct(),

    # Write out the labeled volume
    florin.save('labeled.tiff')
)

# Run the pipeline
segmented = pipeline()
```

In this case, an implicit join after the MPI pipeline converts merges the segmented tiles into a single volume. Connected components are then computed over the whole volume and classified concurrently using a multithreading model.

## Closing Remarks

Parallel processing with FLoRIN is as easy as specifying the type of parallel pipeline to use, and they are roughly interchangeable (MPI requires using the standard `mpirun` or `mpiexec` invocations, or an equivalent).

## 2.2.3 Using Custom Functions in FLoRIN

Because of the wide array of computer vision methods, FLoRIN comes with utilities to prepare functions. This section will go over the two cases for preparing functions: without parameters, and with parameters.

### Single-Argument Functions

Functions with a single argument (e.g., those taking a single image or a single numpy array and no other arguments) require no additional preparation. This example shows how to incorporate `np.squeeze` into a pipeline:

```
import florin
import florin.conncomp as conncomp
import florin.morphology as morphology
import florin.thresholding as thresholding

import numpy as np

# Set up a serial pipeline
pipeline = florin.Serial(
    # Load in the volume from file
    florin.load(),

    # Tile the volume into overlapping 64 x 64 x 10 subvolumes
    florin.tile(shape=(10, 64, 64), stride=(10, 32, 32)),

    # Remove any axes with shape 1. Simply pass np.squeeze without invoking
    np.squeeze,

    # Threshold with NDNT
    thresholding.ndnt(shape=(10, 64, 64), threshold=0.3),

    # Clean up a little bit
    morphology.binary_opening(),

    # Save the output to a TIFF stack
    florin.save('segmented.tiff')
)

# Run the pipeline
segmented = pipeline()
```

Note that `np.squeeze` is not invoked. The function is just passed to the pipeline as-is, and FLoRIN will call it later.



## Parameterizing Functions with florinate

Functions with parameters can also be used within FLoRIN by wrapping them with `florin.florinate`. This function records any parameters passed while setting up the pipeline and then automatically applies them when the data comes through (i.e. partial function application):

```
.. content-tabs::
```

### Decorator

```
import florin
import florin.conncomp as conncomp
import florin.morphology as morphology
import florin.thresholding as thresholding

# Create the custom function and decorate it with ``florinate``
@florin.florinate
def scale(image, scalar=1):
    """Scale an images values by some number.

    Parameters
    -----
    image : array_like
    scale : int or float

    Returns
    -----
    image * scale
    """
    return image * scale

# Set up a serial pipeline
pipeline = florin.Serial(
    # Load in the volume from file
    florin.load(),

    # Tile the volume into overlapping 64 x 64 x 10 subvolumes
    florin.tile(shape=(10, 64, 64), stride=(10, 32, 32)),

    # Add the custom function to the pipeline
    scale(scalar=2.0),

    # Threshold with NDNT
    thresholding.ndnt(shape=(10, 64, 64), threshold=0.3),

    # Clean up a little bit
    morphology.binary_opening(),

    # Save the output to a TIFF stack
    florin.save('segmented.tiff')
)

# Run the pipeline
segmented = pipeline()
```

### In-Line

```
import florin
import florin.conncomp as conncomp
import florin.morphology as morphology
import florin.thresholding as thresholding

# Create the custom function
def scale(image, scalar=1):
    """Scale an images values by some number.

    Parameters
    -----
    image : array_like
    scale : int or float

    Returns
    -----
    image * scale
    """
    return image * scale

# Set up a serial pipeline
pipeline = florin.Serial(
    # Load in the volume from file
    florin.load(),

    # Add the custom function to the pipeline and wrap it in ``florinate``
    florin.florinate(scale)(scalar=2.0),

    # Tile the volume into overlapping 64 x 64 x 10 subvolumes
    florin.tile(shape=(10, 64, 64), stride=(10, 32, 32)),

    # Add the custom function to the pipeline
    scale(scalar=2.0),

    # Threshold with NDNT
    thresholding.ndnt(shape=(10, 64, 64), threshold=0.3),

    # Clean up a little bit
    morphology.binary_opening(),

    # Save the output to a TIFF stack
    florin.save('segmented.tiff')
)

# Run the pipeline
segmented = pipeline()
```

`florinate` will handle any number of arguments and keyword arguments passed to it, applying them every time the function is called during the pipeline.

## Why florinate?

The `functools` module already has an implementation of partial functions (`functools.partial`), the the natural question is: why reinvent the wheel? When building FLoRIN, we noticed that most computer vision functions take the image as the *first* argument; `functools.partial`, however will only *append* arguments when called. `florinate` solves this by *prepending* the argument(s) when called, lining up with the norm for computer vision APIs.

If a custom function takes the image as the *last* argument, `functools.partial` can be used in place of `florinate` with no changes.

## 2.2.4 Adding New Pipeline Types to FLoRIN

FLoRIN offers a number of pipeline options (Serial, Multithread, Multiprocess, etc.) out of the box, but what if you need a different model? This example will show how to create a custom pipeline class with a different style of execution.

### SLURMPipeline

Suppose you work on a cluster that uses SLURM and want to submit a job to a queue. This requires a pipeline that

1. Accepts parameters to configure `sbatch`
2. Sets up a job script
3. Submits the job script for processing
4. Blocks until all jobs are finished

Such a pipeline may look like this

```
import re
import subprocess
import time

import dill # dill is installed with florin

from florin.pipelines import Pipeline

class SLURMPipeline(Pipeline):
    """Pipeline that sets up and runs a SLURM job.

    Parameters
    -----
    operations : callables
        The functions of the pipeline.

    Other Parameters
    -----
    Keyword arguments corresponding to SLURM directives, e.g. qos='debug',
    time=60, etc. These are dynamically added to the jobscript before
    submission.
    """

    def __init__(self, *operations, **kwargs):
        super(SLURMPipeline, self).__init__(*operations)
        self.slurm_directives = kwargs

    def run(self, data):
        """Submit and run a pipeline on SLURM.

        Parameters
        -----
        data : list
            The input to the first function in the pipeline, e.g. a
```

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```

        filepath for florin.load().
    """
    # Serialize this current pipeline
    pipeline_path = 'my_pipeline.pkl'
    self.dump(pipeline_path)

    # Set up the job script. This sets up the shebang header, then
    # iterates over the provided #SBATCH directives and sets each one
    # up on its own line, then finally invokes srun to deserialize the
    # pipeline and run it on the data.
    jobscript = "#!/usr/bin/env bash"
    jobscript = '\n'.join(
        ['#!/usr/bin/env bash'] +
        ['#SBATCH --{}={}'.format(key, val) for key, val in self.slurm_directives.
        ↪items()] +
        ['srun python -m florin.run {} $1'.format(pipeline_path)])

    # Dump the jobscript to file
    with open('my_jobscript.job', 'w') as f:
        f.write(jobscript)

    jobids = []

    # Submit one job for each data item.
    for item in data:
        out = subprocess.check_output(['sbatch', my_jobscript, item])
        jobids.append(re.search(r'([\d]+)', out).group())

    # Wait until all jobs have completed to exit.
    while len(jobids) > 0:
        time.sleep(10)
        completed = []

        for jid in jobids:
            out = subprocess.check_output(['sacct', '-j', jid])
            if re.search(r'(COMPLETE)', out):
                completed.add(jid)

        for jid in completed:
            jobids.remove(jid)

```

Note that this code is untested and by no means guaranteed to work, it is only meant to be a non-trivial example of what a custom pipeline may look like.

## Other Examples

Another great source of examples for setting up custom pipelines is the `florin.pipelines` module, where the source code for the officially supported pipelines.

## 2.3 API Documentation

<i>florin</i>	The FLoRIN pipeline for large-scale learning-free computer vision.
<i>florin.classification</i>	Utilities for classifying connected components.
<i>florin.closure</i>	Closure decorator for delayed processing.
<i>florin.compose</i>	Deferred function composition with functools.
<i>florin.conncomp</i>	Convenience functions for image connected components operations.
<i>florin.io</i>	I/O functions for loading and saving data in a variety of formats.
<i>florin.morphology</i>	Convenience functions for image morphological operations.
<i>florin.ndnt</i>	N-Dimensional Neighborhood Thresholding for any-dimensional data.
<i>florin.pipelines</i>	Deferred execution pipelines with different computational models.
<i>florin.reconstruction</i>	Reconstruct connected components as an array of pixel-wise class labels.
<i>florin.thresholding</i>	Convenience functions for image thresholding operations.
<i>florin.tiling</i>	Utilities for tiling images and volumes.

### 2.3.1 florin

The FLoRIN pipeline for large-scale learning-free computer vision.

#### Classes

**Balsam** Distributed computation using the Balsam job submission database.

**MPI** Multicore/multi-node parallel computation with MPI.

**Multiprocessing** Multiprocessing using the standard fork/join model.

**Multithreading** Multithreading using the Python multithreading library.

**Serial** Single-core serial deferred computation.

**WorkQueue** Distributed computing using Work Queue to manage tasks.

#### Functions

**bounds\_classifier** Classify connected components based on boundary conditions.

**classify** Classify connected components into multiple classes.

**florinate** Prepare a function for use in the FLoRIN pipeline.

**join** Join one or more tiles into a single array.

**load** Load image data into FLoRIN.

**reconstruct** Create a label array from connected component classification labels.

**save** Save image data from FLoRIN.

**tile** Split a single array into sub-arrays.

## 2.3.2 florin.classification

Utilities for classifying connected components.

### Classes

**FlorinClassifier** Classification unit for weak object grouping.

### Functions

**classify** Classify a segmented object.

### Functions

---

<code>classify(obj, *classes)</code>	Multiclass classificaiton based on human-tuned boundaries.
--------------------------------------	--

---

### Classes

---

<code>FlorinClassifier(label, **kwargs)</code>	Classify connected components based on boundary conditions.
--	---

---

**class** `florin.classification.FlorinClassifier` (*label*, *\*\*kwargs*)  
Classify connected components based on boundary conditions.

#### Parameters

- **label** – The class label identifying this class. Can be any arbitrary label.
- **boundaries** – Pairs of values (2-tuples) passed as keyword arguments defining the boundaries to classify along. For example, passing `area=(5, 10)` tells this class that the objects it contains have an area/volume of  $5 \leq \text{obj.area} \leq 10$ .

### Methods

---

<code>classify(self, obj)</code>	Determine if an object is in this class.
----------------------------------	--

---

**classify** (*self*, *obj*)  
Determine if an object is in this class.

**Parameters** *obj* (*skimage.measure.\_regionprops.RegionProperties*) – The object to classify.

**Returns** True if the object is within all defined boundaries else False. If no boundaries were provided, return True (e.g., the default class).

**Return type** bool

`florin.classification.classify` (*obj*, *\*classes*)  
Multiclass classificaiton based on human-tuned boundaries.

#### Parameters

- **obj** (*skimage.measure.\_regionprops.RegionProperties*) – The object to classify.
- **classes** (*florin.classify.FlorinClassifiers*) – The classes to select from.

**Returns** Updates `obj` with a class label (`obj.class_label`) and passes it on for further processing.

**Return type** `obj`

### Notes

In a typical FLoRIN pipeline, `florin.reconstruct()` will be called immediately after `florin.classify()`.

## 2.3.3 florin.closure

Closure decorator for delayed processing.

### Functions

**florinate** Decorator to wrap arbitrary functions and enable delayed evaluation.

### Functions

<code>florinate(func)</code>	Decorator to wrap arbitrary functions and enable delayed evaluation.
------------------------------	--

`florin.closure.florinate(func)`

Decorator to wrap arbitrary functions and enable delayed evaluation.

**Parameters** **func** (*callable*) – The function/Python callable to wrap.

**Returns** **wrapper** – The wrapped `func` which stores any arguments passed to `func` and may be called on new data at a future time.

**Return type** `callable`

### Notes

`florinate` is essentially a rebranding of `functools.partial` to allow passing the deferred arguments at the front of the call instead of the tail. This conforms with the signatures of many computer vision API functions, which tend to accept image data as the first argument.

### Examples

`florinate` may be applied as a decorator to standard function definitions to then make subsequent calls return the deferred function.

```
>>> @florinate
... def add(x, y):
...     return x + y
>>> plus_one = add(1)
```

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```
>>> plus_one(5)
6
```

Functions may also be florinated on the fly by using it as a standard function:

```
>>> def concat(str1, str2):
...     return ' '.join([str1, str2])
>>> worlde = florinate(concat)('World')
>>> worlde('Hello')
'Hello World'
```

## 2.3.4 florin.compose

Deferred function composition with functools.

### Functions

**compose** Compose a chain of functions on an initial input.

### Functions

---

<code>compose(*functions)</code>	Compose a chain of functions on an initial input.
----------------------------------	---

---

`florin.compose.compose(*functions)`

Compose a chain of functions on an initial input.

Applies a sequence of functions in order to some initial data, performing a reduce over the entire function chain.

**Parameters** **functions** (*list of callable*) – The functions to execute. List contents may be any callable, including `functools.partial` objects to enable parameterizing deferred functions.

**Returns**

**Return type** A partial function to be applied to data at a later time.

## 2.3.5 florin.conncomp

Convenience functions for image connected components operations.

### Functions

**label** Integer labeling for binary connected components.

**regionprops** Compute various properties of labeled connected components.

### Functions

---

<code>label(image, *args, **kwargs)</code>	Wrapper that casts arrays to integers before labeling
--	---

---

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Table 7 – continued from previous page

<code>regionprops(image, \**kwargs)</code>	Compute the properties of connected components.
--	---

`florin.conncomp.label` (*image*, \*args, \*\*kwargs)

Wrapper that casts arrays to integers before labeling

`florin.conncomp.regionprops` (*image*, \*\*kwargs)

Compute the properties of connected components.

#### Parameters

- **image** (*array\_like*) – The labeled image to process for connected components.
- **intensity\_image** (*array\_like*) – The original image from which *image* was computed. Passing this enables computing summary statistics about the image pixel intensities.

#### Notes

This function wraps `skimage.measure.regionprops` to allow for additional bookkeeping and feature computation.

## 2.3.6 florin.io

I/O functions for loading and saving data in a variety of formats.

### Functions

**load** Load image(s) from a file.

**load\_hdf5** Load data from an HDF5 file.

**load\_image** Load an image file.

**load\_images** Load a directory of image files.

**load\_npy** Load data from a numpy array file.

**load\_tiff** Load a TIFF stack.

**save** Save image(s) in a variety of formats.

**save\_hdf5** Save an image to HDF5 format.

**save\_image** Save an image.

**save\_images** Save a sequence of images.

**save\_npy** Save an image to a numpy array file.

**save\_tiff** Save an image to TIFF format.

### Functions

<code>load(path, \**kwargs)</code>	Load images from a file.
<code>load_hdf5(path[, key])</code>	Load data from an HDF5 file.
<code>load_image(path)</code>	Load an image file.
<code>load_images(path[, ext])</code>	Load a directory of image files.

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<code>load_npy(path)</code>	Load data from a numpy array file.
<code>load_tiff(path)</code>	Load a TIFF stack.
<code>save(img, path, **kwargs)</code>	Save image(s) in a variety of formats.
<code>save_hdf5(img, path[, key])</code>	Save an image to HDF5 format.
<code>save_image(img, path)</code>	Save an image.
<code>save_images(img, path[, ext])</code>	Save a sequence of images.
<code>save_npy(img, path)</code>	Save an image to a numpy array file.
<code>save_tiff(img, path)</code>	Save an image to TIFF format.

`florin.io.load(path, **kwargs)`

Load images from a file.

Generic loader function that uses the file extension to determine how to load the data.

**Parameters** `path` (*str*) – Path to the image file(s) to load.

**Other Parameters** `key` – Key to load data from when working with key/value stores (e.g. HDF5, npz, etc.)

**Returns** `data`

**Return type** `numpy.ndarray`

`florin.io.load_hdf5(path, key='stack')`

Load data from an HDF5 file.

**Parameters**

- `path` (*str*) – Path to the HDF5 file to load.
- `key` – Key to load data from.

**Returns** `data`

**Return type** `h5py.Dataset`

`florin.io.load_image(path)`

Load an image file.

**Parameters** `path` (*str*) – Path to the image file to load.

**Returns** `data`

**Return type** `numpy.ndarray`

`florin.io.load_images(path, ext='png')`

Load a directory of image files.

**Parameters**

- `path` (*str*) – Path to the image file(s) to load.
- `ext` (*str*) – The file extension to match. Only files with this extension will be loaded. Default: 'png'

**Returns** `data`

**Return type** `numpy.ndarray`

`florin.io.load_npy(path)`

Load data from a numpy array file.

**Parameters** `path` (*str*) – Path to the array file to load.

**Returns data****Return type** numpy.ndarray`florin.io.load_tiff(path)`

Load a TIFF stack.

**Parameters** `path` (*str*) – Path to the TIFF stack to load.**Returns data****Return type** numpy.ndarray`florin.io.save(img, path, **kwargs)`

Save image(s) in a variety of formats.

**Parameters**

- **img** (*array\_like*) – The image/volume to save.
- **path** (*str*) – The filepath to save the data to. This path determines which format the data will be saved as.

**Returns** The unaltered image/volume.**Return type** img**Other Parameters**

- See “`save_hdf5`“, “`save_image`“, “`save_images`“, “`save_npy`“, and
- “`save_tiff`“ for filetype-specific arguments.

**Notes**

The filetype passed as `path` will determine the format of the saved file. If no extension is found, 3D arrays will automatically be saved as numbered PNG files in a directory created at `path` and 2D arrays will be saved to `path` directly as a PNG.

`florin.io.save_hdf5(img, path, key='stack')`

Save an image to HDF5 format.

**Parameters**

- **img** (*array\_like*) – The image/volume to save.
- **path** (*str*) – The filepath to save the data to.

`florin.io.save_image(img, path)`

Save an image.

**Parameters**

- **img** (*array\_like*) – The image/volume to save.
- **path** (*str*) – The filepath to save the data to.

`florin.io.save_images(img, path, ext='png')`

Save a sequence of images.

**Parameters**

- **img** (*array\_like*) – The image/volume to save.
- **path** (*str*) – The filepath to save the data to.
- **ext** (*str*) – The file extension to save each image with.

`florin.io.save_npy (img, path)`  
Save an image to a numpy array file.

**Parameters**

- **img** (*array\_like*) – The image/volume to save.
- **path** (*str*) – The filepath to save the data to.

`florin.io.save_tiff (img, path)`  
Save an image to TIFF format.

**Parameters**

- **img** (*array\_like*) – The image/volume to save.
- **path** (*str*) – The filepath to save the data to.

## 2.3.7 florin.morphology

Convenience functions for image morphological operations.

### Functions

**closing** Perform a grayscale morphological closing on an image.

**dilation** Perform a grayscale morphological dilation on an image.

**erosion** Perform a grayscale morphological erosion on an image.

**opening** Perform a grayscale morphological opening on an image.

**binary\_closing** Perform a binary morphological closing on an image.

**binary\_dilation** Perform a binary morphological dilation on an image.

**binary\_erosion** Perform a binary morphological erosion on an image.

**binary\_opening** Perform a binary morphological opening on an image.

**remove\_small\_holes** Fill in contiguous holes smaller than the specified size.

**remove\_small\_objects** Remove contiguous objects smaller than the specified size.

## 2.3.8 florin.ndnt

N-Dimensional Neighborhood Thresholding for any-dimensional data.

### Functions

**ndnt** Binarize data with N-Dimensional Neighborhood Thresholding.

**integral\_image** Compute the integral image of a n image or volume.

**integral\_image\_sum** Compute the neighborhood sum of an integral image.

### Classes

`InvalidThresholdError`

## Functions

<code>integral_image(img[, inplace])</code>	Compute the integral image of an image or image volume.
<code>integral_image_sum(int_img[, shape, ...])</code>	Compute pixel neighborhood statistics.
<code>ndnt(img[, shape, threshold, inplace])</code>	Compute an n-dimensional Bradley thresholding of an image or volume.

## Exceptions

<code>InvalidThresholdError(t)</code>	Raised when the NDNT threshold value is out of domain.
---------------------------------------	--

**exception** `florin.ndnt.InvalidThresholdError(t)`

Raised when the NDNT threshold value is out of domain.

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

`florin.ndnt.integral_image(img, inplace=False)`

Compute the integral image of an image or image volume.

### Parameters

- **img** (*array-like*) – The original 2D image or 3D volume.
- **inplace** (*bool, optional*) – If True, compute the integral image in the same array as the original image.

**Returns** `int_img` – The integral image of the original image or volume.

**Return type** `array-like`

## Notes

This function extends the integral image to  $n$  dimensions as described in [1].

## References

`florin.ndnt.integral_image_sum(int_img, shape=None, return_counts=True)`

Compute pixel neighborhood statistics.

### Parameters

- **int\_image** (*array\_like*) – The integral image.
- **shape** (*tuple of int*) – The shape of the neighborhood around each pixel.
- **return\_counts** (*bool*) – If True, in addition to neighborhood pixel sums, return the number of pixels used to compute each sum.

### Returns

- **sums** (*array\_like*) – An array where each entry is the sum of pixel values in a neighborhood. The same shape as `int_img`.

- **counts** (*array\_like*) – An array where each entry is the number of pixels used to compute each entry in `sums`. The same shape as `int_img`.

`florin.ndnt.ndnt (img, shape=None, threshold=0.25, inplace=False)`

Compute an n-dimensional Bradley thresholding of an image or volume.

The Bradley thresholding, also called Local Adaptive Thresholding, uses the integral image of an image or volume to threshold an image based on local mean greyscale intensities. The underlying assumption is that while the mean intensity may shift, the distribution of intensities will remain roughly constant across an entire image or volume.

#### Parameters

- **img** (*array-like*) – The image to threshold.
- **shape** (*array-like, optional*) – The dimensions of the local neighborhood around each pixel/voxel.
- **threshold** (*float*) – The threshold value as the percentage of greyscale value to keep. Must be in [0, 1].

#### Notes

The original Bradley thresholding was introduced in [1] as a means for quickly thresholding images or video. Shabbazi *et al.* [2] extended this method to operate on data of arbitrary dimensionality using the method described by Tapia [3].

#### References

### 2.3.9 florin.pipelines

Deferred execution pipelines with different computational models.

#### Classes

**BalsamPipeline** Distributed computation using the Balsam job submission database.

**MPIPipeline** Multicore/multi-node parallel computation with MPI.

**MultiprocessingPipeline** Multiprocessing using the standard fork/join model.

**MultithreadingPipeline** Multithreading using the Python multithreading library.

**SerialPipeline** Single-core serial deferred computation.

**WorkQueuePipeline** Distributed computing using Work Queue to manage tasks.

**class** `florin.pipelines.BalsamPipeline (*operations)`

#### Methods

<code>__call__(self, data)</code>	Call self as a function.
<code>add(self, func)</code>	Append a callable to this pipeline.
<code>dump(self, path)</code>	Save this pipeline to file.
<code>dumps(self)</code>	Serialize this pipeline as a string.

Continued on next page

Table 11 – continued from previous page

<code>run(self, data)</code>	Run data through the pipeline.
------------------------------	--------------------------------

**add** (*self*, *func*)

Append a callable to this pipeline.

**Parameters** *func* (*callable*) – New function to add.

**dump** (*self*, *path*)

Save this pipeline to file.

**Parameters** *path* (*str*) – Path to the file to write this pipeline to.

**dumps** (*self*)

Serialize this pipeline as a string.

**run** (*self*, *data*)

Run data through the pipeline.

**Parameters** *data* – Input to the first function in the pipeline.

**Returns** The result of applying the pipeline to *data*.

**Return type** *result*

**class** `florin.pipelines.MPIPipeline` (*\*operations*)

MPI-based multiprocessing pipeline.

**Parameters** *operations* (*callables*) – Sequence of operations to run in the pipeline.

## Notes

MPI is configured by wrapping Python in an `mpiexec` or `mpirun` call at runtime.

## Methods

<code>__call__(self, data)</code>	Call self as a function.
<code>add(self, func)</code>	Append a callable to this pipeline.
<code>dump(self, path)</code>	Save this pipeline to file.
<code>dumps(self)</code>	Serialize this pipeline as a string.
<code>run(self, data)</code>	Run data through the pipeline.

**add** (*self*, *func*)

Append a callable to this pipeline.

**Parameters** *func* (*callable*) – New function to add.

**dump** (*self*, *path*)

Save this pipeline to file.

**Parameters** *path* (*str*) – Path to the file to write this pipeline to.

**dumps** (*self*)

Serialize this pipeline as a string.

**run** (*self*, *data*)

Run data through the pipeline.

**Parameters** *data* – Input to the first function in the pipeline.

**Returns** The result of applying the pipeline to `data`.

**Return type** `result`

**class** `florin.pipelines.MultiprocessingPipeline` (\**operations*, *processes*=None)

Pipeline for multi-core parallel processing on a single machine.

#### Parameters

- **operations** (*callable*s) – The operations/functions/callable classes to run in this pipeline.
- **processes** (*int*, *optional*) – The number of processes to use. Setting None will attempt to use as many as can be supported.

#### Methods

<code>__call__(self, data)</code>	Call self as a function.
<code>add(self, func)</code>	Append a callable to this pipeline.
<code>dump(self, path)</code>	Save this pipeline to file.
<code>dumps(self)</code>	Serialize this pipeline as a string.
<code>run(self, data)</code>	Run data through the pipeline.

**add** (*self*, *func*)

Append a callable to this pipeline.

**Parameters** **func** (*callable*) – New function to add.

**dump** (*self*, *path*)

Save this pipeline to file.

**Parameters** **path** (*str*) – Path to the file to write this pipeline to.

**dumps** (*self*)

Serialize this pipeline as a string.

**run** (*self*, *data*)

Run data through the pipeline.

**Parameters** **data** – Input to the first function in the pipeline.

**Returns** The result of applying the pipeline to `data`.

**Return type** `result`

**class** `florin.pipelines.MultithreadingPipeline` (\**operations*, *threads*=None)

Pipeline for multithreaded parallel processing on a single machine.

#### Parameters

- **operations** (*callable*s) – Sequence of operations to run in the pipeline.
- **threads** (*int*, *optional*) – The number of threads to use. Setting None will attempt to use as many as can be supported.

#### Methods

<code>__call__(self, data)</code>	Call self as a function.
<code>add(self, func)</code>	Append a callable to this pipeline.

Continued on next page



Table 14 – continued from previous page

<code>dump(self, path)</code>	Save this pipeline to file.
<code>dumps(self)</code>	Serialize this pipeline as a string.
<code>run(self, data)</code>	Run data through the pipeline.

**add** (*self*, *func*)

Append a callable to this pipeline.

**Parameters** *func* (*callable*) – New function to add.

**dump** (*self*, *path*)

Save this pipeline to file.

**Parameters** *path* (*str*) – Path to the file to write this pipeline to.

**dumps** (*self*)

Serialize this pipeline as a string.

**run** (*self*, *data*)

Run data through the pipeline.

**Parameters** *data* – Input to the first function in the pipeline.

**Returns** The result of applying the pipeline to *data*.

**Return type** *result*

**class** `florin.pipelines.SerialPipeline` (\**operations*)

Pipeline for single-core serial computation.

**Parameters** *operations* (*callables*) – The operations/functions/callable classes to run in this pipeline.

## Methods

<code>__call__(self, data)</code>	Call self as a function.
<code>add(self, func)</code>	Append a callable to this pipeline.
<code>dump(self, path)</code>	Save this pipeline to file.
<code>dumps(self)</code>	Serialize this pipeline as a string.
<code>run(self, data)</code>	Run data through the pipeline.

**add** (*self*, *func*)

Append a callable to this pipeline.

**Parameters** *func* (*callable*) – New function to add.

**dump** (*self*, *path*)

Save this pipeline to file.

**Parameters** *path* (*str*) – Path to the file to write this pipeline to.

**dumps** (*self*)

Serialize this pipeline as a string.

**run** (*self*, *data*)

Run data through the pipeline.

**Parameters** *data* – Input to the first function in the pipeline.

**Returns** The result of applying the pipeline to *data*.

**Return type** result

**class** florin.pipelines.**WorkQueuePipeline**(\*operations)

### Methods

<code>__call__(self, data)</code>	Call self as a function.
<code>add(self, func)</code>	Append a callable to this pipeline.
<code>dump(self, path)</code>	Save this pipeline to file.
<code>dumps(self)</code>	Serialize this pipeline as a string.
<code>run(self, data)</code>	Run data through the pipeline.

**add** (*self*, *func*)

Append a callable to this pipeline.

**Parameters** **func** (*callable*) – New function to add.

**dump** (*self*, *path*)

Save this pipeline to file.

**Parameters** **path** (*str*) – Path to the file to write this pipeline to.

**dumps** (*self*)

Serialize this pipeline as a string.

**run** (*self*, *data*)

Run data through the pipeline.

**Parameters** **data** – Input to the first function in the pipeline.

**Returns** The result of applying the pipeline to *data*.

**Return type** result

## 2.3.10 florin.reconstruction

Reconstruct connected components as an array of pixel-wise class labels.

### Functions

**reconstruct** Create a labeled image or volume from classified connected components.

### Functions

<code>reconstruct(objs)</code>	Create a labeled image or volume from classified connected components.
--------------------------------	--

florin.reconstruction.**reconstruct** (*objs*)

Create a labeled image or volume from classified connected components.

**Parameters** **objs** (*list of obj : skimage.measure.\_regionprops.RegionProperties*) – Classified objects to be labeled.

### 2.3.11 florin.thresholding

Convenience functions for image thresholding operations.

#### Functions

**ndnt** Binarize data with N-Dimensional Neighborhood Thresholding.

### 2.3.12 florin.tiling

Utilities for tiling images and volumes.

#### Functions

**tile\_generator** Subdivide an array into equally-sized tiles.

**join\_tiles** Join a sequence of tiles into a single array.

#### Functions

<i>join(tiles)</i>	Join a set of tiles into a single array.
<i>join_tiles(tiles)</i>	Join a set of tiles into a single array.
<i>tile(img[, shape, stride, offset, tile_store])</i>	Tile data into n-dimensional subdivisions.
<i>tile_generator(img[, shape, stride, offset, ...])</i>	Tile data into n-dimensional subdivisions.

#### Exceptions

<i>DimensionMismatchError</i>
<i>InvalidTileShapeError</i>
<i>InvalidTileStepError</i>
<i>ShapeStepMismatchError</i>

**exception** florin.tiling.DimensionMismatchError

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** florin.tiling.InvalidTileShapeError

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** florin.tiling.InvalidTileStepError

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

**exception** florin.tiling.ShapeStepMismatchError

**with\_traceback()**

Exception.with\_traceback(tb) – set self.\_\_traceback\_\_ to tb and return self.

`florin.tiling.join(tiles)`

Join a set of tiles into a single array.

**Parameters**

- **tiles** (*collection of FlorinArray*) – The collection of tiles to join.
- **shape** (*tuple of int*) – The shape of the joined array.

**Returns joined** – The array created by joining the tiles and inserting them into the correct positions.

**Return type** array\_like

`florin.tiling.join_tiles(tiles)`

Join a set of tiles into a single array.

**Parameters**

- **tiles** (*collection of FlorinArray*) – The collection of tiles to join.
- **shape** (*tuple of int*) – The shape of the joined array.

**Returns joined** – The array created by joining the tiles and inserting them into the correct positions.

**Return type** array\_like

`florin.tiling.tile(img, shape=None, stride=None, offset=None, tile_store=None)`

Tile data into n-dimensional subdivisions.

**Parameters**

- **img** (*array\_like*) – The data to subdivide.
- **shape** (*tuple of int*) – The shape of the subdivisions.
- **stride** (*tuple of int*) – The stride between subdivisions.

**Yields**

- **tile** (*florin.FlorinVolume*) – A subdivision of `img`. Subdivisions are yielded in sequence from the start of `img`.
- **metadata** (*dictionary*) – Key/value store of metadata, e.g. for joining tiles.

## Notes

Everything up to the for loop will be run exactly once when the first tile is requested.

`florin.tiling.tile_generator(img, shape=None, stride=None, offset=None, tile_store=None)`

Tile data into n-dimensional subdivisions.

**Parameters**

- **img** (*array\_like*) – The data to subdivide.
- **shape** (*tuple of int*) – The shape of the subdivisions.
- **stride** (*tuple of int*) – The stride between subdivisions.

**Yields**

- **tile** (*florin.FlorinVolume*) – A subdivision of `img`. Subdivisions are yielded in sequence from the start of `img`.

- **metadata** (*dictionary*) – Key/value store of metadata, e.g. for joining tiles.

## Notes

Everything up to the for loop will be run exactly once when the first tile is requested.



---

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