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**pystem**  
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## SYSTEM USER GUIDE

### 1.1 Introduction

#### 1.1.1 What is pystem

pystem is an open source Python library which provides tools to reconstruct partially sampled 2D images as multi-band images.

pystem's core is a set of reconstruction techniques such as interpolation, regularized least-square and dictionary learning methods. It provides a user interface which simplify the use of these techniques.

pystem is mainly at the destination of the microscopy community so that it highly depends on the good library [HyperSpy](#).

This library was originally developed by its creator Etienne Monier to handle EELS data and develop reconstruction algorithms. This was proposed afterwards to the microscopy community as a tool.

#### 1.1.2 About the developer

This library is developed by Etienne Monier, a French PhD student.

His research interests are in new methods and algorithms to solve challenging acquisition problems encountered in the acquisition of multi-band microscopy images. In particular, he is interested in acquiring high-SNR Electron Energy Loss Spectroscopy (EELS) images with extremely low beam energy to prevent destruction of sensitive microscopy samples. His goal is to provide to the EELS community precise algorithms to detect rapidly the presence of a chemical element inside a sample to reduce irradiation as much as possible. Such problem requires **signal processing** methods, such as **convex optimization** and **proximal splitting** methods.

### 1.2 Installing pystem

Well, for the moment, please use.

```
pip install git+https://github.com/etienne-monier/pystem
```

### 1.3 Getting started

In this documentation, we will assume that the reader can write some command line or jupyter python.

### 1.3.1 Starting system in python

system can be imported in python just as any python package.

```
>>> import system
```

In addition to system, the `HyperSpy` library is required to construct the system objects as some arguments should be `HyperSpy` data.

```
>>> import hyperspy.api as hs
```

Last, note that most of the scientific python applications require libraries such as `numpy` and `matplotlib`. It is recommended to import them as well.

```
>>> import numpy as np
>>> import matplotlib.pyplot as plt
```

### 1.3.2 The base: What is a STEM acquisition here ?

A STEM acquisition here is the result of two main informations:

- **The scan pattern** which is basically the array of the visited pixels indexes,
- **The data** which are the values of the data at the sampled pixels.

Be aware that the system library can handle 2D (e.g. HAADF data) as 3D data (e.g. EELS data). The data that are acquired at a spatial position (or pixel) can then be a single value (for 2D) or a spectrum (for 3D).

### 1.3.3 The first basic object is the scan

The basic object to understand is the `Scan` class. This is an object which stores the scan pattern. To create one, the data spatial shape and the path indexes should be given.

```
>>> shape = (3, 4) # This is the spatial shape of the data : 3 rows, 4 columns.
>>> path = [ 1, 3, 6, 4, 7, 11, 8, 0] # These are the sampled pixels indexes.
>>> scan = system.Scan(shape, path)
>>> scan
<Scan, shape: (3, 4), ratio: 0.667>
```

---

**Note:** Note that in this documentation, the matrix indexes are denoted in the rows major order (which is the order chosen in python).

It mean that if the spatial dimensions are  $(M, N)$ , then the  $i$ 'th index refers to the pixels which coordinates are  $(i // N, i \% N)$ . In the above example, the first visited pixel is the second pixel of the first line.

Be careful also that **python coordinates begin at 0**, not 1.

---

Additionally, the `Scan` object allows you to select a fraction of the scan pattern. Let us consider a fully sampled acquisition which spatial shape is  $(M, N)$ , then only 10% of the pixels can be selected by setting the `ratio` argument to `0.1`. This argument can be modified after the object definition.

Thought, be careful in case the acquisition is partially sampled (or example, if only  $r*M*N$  pixels were acquired, with  $r$  below 1). In such case, if `ratio` is below  $r$ , then only `ratio*M*N` pixels are kept. If `ratio` is above  $r$ , then all  $r*M*N$  pixels are kept.

```

>>> scan
<Scan, shape: (3, 4), ratio: 0.667>
>>> scan.ratio = 0.8 # Here, we ask for a ratio which is higher than 0.667.
WARNING:root:Input ratio is higher than higher maximal ratio (0.667). Ratio is set to
↳the maximal value.
>>> scan.ratio = 0.5 # Here, the value is correct.
>>> scan
<Scan, shape: (3, 4), ratio: 0.500>

>>> scan = pystem.Scan(shape, path, ratio=0.5) # The ratio can be given at
↳initialization.
>>> scan
<Scan, shape: (3, 4), ratio: 0.500>
>>> scan.ratio = 0.667 # But don't worry, the additional visited pixels are not lost.
>>> scan
<Scan, shape: (3, 4), ratio: 0.667>

```

In fact, the pixels that are given at initialization of `scan` are not lost when a below ratio is given as the currently visited index are stored in `path` attribute while the `path_0` attribute stores all pixels at initialization.

```

>>> scan = pystem.Scan(shape, path, ratio=0.5) # The ratio can be given at
↳initialization.
>>> scan
<Scan, shape: (3, 4), ratio: 0.500>
>>> scan.path
.. code-block:: python
>>> scan.path_0
array([ 1,  3,  6,  4,  7, 11,  8,  0])
>>> scan.ratio
0.5

```

**Note:** The Scan object data can be represented with a sampling mask  $M$  defined as

$$M_i = \begin{cases} 1, & \text{if pixel \# } i \text{ is acquired} \\ 0, & \text{otherwise} \end{cases}$$

This representation suffer from information deficiency, but is interesting to study the acquired pixels repartition. This sampling mask which shape is the same as the spatial shape can be obtained using the `get_mask()` method of `Scan`. This one can also be plotted using the method `plot()` (see [Data Visualization](#)).

### 1.3.4 The second basic object is data

Well, data here are nothing else than `HyperSpy` data. Please refer to its [documentation](#) for more info about it.

### 1.3.5 The result is pystem data

As explained previously, the pystem data is the combination of a `Scan` object and an `HyperSpy` data. Two classes are proposed to the user:

- `Stem2D` for 2D data,
- `Stem2D` for 3D data.

Both are initialized with a scan pattern and the associated data. Though, the scan pattern is optional as the default scan pattern is raster scan (line-by-line) full sampling.

```
>>> import hyperspy.api as hs
>>> haadf_hs = hs.load('haadf_data.dm4')
>>> acquisition_1 = pystem.Stem2D(haadf_hs) # fully sampled HAADF image.

>>> m, n = haadf_hs.data.shape
>>> N = int(0.5*m*n) # The number of pixels to visit.
>>> path = np.random.permutation(m*n)[:N]
>>> scan = pystem.Scan(m, n, path)
>>> acquisition_2 = pystem.Stem2D(haadf_hs, scan) # partially sampled HAADF image.

>>> eels_hs = hs.load('eels_data.dm4')
>>> acquisition_3 = pystem.Stem3D(eels_hs) # fully sampled EELS image.
```

### 1.3.6 Loading your data is faster

pystem offers you a way to accelerate the data definition. To that end, pystem proposes you to setup a data directory (let's say `/my/wonderful/data/dir/`) and to put inside your data so that the structure looks like this:

```
/my/wonderful/data/dir/
|
+-- MyData1
|   |
|   +-- eels_data.dm4
|   +-- haadf_data.dm4
|   +-- scan.dm4
|   +-- MyData1.conf
|
+-- MyData2
|   |
|   +-- eels_data_2.dm4
|   +-- MyData2.conf
```

**Note:** The data directory is not set by default. You should use the `set_data_path()` function to set the path. Then, it can be read with the `read_data_path()`.

```
>>> pystem.set_data_path('/my/wonderful/data/dir/')
>>> pystem.read_data_path()
'/my/wonderful/data/dir/'
```

The data directory contains sub-directories which host:

- the data files (2D/3D data, scan pattern),
- the **configuration file** (such as `MyData1.conf` in the above tree).

The configuration file has the structure of a `.ini` file (have a look at [this page](#) for an example format) and defines the relative location of data files. This would look like this (be aware that the section names such as `2D DATA` is case sensitive while keys such as `file` are not).

```
#
# This is a demo MyData1.conf file
#
```

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```

[2D DATA]
# This section defines all info about 2D data
file = haadf_data.dm4

[3D DATA]
# This section defines all info about 3D data
File = eels_data.dm4

[SCAN]
# This section defines all info about scan pattern
FILE = scan.dm4

```

This file defines all is necessary to define the pystem data objects. To load the corresponding data, one should use the `load_file()` function which loads the data based on the `.conf` configuration file. Alternatively, pystem can load the `mydata.conf` data directly by using the `load_key()` with the `mydata` key (as long as `mydata.conf` is located inside the data directory). The difference between the two functions? `load_file()` **allows you to load a file which is not in the data directory.**

In addition to the configuration file path, the user should specify which data to load with the `ndim` argument (2 for 2D data and 3 for 3D data).

```

>>> pystem.get_data_path()
/my/wonderful/data/dir/
>>> acquisition = pystem.load_key('MyData1')
>>> acquisition = pystem.load_file('/my/wonderful/data/dir/MyData2.conf', ndim=2)

```

Other arguments (such as the scan pattern ratio) can be passed to the two load function. That will be seen later.

### 1.3.7 What about restoration ?

Well, everything was loaded and is ready for reconstruction. Lets us consider that your acquisition was partially sampled with a ratio of 0.2. So, to use any reconstruction method, use the `restore()` method of pystem objects.

The methods to reconstruct the data include nearest neighbor interpolation, regularized least-square and dictionary learning. Let's try with an example data (pystem has three dataset that can be loaded easily, this will be mentioned in).

```

>>> import pystem
>>> data = pystem.load_example('HR-sample', ndim=2, scan_ratio=0.2) # This loads_
↳example data.
Reading configuration file ...
Generating data ...
Creating STEM acquisition...
Correcting STEM acquisition...

>>> data
<Stem2D, title: HR-sample, dimensions: (|113, 63), sampling ratio: 0.20>
>>> reconstructed_data, info = data.restore('interpolation', parameters={'method':
↳'nearest'})
>>> reconstructed_data
<Signal2D, title: HR-sample, dimensions: (|113, 63)> # 2D hs data.
>>> info
{'time': 0.012229681015014648} # Execution time in sec.

```

Have a look at the reconstructed data which is an HyperSpy data. It means that the reconstructed data can analyzed with HyperSpy tools. Additional information are returned in the `info` dictionary (for the nearest neighbor method,

the only information that is returned is the execution time).

### 1.3.8 What about axes\_manager and metadata informations ?

The initialization of *Stem2D* or *Stem3D* objects need an HyperSpy image which stores information about the axes (as the axes\_manager attribute) and other general information (as the metadata attribute). **These informations are transferred to the reconstructed data.**

```

>>> data.hsdata.metadata
├── General
│   ├── original_filename = spim4-2-df-manually aligned image.dm4
│   └── title = HR-sample
└── Signal
    ├── Noise_properties
    │   └── Variance_linear_model
    │       ├── gain_factor = 1.0
    │       └── gain_offset = 0.0
    ├── binned = False
    ├── quantity = Intensity
    └── signal_type =

>>> data.hsdata.axes_manager
<Axes manager, axes: (|113, 63)>
      Name | size | index | offset | scale | units
===== | ===== | ===== | ===== | ===== | =====
----- | ----- | ----- | ----- | ----- | -----
          x | 113 |      |      -0 |      1 |
          y |  63 |      |      -0 |      1 |

>>> reconstructed_data.metadata
├── General
│   ├── original_filename = spim4-2-df-manually aligned image.dm4
│   └── title = HR-sample
└── Signal
    ├── Noise_properties
    │   └── Variance_linear_model
    │       ├── gain_factor = 1.0
    │       └── gain_offset = 0.0
    ├── binned = False
    ├── quantity = Intensity
    └── signal_type =

>>> reconstructed_data.axes_manager
<Axes manager, axes: (|113, 63)>
      Name | size | index | offset | scale | units
===== | ===== | ===== | ===== | ===== | =====
----- | ----- | ----- | ----- | ----- | -----
          x | 113 |      |      -0 |      1 |
          y |  63 |      |      -0 |      1 |
    
```

## 1.4 Initializing the data

### 1.4.1 How to initialize the scan pattern

The scan pattern can be initialized using three recipes:

- initialize it with the shape and path values (see *The first basic object is the scan*),

- initialize it with a Numpy or HyperSpy file,
- initialize it as random sampling.

Recall that a path which is initialized with the data shape only is set to be a full raster (i.e. line-by-line) scan.

Recall also that all scan initialization functions allow to define a ratio argument (see *The first basic object is the scan*).

### Initialize it with a file

The scan pattern can be initialized with a numpy .npz file which should store:

- m (resp. n) which is the data number of rows (resp. columns),
- path which is the path argument

To that end, one should use the `from_file()` method of `Scan`.

```
>>> import numpy as np
>>> m, n = 50, 100
>>> path = np.random.permutation(m*n)
>>> data_2_save = {'m': m, 'n': n, 'path': path}
>>> np.savez('my_scan.npz', **data_2_save) # This saves the Scan numpy file

>>> pystem.Scan.from_file('my_scan.npz', ratio=0.5) # This loads the numpy scan file.
<Scan, shape: (50, 100), ratio: 0.500>
```

### Initialize it as random sampling

The sampling scan can last be initialized with the `random()` method of `Scan`. One should just give the spatial data shape (m, n). In addition to the ratio argument which can also be given, the user can give a seed to the method to have reproducible results.

```
>>> pystem.Scan.random((50, 100))
<Scan, shape: (50, 100), ratio: 1.000>
>>> scan = pystem.Scan.random((50, 100), ratio=0.2)
>>> scan
<Scan, shape: (50, 100), ratio: 0.200>
>>> scan.path[:5]
array([4071, 662, 4168, 3787, 4584])

>>> scan = pystem.Scan.random((50, 100), ratio=0.2, seed=0)
>>> scan.path[:5]
array([ 398, 3833, 4836, 4572, 636])
>>> scan = pystem.Scan.random((50, 100), ratio=0.2, seed=0)
>>> scan.path[:5] # This shows that setting the seed makes the results reproducible.
array([ 398, 3833, 4836, 4572, 636])
```

## 1.4.2 Construct pystem data manually

As explained in *The result is pystem data*, the pystem data is composed of a `Scan` object which defines the sampling pattern and the HyperSpy data which stores the data. Once both have been defined, the pystem structure can be defined by hand.

```
>>> pystem_data = pystem.Stem2D(hsdata, scan=scan_object)
```

### 1.4.3 Construct system data from a Numpy array

In case your image is a numpy array, one should define the HyperSpy data before creating the system data.

```
>>> import numpy as np
>>> import hyperspy.api as hs
>>> shape = (50, 100, 1500)           # This is the 3D data shape
>>> im = np.ones(shape)             # This is our image (which is 3D this_
↳time).
>>> scan = system.Scan.random(shape[:2]) # The scan is created (be careful to have_
↳2-tuple shape).
>>> hsddata = hs.signals.Signal1D(im) # Here, hs data is created from numpy_
↳array.
>>> system.Stem3D(hsddata, scan)
<Stem3D, title: , dimensions: (100, 50|1500), sampling ratio: 1.00>
```

Well, the problem here, which is the same as for numpy-based HyperSpy data, is that both `axes_manager` and `metadata` are empty. To correct that, it is highly recommended to use a configuration file. That's the subject of next section.

### 1.4.4 Construct system data from a configuration file

As explained in *Loading your data is faster*, system can load data from a `.conf` configuration file. This is loaded by using the `load_file()` function (or the `load_key()` function if the configuration file is in the data path). To that end, a configuration file gives to system all important informations.

First, the configuration file is separated in three main sections (case-sensitive, caution !):

- DATA 2D for 2D data,
- DATA 3D for 3D data,
- SCAN for the scan pattern.

Among these sections, only one of DATA 2D and DATA 3D sections is required (if no data is given, system can not do anything ...). And inside this section, the only key which is required is `file` which specifies the location of the data file (numpy `.npz` or `.dm4` or all other file which is allowed by HyperSpy) **relative to the configuration file**. One info: contrary to sections which are case-sensitive, keys are not.

In case no `file` key is given inside a SCAN section, the `load_file()` function **creates automatically a random scan object** (based on its `scan_ratio` and `scan_seed` arguments). Otherwise, a scan file (numpy or dm4/dm3) is loaded (the `scan_ratio` argument of `load_file()` can still be given).

Hence, a basic configuration file could look like this.

```
#
# This is a demo file.
# This text is not used, that's a commentary.
#

[3D DATA]
# This section defines all info about 3D data
File = eels_data.dm4

[SCAN]
# This section defines all info about scan pattern

# If the following line is commented, the scan pattern would be random.
FILE = scan.dm4
```

In the special case where the data file is a numpy . npy file, one could define additional information to fill the HyperSpy axes\_manager attribute. To that end, a set of keys can be given inside the corresponding section. These keys should be like axis\_dim\_info where:

- dim is the axis index (0 for the x axis, 1 for the y axis and 2 in case of 3D data for the spectrum axis),
- info belongs to name, scale, unit and offset.

As an example, the previous section data axes\_manager should look like this.

```
>>> data = pystem.Stem3D(hsdata, scan)
Creating STEM acquisition...

>>> data.hsdata.axes_manager
<Axes manager, axes: (100, 50|1500)>
=====
Name | size | index | offset | scale | units
-----
<undefined> | 100 | 0 | 0 | 1 | <undefined>
<undefined> | 50 | 0 | 0 | 1 | <undefined>
-----
<undefined> | 1500 | | 0 | 1 | <undefined>
```

If the numpy array is save inside a directory with the following configuration file, this issue would be fixed.

```
#
# This is a demo file to define Numpy data axes_manager.
#

[3D DATA]
file = numpy_data.npy

# Infos for the axes_manager
axis_0_name = x
axis_1_name = y
axis_2_name = Energy loss

# Some more info for the energy loss axis
axis_2_offset = 4.6e+02
axis_2_scale = 0.32
axis_2_unit = eV

# No scan section, I want a random scan.
```

And the data would be loaded by simply typing this.

```
>>> pystem.load_file('my-nice-file.conf', scan_ratio=0.5, scan_seed=0)
```

### 1.4.5 Loading example data for fast testing

Last way to load data, use one of the example data provided by pystem. To that end, just use the load\_example() function just as the load\_key() with one of the following keys:

- 'HR-sample': this is a real atomic-scale HAADF/EELS sample,
- 'HR-synth': this is a synthetic EELS image generated to be similar to 'HR-sample',
- 'LR-synth': this is a synthetic low-resolution EELS image.

The first data were acquired in the context of the following works [AZWT+19], [APLML+18]. Authors of these works would like to acknowledge Daniele Preziosi for the LAO-NNO thin film growth, Alexandre Gloter for the FIB lamella preparation and Xiaoyan Li for STEM experiments.

The two last data were generated to compare reconstruction methods in the context of STEM-EELS data inpainting [AMonierOberlinBrun+18]. The high-resolution works were submitted.

## 1.4.6 References

# 1.5 Correcting data

## 1.5.1 Introduction

Sometimes, you can face a situation where your data has outliers, i.e. data that are abnormal because of local dysfunctions. The data *were* acquired, but their value are *not* normal. In such case, you can wish to

- purely remove columns / rows / bands,
- correct particular dead pixels by replacing their value by correct ones.

For the dead pixels, their new value are set to a mean over the nearest correct sampled positions.

In the below example, the user wants to remove the red rows, the green columns and correct a dead pixel in blue.

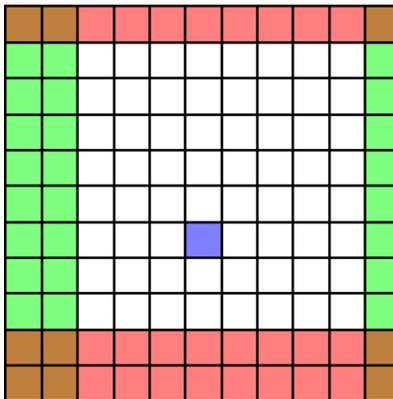


Fig. 1: Correction with a single image

## 1.5.2 Correcting data manually

This is realized easily by using the `correct()` method of the data object. This only requires

- slices objects that define the rows and columns to keep (and the bands in case of 3D data),
- the position of dead pixels.

---

**Note:** Let us recall what a `slice` object is. When you define a numpy array `A` of shape  $(m, n)$ , you can access columns and rows using e.g. `A[1:2:5, :2]`. In each direction, you specify the start, stop and step values.

For example, writing `A[1:, :]` mean you want to select all rows from row 1 to the last row `m`. This is equivalent to write `A[slice(1), :]`. In fact, a `slice` object just defines, for a direction, the start, stop and step values. Let's have some examples:

- `1:` is equivalent to `slice(1)`,
- `:10` is equivalent to `slice(None, 10)`,
- `::10` is equivalent to `slice(None, None, 10)`,
- `2:10` is equivalent to `slice(2, 10)`,
- `:` is equivalent to `slice(None)`.

For the above example, one should write the following code.

```
>>> data
<Stem3D, title: Test, dimensions: (|11, 11), sampling ratio: 0.20>
>>> data.correct(rows=slice(1, 9), columns=slice(2, 10), dpixels=[6*11+5])
Correcting STEM acquisition...

>>> data
<Stem3D, title: Test, dimensions: (|8, 8), sampling ratio: 0.20>
```

### 1.5.3 Correcting data with the configuration file

A lot of information can be given to pystem through the configuration file. To pass correction info to the load functions, all you need is to define slices inside the corresponding 2D DATA or 3D DATA sections. For this, use the following keys: `rows`, `columns`, `bands` and `dpixels`. The slice should be written as for numpy array selection (`1:-60`). Let's illustrate it with the configuration file of the HR-sample example image.

```
[2D DATA]
file = spim4-2-df-manually aligned image.dm4
columns = 15:-60
dpixels = [9384, 8468]

[3D DATA]
file = spim4-2_ali.dm4
columns = 15:-60
bands = 90:
dpixels = [9384, 8468]
```

**Note:** Contrary to the `correct()` method which allows slices, the configuration files require literal slices such as `1:-50`.

One other main difference is that slices objects *do not accept negative values* while the configuration files values are parsed and *accept negative values*. As a consequence, to tell pystem you just want to keep all rows but the first one and the five last ones, you should write `slice(1:m-1)` (where `m` is the number of rows) for the `correct()` method while the configuration file would accept `1:-5`.

## 1.6 Restoration

Welcome to the main page of this documentation. The pystem library is nothing else than a pluggin to HyperSpy to allow reconstruction.

## 1.6.1 Some words about pre and post-processing steps

### For 2D data

2D data are centered and normalized before reconstruction. The reason is to avoid highly variable reconstruction methods parameters.

```
# data numpy array is ready to be reconstructed.
#
# Let's get data mean and standard deviation.
data_mean, data_std = data.mean(), data.std()
# Let's center and normalize the data
data_ready = (data - data_mean) / data_std
#
# Reconstruction is performed
#
# Let's perform the inverse transformation
data_out = reconstructed_data * data_std + data_mean
# data_out is returned
```

### For 3D data

3D data have the same pre and post-processing as for 2D data. But in addition to centering and normalization, a **thresholded principal component analysis** (PCA) is performed to reduce the data dimension along the bands axis and to ensure the low rank assumption. This one states that most multi-band data result in the mixing of  $R$  basic data with  $R$  small compared to the data dimension).

The default behavior is to perform PCA with an automatically estimated threshold (which can be really over-estimated in case of data starvation situations, i.e. if you have almost as many samples as the data size). Though, the user can set both parameters and choose if PCA should be performed and which value the threshold should have.

To sum up, the steps are:

- perform thresholded PCA if required,
- center and normalize the data,
- perform reconstruction,
- re-set the data mean and standard deviation values,
- perform inverse PCA.

## 1.6.2 How to reconstruct my data

To reconstruct the data, the user should use the `restore()` method. Both `Stem2D` and `Stem3D` classes need the following arguments to restore their data:

- `method` which is the method name (default is 'interpolation'),
- `parameters` which should be a dictionary with input parameters,
- `verbose` which allows the method to display information on the console (default is True).

In addition to these common parameters, the *Stem3D* class has the following inputs:

- `PCA_transform` which controls the PCA execution (default is True for PCA execution),
- `PCA_th` which states the PCA threshold.

A common reconstruction task will then look like this.

```
>>> data = pystem.load_example('HR-sample', ndim=2, scan_ratio=0.2)
Reading configuration file ...
Generating data ...
Creating STEM acquisition...
Correcting STEM acquisition...

>>> rec, info = data.restore()
Restoring the 2D STEM acquisition...
-- Interpolation reconstruction algorithm --
Done in 0.01s.
---
>>> rec
<Signal2D, title: HR-sample, dimensions: (|113, 63)>
>>> info
{'time': 0.011758089065551758}
```

### 1.6.3 The reconstruction methods available

All you need to know for each method is:

- what the method do (of course you need to know a little about it),
- his nickname to give to `restore()`,
- his parameters,
- what informations are returned.

#### Restoration cheet sheet

Method input	2D	3D	Parameters	Output info
interpolation	x	x	method (among nearest, linear and cubic)	time
L1	x		Lambda, Nit, init	E, Gamma, nnz_ratio, time
3S		x	Lambda, scale, Nit, init	E, time
SNN		x	Lambda, Mu, Nit, init	E, time
CLS		x	Lambda, Nit, init	E, Gamma, nnz_ratio, time
Post_LS_CLS		x	Lambda, Nit, init	E_CLS, E_post_ls, Gamma, nnz_ratio, time
ITKrMM	x	x	PatchSize, K, L, S, Nit_lr, Nit, CLS_init	dico, E, time
ITKrMM_matlab	x	x	PatchSize, K, L, S, Nit_lr, Nit, CLS_init	dico, E, time
wKSVD	x	x	PatchSize, K, L, S, Nit_lr, Nit, CLS_init	dico, E, time
wKSVD_matlab	x	x	PatchSize, K, L, S, Nit_lr, Nit, CLS_init	dico, E, time
BPFA_matlab	x	x	PatchSize, K, step, Nit	dico, time

Additional info in case `PCA_transform` is `True` is `PCA_info` which stores the following keys:

- `H`: the truncated PCA basis,
- `PCA_th`: the PCA threshold,
- `Ym`: the data mean.

## Interpolation

The interpolation method calls linear, cubic or nearest neighbor interpolation.

The method to give to the `restore()` method is `interpolation`. The associated function is resp. `interpolate()`.

The input parameters are:

- `method`: (optional, str) The interpolation method (among `nearest`, `linear` and `cubic`). Default is `nearest neighbor`.

The output dictionary stores the following informations:

- `time`: the execution time (in sec.),
- `PCA_info`: in case of 3D data with PCA pre-processing, it stores info about PCA.

## L1

This regularized least-square method solves the following optimization problem:

$$\hat{\mathbf{x}} = \arg \min_{\mathbf{x} \in \mathbb{R}^{m \times n}} \frac{1}{2} \|(\mathbf{x} - \mathbf{y}) \cdot \Phi\|_F^2 + \lambda \|\mathbf{x}\Psi\|_1$$

where  $\mathbf{y}$  are the corrupted data,  $\Phi$  is a subsampling operator and  $\Psi$  is a 2D DCT operator.

The method to give to the `restore()` method is `L1`. The associated function is resp. `L1_LS()`.

The input parameters are:

- `Lambda`: (float) The regularization parameter,
- `init`: (optional, numpy array) An initial point for the gradient descent algorithm which should have the same shape as the input data,
- `Nit`: (optional, int) The number of iterations.

The output dictionary stores the following informations:

- `E`: The evolution of the functional value,
- `Gamma`: The set of all pixel positions which coefficient in the DCT basis is non-zero,
- `nnz-ratio`: The ratio of non-zero coefficients over the number of DCT coefficients,
- `time`: the execution time (in sec.).

## Smoothed SubSpace

The 3S algorithm denoise or reconstructs a multi-band image possibly spatially sub-sampled in the case of spatially smooth images. It is well adapted to intermediate scale images.

This algorithm performs a PCA pre-processing operation to estimate:

- the data subspace basis  $\mathbf{H}$ ,
- the subspace dimension  $R$ ,
- the associated eigenvalues in decreasing order  $\mathbf{d}$ ,
- the noise level  $\hat{\sigma}$ .

After this estimation step, the algorithm solves the following regularization problem in the PCA space:

$$\hat{\mathbf{S}} = \arg \min_{\mathbf{S} \in \mathbb{R}^{m \times n \times R}} \frac{1}{2R} \|\mathbf{SD}\|_{\text{F}}^2 + \frac{\lambda}{2} \sum_{m=1}^R w_m \|\mathbf{S}_{m,:}\|_2^2$$

$$\text{s.t. } \frac{1}{R} \|\mathbf{H}_{1:R}^T \mathbf{Y}_{\mathcal{I}(n)} - \mathbf{S}_{\mathcal{I}(n)}\|_2^2 \leq \alpha \hat{\sigma}^2, \forall n \in \{1, \dots, m * n\}$$

where  $\mathbf{Y}$  are the corrupted data,  $\mathbf{D}$  is a spatial finite difference operator and  $\mathcal{I}$  is the set of all sampled pixels. The coefficient  $\alpha$  is a coefficient which scales the power of the data fidelity term.

For more details, see [BMonierOberlinBrun+18].

The method to give to the `restore()` method is `3S`. The associated function is resp. `SSS()`.

The input parameters are:

- `Lambda`: (float) The regularization parameter,
- `scale`: (optional, float) The spectr
- `init`: (optional, numpy array) An initial point for the gradient descent algorithm which should have the same shape as the input data,
- `Nit`: (optional, int) The number of iterations.

The output dictionary stores the following informations:

- `E`: The evolution of the functional value,
- `time`: the execution time (in sec.),
- `PCA_info`: in case of 3D data with PCA pre-processing, it stores info about PCA.

## Smoothed Nuclear Norm

The SNN algorithm denoise or reconstructs a multi-band image possibly spatially sub-sampled in the case of spatially smooth images. It is well adapted to intermediate scale images.

This algorithm solves the following optimization problem:

$$\hat{\mathbf{X}} = \arg \min_{\mathbf{X} \in \mathbb{R}^{m \times n \times B}} \frac{1}{2} \|\mathbf{Y}_{\mathcal{I}} - \mathbf{X}_{\mathcal{I}}\|_{\text{F}}^2 + \frac{\lambda}{2} \|\mathbf{XD}\|_{\text{F}}^2 + \mu \|\mathbf{X}\|_*$$

where  $\mathbf{Y}$  are the corrupted data,  $\mathbf{D}$  is a spatial finite difference operator and  $\mathcal{I}$  is the set of all sampled pixels.

For more details, see [BMonierOberlinBrun+18].

The method to give to the `restore()` method is `SNN`. The associated function is resp. `SNN()`.

The input parameters are:

- `Lambda`: (float) The  $\lambda$  regularization parameter,
- `Mu`: (float) The  $\mu$  regularization parameter,

- `init`: (optional, numpy array) An initial point for the gradient descent algorithm which should have the same shape as the input data,
- `Nit`: (optional, int) The number of iterations.

The output dictionary stores the following informations:

- `E`: The evolution of the functional value,
- `time`: the execution time (in sec.),
- `PCA_info`: in case of 3D data with PCA pre-processing, it stores info about PCA.

## Cosine Least Square

The CLS algorithm denoises or reconstructs a multi-band image possibly spatially sub-sampled in the case of spatially sparse content in the DCT basis. It is well adapted to periodic data.

This algorithm solves the following optimization problem:

$$\hat{\mathbf{X}} = \arg \min_{\mathbf{X} \in \mathbb{R}^{m \times n \times B}} \frac{1}{2} \|\mathbf{Y}_{\mathcal{I}} - \mathbf{X}_{\mathcal{I}}\|_{\mathbb{F}}^2 + \lambda \|\mathbf{X}\Psi\|_{2,1}$$

where  $\mathbf{Y}$  are the corrupted data,  $\mathbf{D}$  is a spatial finite difference operator and  $\mathcal{I}$  is the set of all sampled pixels.

The method to give to the `restore()` method is CLS. The associated function is resp. `CLS()`.

The input parameters are:

- `Lambda`: (float) The  $\lambda$  regularization parameter,
- `init`: (optional, numpy array) An initial point for the gradient descent algorithm which should have the same shape as the input data,
- `Nit`: (optional, int) The number of iterations.

The output dictionary stores the following informations:

- `E`: The evolution of the functional value,
- `Gamma`: The set of all pixel positions which coefficient in the DCT basis is non-zero,
- `nnz-ratio`: The ratio of non-zero coefficients over the number of DCT coefficients,
- `time`: the execution time (in sec.),
- `PCA_info`: in case of 3D data with PCA pre-processing, it stores info about PCA.

## Post-Lasso CLS algorithm

This algorithms consists in applying CLS to restore the data and determine the data support in DCT basis. A post-least square optimization is performed to reduce the coefficients bias.

The method to give to the `restore()` method is `Post_LS_CLS`. The associated function is resp. `Post_LS_CLS()`.

The input parameters are:

- `Lambda`: (float) The  $\lambda$  regularization parameter,
- `init`: (optional, numpy array) An initial point for the gradient descent algorithm which should have the same shape as the input data,

- `Nit`: (optional, int) The number of iterations.

The output dictionary stores the following informations:

- `E_CLS`: The evolution of the functional value for the CLS optimization step,
- `E_post_ls`: The evolution of the functional value for the post-LS optimization step,
- `Gamma`: The set of all pixel positions which coefficient in the DCT basis is non-zero,
- `nnz-ratio`: The ratio of non-zero coefficients over the number of DCT coefficients,
- `time`: the execution time (in sec.),
- `PCA_info`: in case of 3D data with PCA pre-processing, it stores info about PCA.

## ITKrMM and wKSVD

Weighted K-SVD (see [BMairalEladSapiro08]) and Iterative Thresholding and K residual Means for Masked data (see [BNS18]) methods.

The wKSVD and ITKrMM algorithms share a lots of their code so that their input and output are the same. Though, two implementations exist to run these algorithms: one with python (`ITKrMM` and `wKSVD` methods) and one with matlab (`ITKrMM_matlab` and `wKSVD_matlab` methods). The original Matlab codes are broadcasted by “Karin Schnass”. They were translated afterwards into python. Nothing distinguish them but for wKSVD where matlab is faster. The only problem is that you should have the `matlab` command in your system path.

The methods to give to the `restore()` method are `ITKrMM`, `wKSVD`, `ITKrMM_matlab` or `wKSVD_matlab`. The associated functions are resp. `ITKrMM()`, `wKSVD()`, `ITKrMM_matlab()` and `wKSVD_matlab()`.

The input parameters are:

- `Patchsize`: (optional, int) The patch width,
- `K`: (optional, int) The dictionary size (incl. low-rank component),
- `L`: (optional, int) The number of low-rank components to estimate,
- `S`: (optional, int) The sparsity level,
- `Nit`: (optional, int) The number of iterations for the dictionary estimation.
- `Nit_lr`: (optional, int) The number of iterations for the low-rank estimation.

The output dictionary stores the following informations:

- `dico`: The dictionary,
- `E`: The evolution of the error,
- `time`: the execution time (in sec.),
- `PCA_info`: in case of 3D data with PCA pre-processing, it stores info about PCA.

## BPFA

Beta Process Factor Analysis algorithm (see [BXZC+12]).

As for wKSVD and ITKrMM, BPFA is based on a Matlab code from Zhengming Xing (these codes were broadcasted without any license). The python code just calls it, so matlab should be in the path system so that the `matlab` command could be called from the command line.

The method to give to the `restore()` method is `BPFA_matlab`. The associated function is resp. `BPFA_matlab()`.

The input parameters are:

- `Patchsize`: (optional, int) The patch width,
- `K`: (optional, int) The dictionary size,
- `step`: (optional, int) That's the pixel space between two consecutive patches (if 1, full overlap),
- `Nit`: (optional, int) The number of iterations for the dictionary estimation.

The output dictionary stores the following informations:

- `dico`: The dictionary,
- `time`: the execution time (in sec.),
- `PCA_info`: in case of 3D data with PCA pre-processing, it stores info about PCA.

### 1.6.4 That's all folks !

This was the main content of the documentation. Congrats, you understood 90% of this library :)

### 1.6.5 References

## 1.7 Data Visualization

### 1.7.1 Visualizing the data

As for the HyperSpy data, the data objects *Stem2D* and *Stem3D* include a *plot()* method to display the data.

In addition to this basic function, the *Stem3D* class implements four other functions:

- *plot\_sum()* which displays the sum of the 3D data along the last axis,
- *plot\_as2D()* which displays the data as 2D data (the navigation direction is the “channel” axis while the data are spatial),
- *plot\_as1D()* which displays the data as 1D data (the navigation directions are the spatial axes while the data is a spectrum, this is the behavior of the default *plot()* function),
- *plot\_roi()* which considers the data as 1D and enable the user to mean the data over a spatial region-of-interest.

### 1.7.2 Visualizing the scan sampling mask

As explained in *The first basic object is the scan*, a Scan object can be represented with its sampling mask *M* defined as

$$M_i = \begin{cases} 1, & \text{if pixel \# } i \text{ is acquired} \\ 0, & \text{otherwise} \end{cases}$$

This representation suffer from information deficiency, but is interesting to study the acquired pixels repartition. This sampling mask which shape is the same as the spatial shape can be obtained using the *get\_mask()* method of *Scan*. This one can also be plotted using the method *plot()*.

## SYSTEM DEVELOPPER GUIDE

Well, for now, this small library is developed by myself. I don't know yet how much this could be usefull. However, if someone is interested to help me, please let me know at [etienne\[dot\]monier\[at\]enseeiht\[dot\]fr](mailto:etienne[dot]monier[at]enseeiht[dot]fr).

This section just give some informations about the children classes of *Stem2D* and *Stem3D* that helps me to develop algorithms.

### 2.1 Dev data objects

Basically, a signal processing algorithm development aims at testing some method on synthetic (i.e. noise-free) data that has been manually degraded. As the truth image is known, metrics can be computed to test and compare the method.

To that end, two data objects *Dev2D* and *Dev3D* have been developed. These are children classes from *Stem2D* and *Stem3D* (themselves are children of the basic data structure *AbstractStem*).

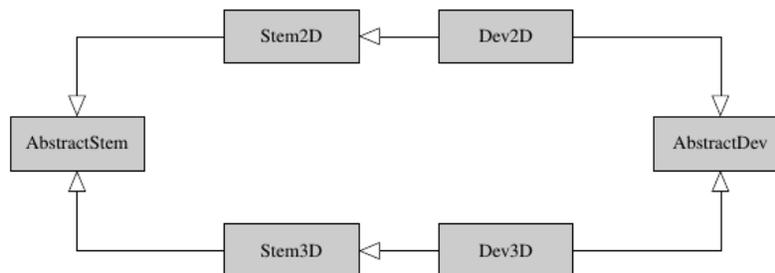


Fig. 1: A simple UML diagram.

These objects basically work as non-dev data objects:

- they are initialized with data and a Scan object,
- loading them can be done with the same functions as for non-dev data,
- they can be corrected with a configuration file,
- they can be reconstructed using the basic *restore()* of *AbstractStem*,
- they can be plotted with the same tools.

Their difference is that:

- noise can be added,

- the results are reproducible,
- new noise can be drawn whenever you want,
- the *Dev3D* allows you to consider the PCA-transformed data as the base data (this is useful for developing 3D restoration algorithm).

### 2.1.1 Initialize Dev data

#### Manually

The Dev data objects could be initialized manually with the same arguments as for *Stem2D* and *Stem3D* classes, i.e.:

- `hsdata`, `scan` and `verbose` for *Stem2D*,
- `hsdata`, `scan`, `PCA_transform`, `PCA_th` and `verbose` for *Stem3D*,

In addition to these arguments, a required input is `key` which is a small descriptive keyword to help referencing. Other optional inputs are:

- `modif_file`: an configuration file which is sent to correction function,
- `sigma`: the desired noise standard deviation in case additional noise is desired,
- `seed`: the noise seed to have reproducible data,
- `normalized`: if set to `True`, the data are normalized at initialization.

```
>>> stem2d_data = pystem.load_example('HR-sample', 2)
Reading configuration file ...
Generating data ...
Creating STEM acquisition...
Correcting STEM acquisition...
>>> scan_shape = stem2d_data.scan.shape
>>> scan = pystem.Scan.random(shape=scan_shape, ratio=0.5)
>>> dev_data = pystem.Dev2D('my-dev-data', hsdata=stem2d_data.hsdata, scan=scan,
↳sigma=0.5, seed=0)
Creating STEM acquisition...
>>> dev_data
<Dev2D, title: HR-sample, dimensions: (|113, 63), sampling ratio: 0.50>
```

#### With load functions

The `load_file()`, `load_key()` and `load_example()` functions also enable to load development data. To that end, the user just has to use the `dev` input which is a dictionary. This dictionary should store the desired inputs:

- for 2D data: `modif_file`, `sigma`, `seed` and `normalized`
- for 3D data: `PCA_transform`, `PCA_th`, `modif_file`, `sigma`, `seed` and `normalized`

```
>>> dev = {'sigma': 0.5, 'seed': 0}
>>> pystem.load_example('HR-sample', 2, dev=dev, scan_ratio=0.5, scan_seed=1)
Reading configuration file ...
Generating data ...
Creating STEM acquisition...
Correcting STEM acquisition...
<Dev2D, title: HR-sample, dimensions: (|113, 63), sampling ratio: 0.50>
```

Note that in case the development data is loaded, the key would be the name of the `.conf` file (e.g. for `my-conf-file.conf`, the key would be `my-conf-file`).

## 2.1.2 Some words about data storage

Contrary to `Stem2D` and `Stem3D` objects, development objects work with numpy techniques (to generate the noise, add it, perform PCA) so that this is the central data to be stored in `Dev` objects.

More precisely, the data are stored twice or three times under the attributes:

- `data` which stores the noise-free data,
- `ndata` which stores the noisy data (in case `sigma` is `None` and no noise-corruption procedure was applied, this attribute is `None`),
- `hsdata` which stores the data as an `HyperSpy` data.

The last attribute only exist to send the data into restoration procedures. To display noisy or noise-free data, prefer the two first attributes.

## 2.1.3 Reproducibility and noise

Inside the data creation procedure, the random effects can come from the scan generation (in case of random initialization) or from the noise generation. For both situations, the seed can be set to get reproducible results. Indeed, the scan seed can be set in the load functions with its `scan_seed` parameter or directly calling the `random()` with its `seed` parameter. The noise seed can be set itself with the `seed` attribute.

**Caution:** The seed values are set for the **startup** procedures. When this is set for the `Dev2D` class, this seed is set just before drawing the noise matrix **for the first time**. If the user wants to draw another noise matrix, the seed will not be the same any more. This is the same for the random scans.

To generate a new noise matrix, just use the `set_ndata()`. To generate a new random scan, just re-run the `random()` method without the `seed` argument.

## 2.1.4 How PCA works for `Dev3D`

At the `Stem3D` initialization, the 3D data are fully stored as an `HyperSpy` data. When the user wants to reconstruct the data, the usual `PCA_transform` and `PCA_th` arguments can be given. This is passed into the reconstruction algorithms which perform PCA as pre and post-processing steps.

In the case of the `Dev3D` class, these parameters are given at initialization. If `PCA_transform` is `False`, then the full data is stored into the `data` attribute. The user could choose to perform PCA by giving `PCA_transform` into the `restore()` as an argument.

```
>>> dev = {'sigma': 0.5, 'PCA_transform': False}
>>> data = pystem.load_example('HR-sample', 3, dev=dev)
Reading configuration file ...
Generating data ...
Creating STEM acquisition...
Correcting STEM acquisition...

>>> data.data.shape
(63, 115, 1510)
```

(continues on next page)

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```
>>> outdata, info = data.restore()
Restoring the 3D STEM acquisition...
-- Interpolation reconstruction algorithm --
- PCA transformation -
Dimension reduced from 1510 to 4.
Estimated sigma^2 is 2.76e-01.
Done in 1.27s.
-
Done in 0.05s.
---
```

```
>>> info['PCA_info']['H'].shape # The PCA basis used for restoration
(1510, 4)
```

In the case of `True PCA_transform` at initialization, a PCA procedure is executed at initialization and the data (and possibly `ndata`) data are reduced in the last axis direction. Additional information is stored in the `PCA_info` attribute. In such case, the user should use the `restore()` method without giving the `PCA_transform` argument.

```
>>> dev = {'sigma': 0.5, 'PCA_transform': True}
>>> data = pystem.load_example('HR-sample', 3, dev=dev)
Reading configuration file ...
Generating data ...
Creating STEM acquisition...
Correcting STEM acquisition...
- PCA transformation -
Dimension reduced from 1510 to 290.
Estimated sigma^2 is 1.43e+03.
Done in 1.27s.
-
```

```
>>> outdata, info = data.restore()
Restoring the 3D STEM acquisition...
-- Interpolation reconstruction algorithm --
Done in 11.12s.
---
```

```
>>> 'PCA_info' in info
False
```

**Note:** The default behavior for the `restore()` `PCA_transform` argument is to take the logical not of the `PCA_transform` argument given at initialization. If the `Dev3D` class has been initialized without PCA, then a PCA is applied by default before restoration. If PCA has been required at initialization, then no PCA will be applied at restoration.

Yet, the user can explicitly ask for additional PCA (which is stupid, I agree) or for no PCA at all. Let's explain it clearly: **if you don't want PCA, say it at initialization and at restoration.**

**Caution:** The two examples above show something important as the estimated PCA threshold is 3 in the case where `PCA_transform` is not given at initialization and 290 otherwise. This means that both orders do not have the same effects.

If `PCA_transform` is `True` at initialization, the PCA transformation is performed **before** adding noise so that

the signal is clear enough to have a high threshold. Besides, the noise is added **to the data in PCA space**.

If `PCA_transform` is `False` at initialization but `True` at restoration, the noise is added to the full dimension data. Besides, the PCA is applied to *noised* data so that few principle components get more powerful than noise and the threshold drops.

To handle easily direct and inverse PCA transformations, two methods are given: `direct_transform()` and `inverse_transform()`. They both allow the user to **perform the same PCA direct/inverse transformation as for the :class:`~.dev.Dev3D` initialization method**. These methods accept HyperSpy as numpy data.

These methods incorporate also normalization procedure inside. This means that the `direct_transform()` method performs also centering and normalization whereas the `inverse_transform()` inject the standard deviation and the mean back.

```
>>> import pystem

# Case with non-PCA-initialized object
>>> dev = {'sigma': 0.5, 'PCA_transform': False, 'normalize': False}
>>> data = pystem.load_example('HR-sample', 3, dev=dev)
>>> direct_data = data.direct_transform(data.data) # Performing direct_
↳transformation to data
>>> inverse_data = data.inverse_transform(data.data) # Performing inverse_
↳transformation to data
>>> import numpy.testing as npt # This is to check arrays are equal
>>> npt.assert_allclose(data.data, direct_data) # Equal
>>> npt.assert_allclose(data.data, inverse_data) # Equal

>>> dev = {'sigma': 0.5, 'PCA_transform': False} # Non-normalized here
>>> data = pystem.load_example('HR-sample', 3, dev=dev)
>>> direct_data = data.direct_transform(data.data)
>>> inverse_data = data.inverse_transform(direct_data)
>>> npt.assert_allclose(data.data, direct_data) # Error because of normalization
>>> npt.assert_allclose(data.data, inverse_data) # Equal: direct, then inverse is_
↳identity :)

# Case with PCA-initialized object
>>> dev = {'sigma': 0.5, 'PCA_transform': True}
>>> data = pystem.load_example('HR-sample', 3, dev=dev)
>>> inverse_data = data.inverse_transform(data.data)
>>> direct_data = data.direct_transform(inverse_data)
>>> npt.assert_allclose(data.data, direct_data) # Equal: direct, then inverse is_
↳still identity :)

>>> data.data.shape # PCA shape
(63, 115, 290)
>>> inverse_data.shape # True image shape
(63, 115, 1510)
>>> direct_data.shape # PCA shape
(63, 115, 290)
```

## 2.1.5 One word about visualization

The development data visualization works as for non-dev classes. Yet, development data visualization methods accept an additional argument which is `noised`. This optional argument that is `False` by default sets which data should be displayed (noise-free data by default or noisy data).

## 2.2 List of todos:

---

**Todo:** Maybe enable PCA\_th in config file for 3D data.

---

(The [original entry](#) is located in `/home/docs/checkouts/readthedocs.org/user_builds/pystem/checkouts/latest/pystem/dataset.py:docstring` of `pystem.dataset.load_file`, line 44.)

## FULL PYSTEM API DOCUMENTATION

PyStem module.

Description here.

### 3.1 signals module

This package defines all sort of classes to handle data for pystem.

#### 3.1.1 The Scan class

**class** `pystem.signals.Scan` (*shape, path, ratio=1*)

Scan pattern class.

This class stores the data spatial shape and two copies of the scan pattern. One of these copies is the initial scan pattern which is given to the class. At the same time, a `ratio` argument can be given to keep only a portion of the available samples. See Notes for more details.

##### Variables

- **shape** (*2-length tuple*) – The spatial shape (m, n) where m is the number of rows and n is the number of columns.
- **path** (*numpy array*) – The sampling path to be used in the study.
- **path\_0** (*numpy array*) – The initial sampling path to be kept in case the ratio is changed.
- **ratio** (*float*) – The current ratio value such that `path` has size `ratio*m*n`. This attribute can be changed with automatic update of `path`.

---

**Note:** Consider only `r*m*n` pixels hve been sampled, then the `path_0` attribute has shape `(r*m*n, )` and its elements lay between 0 and `m*n-1`.

Meanwhile, if the user wants to consider only `ratio` percent of the samples, the `ratio` argument should be given. The `path` attribute would then have shape `(ratio*m*n, )`. In such case, `path_0[:ratio*m*n]` will be equal to `path`. Be aware that `ratio`ratio`` should be lower than `ratio`r`.

Each element of these arrays is the pixel index in row major order. To recover the row and column index array, type the following commands.

**::code:** `i = path // n`  
`j = path % n`

---

`__init__` (*shape, path, ratio=1*)

Scan pattern constructor.

**Parameters**

- **shape** (*(m, n) tuple*) – The spatial shape where m is the number of rows and n is the number of columns.
- **path** (*tuple, numpy array*) – The sampling path. See class Notes for more detail.

**property ratio**

Ratio getter.

**Returns** The ratio property value.

**Return type** float

**classmethod from\_file** (*data\_file, ratio=1*)

Creates a scan pattern object from a data file (such as .dm3, .dm4 or npz).

In the case of a .npz file, this one should contain the :code:'m', :code:'n' and :code:'path' variables which are resp. the number of rows and columns and the path array.

Concerning the .dm3/.dm4 files, the data storage is specific to the LPS Lab (Orsay, France) implementation.

An additional argument :code:'ratio' allows you to select only a given ratio of the sampled pixels. This should lay between 0 (excl.) and 1.

**Parameters**

- **data\_file** (*str*) – The data file path.
- **ratio** (*optional, float*) – The ratio of sampled pixels. This should lay between 0 (excl.) and 1. Default is 1 for full sampling.

**Returns** The scan pattern.

**Return type** Scan object

**classmethod random** (*shape, ratio=1, seed=None*)

Creates a random scan pattern object.

**Parameters**

- **shape** (*(m, n) tuple*) – The data spatial shape.
- **ratio** (*optional, float*) – The ratio of sampled pixels. It should lay between 0 (excluded) and 1. Default is 1 for full sampling.
- **seed** (*optional, int*) – Seed for random sampling. Default is None for random seed.

**Returns** The scan pattern.

**Return type** Scan object

**get\_mask** ()

Returns the sampling mask.

The sampling mask is boolean and True is for sampled pixels.

**Returns** **mask** – The sampling mask.

**Return type** (m, n) numpy array

**plot()**  
Plots the sampling mask.  
White (resp. black) pixels are sampled (resp. non-sampled).

### 3.1.2 The Stem classes

**class** `pystem.signals.AbstractStem` (*hsdata*, *scan=None*, *verbose=True*)  
Abstract STEM acquisition class.

This is an *abstract* class, which mean you can not instantiate such object.

It defines the structure for a STEM acquisition object.

#### Variables

- **hsdata** (*hs BaseSignal*) – The acquired STEM data hyperspy object.
- **scan** (*Scan object*) – The sampling scan object associated with the data.
- **verbose** (*bool*) – If True, information is sent to standard output. Default is True.

**\_\_init\_\_** (*hsdata*, *scan=None*, *verbose=True*)  
AbstractStem constructor.

#### Parameters

- **hsdata** (*hs BaseSignal*) – The acquired STEM data hyperspy object.
- **scan** (*optional, Scan object*) – The sampling scan object associated with the data. Default is None for full sampling.
- **verbose** (*bool*) – If True, information is sent to standard output. Default is True.

**correct** (*rows=slice(None, None, None)*, *cols=slice(None, None, None)*, *bands=slice(None, None, None)*, *dpixels=None*)  
Correct deffective data.

Deffective data correspond to:

1. Rows to remove at the begging or at the end of the image.
2. Columns to remove at the begging or at the end of the image.
3. Bands to remove at the begging or at the end of the image.
4. Located dead pixels at the center of the image.

In the cases 1, 2 or 3, the rows and columns are purely removed. The dead pixels are filled with the mean over a neighbourhood.

A `slice` object for an object A of length L defines a continuous portion of A such as `A[n_1]`, `A[n_1+1]`, ..., `A[n_2-1]` with `n_1 < n_2`. In such case, a slice object definition is `slice(n_1, n_2)`. If `n_1` is 0, then use `slice(None, n_2)`. If `n_2` is L use `slice(n_1, None)`. Last, if all the elements of A should be kept, use `slice(None)`.

#### Parameters

- **rows** (*slice object*) – The range of rows to keep.
- **cols** (*slice object*) – The range of columns to keep.
- **bands** – The range of bands to keep.
- **dpixels** (*list*) – The positions of the dead pixels.

**correct\_fromfile** (*file*)

**abstract restore** ()  
Restores corrupted data.

**plot** ()  
Plots the masked data.

**class** `system.signals.Stem2D` (*hsdata*, *scan=None*, *verbose=True*)  
2D image STEM acquisition.

This defines a 2D STEM image with its associated sampling scan.

#### Variables

- **hsdata** (*hs BaseSignal*) – The acquired STEM data hyperspy object.
- **scan** (*Path object*) – The sampling scan object associated with the data.

**restore** (*method='interpolation'*, *parameters={}*, *verbose=True*)  
Restores the acquisition.

It performs denoising in the case of full scan and performs reconstruction in case of partial sampling.

**class** `system.signals.Stem3D` (*hsdata*, *scan=None*, *verbose=True*)  
3D image STEM acquisition.

This defines a 3D STEM image with its associated sampling scan.

#### Variables

- **hsdata** (*hs BaseSignal*) – The acquired STEM data hyperspy object.
- **scan** (*Path object*) – The sampling scan object associated with the data.

**restore** (*method='interpolation'*, *parameters={}*, *PCA\_transform=True*, *PCA\_th='auto'*, *verbose=True*)  
Restores the acquisition.

It performs denoising in the case of full scan and performs reconstruction in case of partial sampling.

#### Parameters

- **PCA\_transform** (*optional, bool*) – Enables the PCA transformation if True, otherwise, no PCA transformation is processed. Default is True.
- **PCA\_th** (*optional, int, str*) – The desired data dimension after dimension reduction. Possible values are 'auto' for automatic choice, 'max' for maximum value and an int value for user value. Default is 'auto'.

**plot\_sum** ()  
Shows the sum of the data along the last axis.

**plot\_as2D** ()  
Implements the HypersSpy tool to visualize the image for a given band.

**plot\_as1D** ()  
Implements the HypersSpy tool to visualize the spectrum for a given pixel.

**plot\_roi** ()  
Implements the Hyperspy tool to analyse regions of interest.

## 3.2 dev module

This module defines the basic stem acquisitions objects used for processing. These objects are:

1. The 3D spectrum-image,
2. The 2D HAADF image,

**class** `pystem.dev.AbstractDev` (*key, data, mask=None, sigma=None, seed=None, normalize=True, verbose=True*)

Abstract Dev acquisition class.

This is an *abstract* class, which mean you can not instantiate such object.

It defines the structure for a Dev acquisition object.

**key: str** 1-word description of the Dev2D image.

**data: (m,n) or (m, n, l) numpy array** The Dev2D image data before the noise step. Its dimension is (m,n).

**ndata: (m,n) or (m, n, l) numpy array** The noised Dev2D image. If `snr` is `None`, `ndata` is `None`. Its dimension is (m,n).

**sigma: float** The noise standard deviation.

**seed: optional, int** The random noise matrix seed.

**normalize: bool** If `:code:normalize'` is `True`, the data will be centered and normalize before the corruption steps.

**mean\_std: None, 2-tuple** It stores the data mean and std in case `normalize` is `True`.

**verbose: bool** If `True`, information will be displayed. Default is `True`.

**\_\_init\_\_** (*key, data, mask=None, sigma=None, seed=None, normalize=True, verbose=True*)  
AbstractDev constructor.

### Parameters

- **key** (*str*) – 1-word description of the Dev2D image. Generally, it's common to the stem acquisition object.
- **data** (*(m, n) or (m, n, l) numpy array*) – The noise-free image data.
- **mask** (*(m, n) numpy array*) – The sampling mask.
- **sigma** (*optional, None, float*) – The desired standard deviation used to model noise. Default is `None` for no additional noise.
- **seed** (*optional, None, int*) – The random noise matrix seed. Default is `None` for no seed initialization.
- **normalize** (*optional, bool*) – If `:code:normalize'` is `True`, the data will be centered and normalize before the corruption steps. Default is `True`.
- **verbose** (*optional, bool*) – If `True`, information will be displayed. Default is `True`.

**property seed**  
seed property getter.

**property sigma**  
sigma property getter.

**set\_ndata** ()  
Constructs the noised data.

It is also used to draw a new noise matrix.

**class** `system.dev.Dev2D` (*key*, *hsdata*, *scan=None*, *modif\_file=None*, *sigma=None*, *seed=None*, *normalize=True*, *verbose=True*)

Dev2D Class.

#### Variables

- **key** (*str*) – 1-word description of the Dev2D image.
- **hsdata** (*Signal2D hyperspy data*) – The hyperspy Signal2D image. Its dimension is denoted (m,n). This is used to communicate with the parent class.
- **data** (*(m,n) numpy array*) – The Dev2D image data before the noise step. Its dimension is (m,n).
- **ndata** (*(m,n) numpy array*) – The noised Dev2D image. If `snr` is `None`, `ndata` is `None`. Its dimension is (m,n).
- **scan** (*optional, Scan object*) – The sampling scan object associated with the data. Default is `None` for full sampling.
- **sigma** (*float*) – The noise standard deviation.
- **seed** (*optional, int*) – The random noise matrix seed.
- **normalize** (*bool*) – If `:code:normalize` is `True`, the data will be centered and normalized before the corruption steps.
- **mean\_std** (*None, 2-tuple*) – It stores the data mean and std in case `normalize` is `True`.
- **verbose** (*bool*) – If `True`, information will be displayed. Default is `True`.

**\_\_init\_\_** (*key*, *hsdata*, *scan=None*, *modif\_file=None*, *sigma=None*, *seed=None*, *normalize=True*, *verbose=True*)

SpectrumImage constructor.

#### Parameters

- **key** (*str*) – 1-word description of the Dev2D image. Generally, it's common to the stem acquisition object.
- **hsdata** (*Signal2D hyperspy data*) – The noise-free Dev2D image data. Its dimension is denoted (m,n).
- **scan** (*optional, None, Scan object*) – The sampling scan object associated with the data. Default is `None` for full sampling.
- **modif\_file** (*optional, None, str*) – A `.conf` configuration file to remove rows, columns or dead pixels. Default is `None` for no modification.
- **sigma** (*optional, None, float*) – The desired standard deviation used to model noise. Default is `None` for no additional noise.
- **seed** (*optional, None, int*) – The random noise matrix seed. Default is `None` for no seed initialization.
- **normalize** (*optional, bool*) – If `:code:normalize` is `True`, the data will be centered and normalized before the corruption steps. Default is `True`.
- **verbose** (*optional, bool*) – If `True`, information will be displayed. Default is `True`.

**restore** (*method='interpolation', parameters={}, verbose=None*)

**plot** (*noised=False*)

Plots the haadf image.

**Parameters noised** (*optional, bool*) – If True, the noised data is used. If False, the noise-free data is shown. Default is False.

**class** `system.dev.Dev3D` (*key, hsdata, scan=None, modif\_file=None, sigma=None, seed=None, normalize=True, PCA\_transform=False, PCA\_th='auto', verbose=True*)

Dev3D Class

### Variables

- **key** (*str*) – 1-word description of the Dev3D.
- **hsdata** (*Signal1D hyperspy data*) – The hyperspy Signal2D image. Its dimension is denoted (m,n). This is used to communicate with the parent class.
- **data** (*(m,n,l) numpy array*) – The Dev3D data before the noise step. Its dimension is (m,n,l).
- **ndata** (*(m,n,l) numpy array*) – The noised Dev3D data. If snr is None, ndata is None. Its dimension is (m,n,l).
- **snr** (*optional, float*) – The desired snr used for the noising step.
- **sigma** (*float*) – The noise standard deviation.
- **seed** (*optional, int*) – The random noise matrix seed.
- **normalize** (*bool*) – If normalize is True, the data will be centered and normalize before the corruption steps.
- **PCA\_transform** (*bool*) – If PCA\_transformed is True, a PCA transformation has been applied to the data.
- **PCA\_info** (*None, dictionary*) – If PCA\_transformed is True, PCA\_info contains informations about the reduction. Otherwise, it is None.
- **PCA\_operator** (*PcaHandler*) – The PCA operator.
- **verbose** (*bool*) – If True, information will be displayed. Default is True.

**\_\_init\_\_** (*key, hsdata, scan=None, modif\_file=None, sigma=None, seed=None, normalize=True, PCA\_transform=False, PCA\_th='auto', verbose=True*)

Dev3D `__init__` function.

### Parameters

- **key** (*str*) – 1-word description of the Dev3D image. Generally, it's common to the stem acquisition object.
- **hsdata** (*Signal1D hyperspy data*) – The noise-free Dev3D image data. Its dimension is denoted (m,n, l).
- **scan** (*optional, None, Scan object*) – The sampling scan object associated with the data. Default is None for full sampling.
- **modif\_file** (*optional, None, str*) – A .conf configuration file to remove rows, columns or dead pixels. Default is None for no modification.
- **sigma** (*optional, None, float*) – The desired standard deviation used to model noise. Default is None for no additional noise.
- **seed** (*optional, None, int*) – The random noise matrix seed. Default is None for no seed initialization.
- **normalize** (*optional, bool*) – If `normalize` is True, the data will be centered and normalize before the corruption steps. Default is True.

- **PCA\_transform** (*optional, bool*) – If `PCA_transformed` is `True`, a PCA transformation is applied to the data. Default is `False`.
- **PCA\_th** (*optional, str, int*) – The desired data dimension after dimension reduction. Possible values are:
  - ‘auto’ for automatic choice,
  - ‘max’ for maximum value
  - an int value for user value.
 Default is ‘auto’.
- **verbose** (*optional, bool*) – If `True`, information will be displayed. Default is `True`.

**direct\_transform** (*data*)

Applies the Dev3D PCA transformation and normalization steps to data.

**Parameters data** (*(m, n, l) numpy array, hs image*) – Data whose shape is the same as `self.data`.

**inverse\_transform** (*data*)

Applies the Dev3D PCA inverse transformation and inverse normalization steps to `spim`.

**Parameters data** (*(m, n, l) numpy array, hs image*) – Data whose shape is the same as `self.data`.

**restore** (*method='interpolation', parameters={}, PCA\_transform=None, PCA\_th='auto', verbose=None*)

**show\_sum** (*noised=False*)

Shows the sum of the data along the last axis.

**Parameters noised** (*optional, bool*) – If `True`, the noised data is used. If `False`, the noise-free data is shown. Default is `False`.

**plot\_as2D** (*noised=False*)

Implements the Hyperspy tool to visualize the image for a given band.

**Parameters noised** (*optional, bool*) – If `True`, the noised data is used. If `False`, the noise-free data is shown. Default is `False`.

**plot\_as1D** (*noised=False*)

Implements the Hyperspy tool to visualize the spectrum for a given pixel.

**Parameters noised** (*optional, bool*) – If `True`, the noised data is used. If `False`, the noise-free data is shown. Default is `False`.

**plot\_roi** (*noised=False*)

Implements the Hyperspy tool to analyse regions of interest.

**Parameters noised** (*optional, bool*) – If `True`, the noised data is used. If `False`, the noise-free data is shown. Default is `False`.

### 3.3 dataset module

This module defines important tools to import data from dataset.

### 3.3.1 Data path functions

`pystem.dataset.read_data_path()`

Read the saved data folder path.

The pystem library proposes to store all data in a particular directory with associated configuration files. This folder is saved in pystem. To access to this folder path, use this function.

If no data path is saved, the function returns `None`. Else, the path is returned.

**Returns** `None` is returned if no path is saved. Else, the data path is returned.

**Return type** `None, str`

`pystem.dataset.set_data_path(path)`

Sets the saved data folder path.

The pystem library proposes to store all data in a particular directory with associated configuration files. This folder is saved in pystem. To set to this folder path, use this function.

A boolean is returned to confirm that the change is effective.

**Parameters** `path (str)` – The desired data path.

**Returns** If the data path has really been changed, the function returns `True`. Else, it returns `False`.

**Return type** `bool`

### 3.3.2 Load functions

`pystem.dataset.load_file(file, ndim, scan_ratio=1, scan_seed=None, dev=None, verbose=True)`

This function loads a STEM acquisition based on a configuration `.conf` file path.

The number of dimensions `ndim` should also be given.

The Path is generated from a scan file given in the configuration file or is randomly drawn. Whatever the case, the Scan object `ratio` property can be set through the `scan_ratio` argument. Additionally, in the case where no file is provided for the scan pattern, use the `scan_seed` argument to have reproducible data.

The function allows the user to ask for development data by setting the `dev` argument. If `dev` is `None`, then the usual `Stem2D` and `Stem3D` classes are returned. If `dev` is a dictionary, then `Dev2D` and `Dev3D` classes are returned. This dictionary could contain additional class arguments such as:

- `snr`, `seed` and `normalized` for `Dev2D`,
- `snr`, `seed`, `normalized`, `PCA_transformed` and `PCA_th` for `Dev3D`.

#### Parameters

- **file** (`str`) – The configuration file path.
- **ndim** (`int`) – The data dimension. Should be 2 or 3.
- **scan\_ratio** (`optional, float`) – The Path object ratio. Default is 1.
- **scan\_seed** (`int`) – The seed in case of random scan initialization. Default is `None` for random seed.
- **dev** (`optional, None, dictionary`) – This arguments allows the user to ask for development data. If this is `None`, usual data is returned. If this argument is a dictionary, then development data will be returned and the dictionary will be given to the data constructors. Default is `None` for usual data.

- **verbose** (*optional, bool*) – If True, information will be sent to standard output.. Default is True.

**Returns** The pystem data.

**Return type** *Stem2D, Stem3D, Dev2D, Dev3D*

---

**Todo:** Maybe enable PCA\_th in config file for 3D data.

---

`pystem.dataset.load_key(key, ndim, scan_ratio=1, scan_seed=None, dev=None, verbose=True)`

This function loads a STEM acquisition based on a key.

A key is a string which can be:

- an example data name,
- the name of some data located in the pystem data path (which is defined with the `pystem.dataset.set_data_path()` function).

The key should always be the name of the configuration file without the suffix (.conf). As an example, if a configuration file located in the data folder is named my-sample.conf, then its data could be loaded with the my-sample key.

The number of dimensions `ndim` should also be given.

The Path is generated from a scan file given in the configuration file or is randomly drawn. Whatever the case, the Scan object `ratio` property can be set through the `scan_ratio` argument. Additionally, in the case where no file is provided for the scan pattern, use the `scan_seed` argument to have reproducible data.

The function allows the user to ask for development data by setting the `dev` argument. If `dev` is `None`, then the usual `Stem2D` and `Stem3D` classes are returned. If `dev` is a dictionary, then `Dev2D` and `Dev3D` classes are returned. This dictionary could contain additional class arguments such as:

- `snr`, `seed`, `normalized` and `verbose` for `Dev2D`,
- `snr`, `seed`, `normalized`, `PCA_transformed`, `PCA_th` and `verbose` for `Dev3D`.

This function only searches for the configuration file to use the `load_file` function afterwards.

#### Parameters

- **key** (*str*) – The data key.
- **ndim** (*int*) – The data dimension. Should be 2 or 3.
- **scan\_ratio** (*optional, float*) – The Path object ratio. Default is 1.
- **scan\_seed** (*int*) – The seed in case of random scan initialization. Default is `None` for random seed.
- **dev** (*optional, None, dictionary*) – This arguments allows the user to ask for development data. If this is `None`, usual data is returned. If this argument is a dictionary, then development data will be returned and the dictionary will be given to the data constructors. Default is `None` for usual data.
- **verbose** (*optional, bool*) – If True, information will be sent to standard output.. Default is True.

**Returns** The pystem data.

**Return type** *Stem2D, Stem3D, Dev2D, Dev3D*

## 3.4 pystem.tools subpackage

This introduces some tools for pystem.

### 3.4.1 pystem.tools.PCA module

This module implements tools to perform PCA transformation.

The main element is the **PcaHandler** class which is a user interface. It performs direct and inverse PCA transformation for 3D data.

**Dimension\_Reduction** is the background function which performs PCA while the **EigenEstimate** function improves the estimation of PCA eigenvalues.

#### The PcaHandler interface

```
class pystem.tools.PCA.PcaHandler (Y, mask=None, PCA_transform=True, PCA_th='auto', verbose=True)
```

Interface to perform PCA.

The PCA is applied at class initialization based on the input data. This same operation can be applied afterward to other data using the `direct` and `inverse` methods.

#### Variables

- **Y** ( $(m, n, l)$  *numpy array*) – Multi-band data.
- **Y\_PCA** ( $(m, n, PCA\_th)$  *numpy array*) – The data in PCA space.
- **mask** (*optional*,  $(m, n)$  *numpy array*) – Spatial sampling mask. Default is full sampling.
- **PCA\_transform** (*optional*, *bool*) – Flag that sets if PCA should really be applied. This is useful in some cases where PCA has already been applied. Default is True.
- **verbose** (*optional*, *bool*) – If True, information is sent to output.
- **H** ( $(l, PCA\_th)$  *numpy array*) – The subspace base.
- **Ym** ( $(m, n, l)$  *numpy array*) – Matrix whose spectra are all composed of the data spectral mean.
- **PCA\_th** (*int*) – The estimated data dimension.
- **InfoOut** (*dict*) – The dictionary containing additional information about the reduction. See Note.

---

**Note:** The InfoOut dictionary containing the three following keys:

1. 'H' which is the base of the reduced subspace. Its shape is  $(l, PCA\_th)$  where  $PCA\_th$  is the estimated data dimension.
  2. 'd' which is the evolution of the PCA-eigenvalues after estimation.
  3. 'PCA\_th' which is the estimated data dimension.
  4. 'sigma' which is the estimated Gaussian noise standard deviation.
  5. 'Ym' which is a  $(m, n, l)$  *numpy array* where the data mean over bands is repeated for each spatial location.
-

`__init__` (*Y*, *mask=None*, *PCA\_transform=True*, *PCA\_th='auto'*, *verbose=True*)  
PcaHandler constructor.

**Parameters**

- **Y** (*(m, n, l) numpy array*) – Multi-band data.
- **mask** (*(m, n) numpy array*) – Spatial sampling mask.
- **PCA\_transform** (*optional, bool*) – Flag that sets if PCA should really be applied. This is useful in some cases where PCA has already been applied. Default is True.
- **verbose** (*optional, bool*) – If True, information is sent to output.

**direct** (*X=None*)

Performs direct PCA transformation.

The input X array can be data to project into the PCA subspace or None. If input is None (which is default), the output will be simply self.Y\_PCA.

**Caution:** The input data to transform should have the same shape as the Y initial data.

**Parameters X** (*(m, n, l) numpy array*) – The data to transform into PCA space.

**Returns** Multi-band data in reduced space.

**Return type** (m, n, PCA\_th) numpy array

**inverse** (*X\_PCA*)

Performs inverse PCA transformation.

**Caution:** The input data to transform should have the same shape as the self.Y\_PCA transformed data.

**Parameters X\_PCA** (*(m, n, PCA\_th) numpy array*) – The data to transform into data space.

**Returns** Multi-band data after inverse transformation.

**Return type** (m, n, l) numpy array

## Background functions

`system.tools.PCA.Dimension_Reduction` (*Y*, *mask=None*, *PCA\_th='auto'*, *verbose=True*)

Reduces the dimension of a multi-band image.

**Parameters**

- **Y** (*(m, n, l) numpy array*) – The multi-band image where the last axis is the spectral one.
- **mask** (*optional, (m, n) numpy array*) – The spatial sampling mask filled with True where pixels are sampled. This is used to remove correctly the data mean. Default if a matrix full of True.
- **PCA\_th** (*optional, str, int*) – The PCA threshold. ‘auto’ for automatic estimation. ‘max’ to keep all components. An integer to choose the threshold.

- **verbose** (*optional, bool*) – Prints output if True. Default is True.

**Returns**

- (*m, n, PCA\_th*) *numpy array* – The data in the reduced subspace. Its shape is (m, n, PCA\_th) where PCA\_th is the estimated data dimension.
- *dict* – The dictionary containing additional information about the reduction. See Note.

---

**Note:** The InfoOut dictionary containing the three following keys:

1. ‘H’ which is the base of the reduced subspace. Its shape is (l, PCA\_th) where PCA\_th is the estimated data dimension.
  2. ‘d’ which is the evolution of the PCA-eigenvalues after estimation.
  3. ‘PCA\_th’ which is the estimated data dimension.
  4. ‘sigma’ which is the estimated Gaussian noise standard deviation.
  5. ‘Ym’ which is a (m, n, l) *numpy array* where the data mean over bands is repeated for each spatial location.
- 

`system.tools.PCA.EigenEstimate` (*l, Ns*)

Computes an estimate of the covariance eigenvalues given the sample covariance eigenvalues. The Stein estimator coupled with isotonic regression has been used here.

For more information, have a look at:

- 
- MESTRE, Xavier. Improved estimation of eigenvalues and eigenvectors of covariance matrices using their sample estimates. *IEEE Transactions on Information Theory*, 2008, vol. 54, no 11, p. 5113-5129.s

**Parameters**

- **l** (*numpy array*) – Sample eigenvalues
- **Ns** (*int*) – Number of observations

**Returns**

- *numpy array* – Estimated covariance matrix eigenvalues.
- *float* – Estimated Gaussian noise standard deviation.
- *int* – Estimated dimension of the signal subspace.

### 3.4.2 system.tools.FISTA module

This module implements interfacing tools for the FISTA algorithm.

For further informations about the FISTA algorithm, have a look at<sup>1</sup>.

**class** `system.tools.FISTA.FISTA` (*f, df, L, g, pg, shape, Nit=None, init=None, verbose=True*)  
 Fast Iterative Shrinkage-Thresholding Algorithm implementation.

**Variables**

- **f** (*function*) –  $C^{1,1}$  convex function.
- **df** (*function*) – derivative function of f.

---

<sup>1</sup> BECK, Amir et TBOULLE, Marc. A fast iterative shrinkage-thresholding algorithm for linear inverse problems. *SIAM journal on imaging sciences*, 2009, vol. 2, no 1, p. 183-202.

- **L** (*float*) – Lipschitz constant of *f*.
- **g** (*function*) – Non-smooth function.
- **pg** (*function*) – *g* proximal operator.
- **shape** (*tuple*) – The data shape.
- **Nit** (*None, int*) – Number of iteration. If *None*, the iterations will stop as soon as the functional no longer evolve. Default is *None*.
- **init** (*numpy array*) – Init point which shape is the same as the data. If *None*, a random initialization is drawn. Default is *None*.
- **verbose** (*bool*) – If *True*, process informations are sent to the output. Default is *True*.
- **Nit\_max** (*int*) – Maximum number of iterations.
- **tau** (*float*) – Descent step.
- **E** (*numpy array*) – Functional evolution across iterations.
- **lim** (*float*) – Controls the stop condition in case *Nit* is *None*. The smallest *lim*, the more iterations before stopping. *lim* is usually  $1e-4$ .

`__init__` (*f, df, L, g, pg, shape, Nit=None, init=None, verbose=True*)  
 Initialization function for FISTA.

**Parameters**

- **f** (*function*) –  $C^{1,1}$  convex function.
- **df** (*function*) – derivative function of *f*.
- **L** (*float*) – Lipschitz constant of *f*.
- **g** (*function*) – Non-smooth function.
- **pg** (*function*) – *g* proximal operator.
- **shape** (*tuple*) – The data shape.
- **Nit** (*None, int*) – Number of iteration. If *None*, the iterations will stop as soon as the functional no longer evolve. Default is *None*.
- **init** (*numpy array*) – Init point which shape is the same as the data. If *None*, a random initialization is drawn. Default is *None*.
- **verbose** (*bool*) – If *True*, process informations are sent to the output. Default is *True*.

**StopCriteria** (*n*)

This function computes a criteria that informs about the algorithm convergence at step *n*.

**Parameters** *n* (*int*) – Current step

**Returns** Value of the criteria.

**Return type** float

**StopTest** (*n*)

This function choose if iterations should be stopped at step *n*. If *Nit* is not *None*, it returns *True* as long as *n* is smaller than *Nit*. If *Nit* is *None*, it returns *True* as long as the functional is evolving fast.

**Parameters** *n* (*int*) – Current step.

**Returns** Should the iterations go on ?

**Return type** bool

**execute ()**

Method that executes the FISTA algorithm.

**Returns**

- *numpy array* – The optimum of the optimization problem.
- *dict* – Extra informations about convergence.

---

**Note:** Infos in output dictionary:

- *E*: Evolution of the functional along the iterations.
  - *time*: Execution time.
- 

### 3.4.3 pystem.tools.matlab\_interface module

This module defines an interface to run matlab codes from python.

`pystem.tools.matlab_interface.matlab_interface (program, dataDico)`

Interfaces a matlab code with python3.

The functions needs a **matlab program** to run and **input data** to be given to the matlab program.

The input data should be given in dictionary format where keys are the matlab variable names and values are the variable data.

**Parameters**

- **program** (*Path object*) – The program path.
- **dataDico** (*dict*) – The dico containing the data to give to the program.

**Returns** The data returned by the program.

**Return type** dict

---

**Note:** A matlab command *matlab* should be accessible in the command line to make this code work.

If this does not work, please be sure the `PATH` variable is perfectly set. For exemple, please add this to your `.bashrc` for Linux Users:

Listing 1: `.bashrc`

```
export PATH:$PATH:/path/to/matlab/bin
```

and for Windows users, please have a search about how to add a location into your path (this is a graphical task).

---

### 3.4.4 pystem.tools.dct module

This module defines some functions related to DCT decomposition including:

- direct and inverse normalized 2D DCT transform,
- direct and inverse band-by-band DCT transform for multi-band data.

## 2D transformations

`pystem.tools.dct.dct2d(a)`

Computes the 2D Normalized DCT-II.

**Parameters** **X** ( $(m, n)$  *numpy array*) – 2D image.

**Returns** DCT coefficient matrix.

**Return type**  $(m, n)$  *numpy array*

### Example

```
>>> from pystem.tools.dct import dct2d
>>> import scipy.misc
>>> face = scipy.misc.face()
>>> A = dct2d(face.sum(2))
```

`pystem.tools.dct.idct2d(a)`

Computes the 2D Normalized Inverse DCT-II.

**Parameters** **A** ( $(m, n)$  *numpy array*) – DCT coefficient matrix

**Returns** 2D image.

**Return type**  $(m, n)$  *numpy array*

### Example

```
>>> from pystem.tools.dct import dct2d, idct2d
>>> import scipy.misc
>>> face = scipy.misc.face()
>>> A = dct2d(face.sum(2))
>>> X = idct2d(A)
```

## Band-by-band transformations

`pystem.tools.dct.dct2d_bb(x, size=None)`

Computes the band-by-band 2D Normalized DCT-II

If the input X is a 3D data cube, the 2D dct will be computed for each 2D images staked along the 2nd axis.

### Parameters

- **X** ( $(l, m*n)$  or  $(m, n, l)$  *numpy array*) – 2D or 3D multi-band data. If the data has 3 dimensions, the last axis is for spectra. If the data is 2D, the first axis is for spectra.
- **size** (*optional*,  $(m, n)$  *tuple*) – This is the spatial size. This parameter is required only if input data are 2D.

**Returns** DCT coefficient matrix.

**Return type**  $(l, m*n)$  or  $(m, n, l)$  *numpy array*

### Example

```
>>> from pystem.tools.dct import dct2d_bb
>>> import scipy.misc
>>> face = scipy.misc.face()
>>> A = dct2d_bb(face)
```

`pystem.tools.dct.idct2d_bb` (*a*, *size=None*)

Computes the band-by-band inverse 2D Normalized DCT-II

If the input *a* is a 3D data cube, the 2D dct will be computed for each 2D images staked along the 2nd axis.

#### Parameters

- **A** (*(l, m\*n)* or *(m, n, l)* numpy array) – 2D or 3D multi-band data DCT decomposition. If the data has 3 dimensions, the last axis is for spectra. If the data is 2D, the first axis is for spectra.
- **size** (*optional, (m, n) tuple*) – This is the spatial size. This parameter is required only if input data are 2D.

**Returns** The image matrix.

**Return type** *(l, m\*n)* or *(m, n, l)* numpy array

### Example

```
>>> from pystem.tools.dct import dct2d_bb, idct2d_bb
>>> import scipy.misc
>>> import numpy.testing as npt
>>> face = scipy.misc.face()
>>> A = dct2d_bb(face)
>>> X = idct2d_bb(A)
>>> npt.assert_allclose(X, face, atol=1e-12)
```

## 3.4.5 pystem.tools.sec2str module

This small module only contain `sec2str`, which is a function to display time in human-readable format.

`pystem.tools.sec2str.sec2str` (*t*)

Returns a human-readable time str from a duration in s.

**Parameters** **t** (*float*) – Duration in seconds.

**Returns** Human-readable time str.

**Return type** str

### Example

```
>>> from pystem.tools.sec2str import sec2str
>>> sec2str(5.2056)
5.21s
>>> sec2str(3905)
'1h 5m 5s'
```

### 3.4.6 pystem.tools.metrics module

This module contains several metric functions.

`pystem.tools.metrics.SNR(xhat, xref)`

Computes the SNR metric.

**Parameters**

- **xhat** (*numpy array*) – The noised data.
- **xref** (*numpy array*) – The noise-free image.

**Returns** The SNR value in dB.

**Return type** float

`pystem.tools.metrics.NMSE(xhat, xref)`

Computes the normalized mean square metric.

**Parameters**

- **xhat** (*numpy array*) – The noised data.
- **xref** (*numpy array*) – The noise-free image.

**Returns** The NMSE value in dB.

**Return type** float

`pystem.tools.metrics.aSAD(xhat, xref)`

Computes the averaged Spectral Angle Distance metric.

The input data number of dimensions can be:

- 1: the data are spectra,
- 2: the data are matrices of shape (n, M),
- 3: the data are matrices of shape (m, n, M)

where M is the spectrum size.

**Parameters**

- **xhat** (*numpy array*) – The noised data.
- **xref** (*numpy array*) – The noise-free image.

**Returns** The SNR value in dB.

**Return type** float

### 3.4.7 pystem.tools.misc module

This module defines some miscellaneous functions.

`pystem.tools.misc.toslice(text=None, length=None)`

Parses a string into a slice.

Input strings can be eg. '5:10', ':10', '1:'. Negative limits are allowed only if the data length is given. In such case, input strings can be e.g. '1:-10'.

If no text not length is given, default slice is slice(None).

**Parameters**

- **text** (*optional, None, str*) – The input text to parse. Default is None.
- **length** (*None, int*) – The data length. This is not mandatory if no slice limit is negative. Default is None.

**Returns** The parsed slice object.

**Return type** slice

## 3.5 pystem.restore subpackage

This package implements a variety of reconstruction algorithms for 2D as 3D data.

These methods include:

- interpolation methods that are known to be fast but with low-quality results,
- regularized least-square methods which are a slower than interpolation but with higher quality,
- dictionary-learning methods which are very efficient at the price of long reconstruction procedures.

### 3.5.1 pystem.restore.interpolation module

This module implement the interpolate function which is an interface between 2D as 3D data and the interpolation function of scipy.

```
system.restore.interpolation.interpolate(Y, mask=None, method='nearest',
                                         PCA_transform=True, PCA_th='auto', verbose=True)
```

Implements data interpolation.

Three interpolation methods are implemented: nearest neighbor, linear interpolation and cubic interpolation.

Note that cubic interpolation is performed band-by-band in the case of 3D data while other methods perform in 3D directly.

#### Parameters

- **Y** (*(m, n) or (m, n, l) numpy array*) – Input data
- **mask** (*optional, None, (m, n) numpy array*) – Sampling mask. True for sampled pixel. Default is None for full sampling.
- **method** (*optional, 'nearest', 'linear' or 'cubic'*) – Interpolation method. Default is 'nearest'.
- **PCA\_transform** (*optional, bool*) – Enables the PCA transformation if True, otherwise, no PCA transformation is processed. Default is True.
- **PCA\_th** (*optional, int, str*) – The desired data dimension after dimension reduction. Possible values are 'auto' for automatic choice, 'max' for maximum value and an int value for user value. Default is 'auto'.
- **verbose** (*optional, bool*) – Indicates if information text is desired. Default is True.

#### Returns

- (*m, n*) or (*m, n, l*) *numpy array* – Interpolated data.
- *float* – Execution time (s).

### 3.5.2 system.restore.LS\_2D module

This module gathers regularized least square restoration methods adapted to 2D data.

The only method it implements for the moment is the **L1-LS** algorithm.

`system.restore.LS_2D.L1_LS (Y, Lambda, mask=None, init=None, Nit=None, verbose=True)`

L1-LS algorithm.

The L1-LS algorithm denoises or reconstructs an image possibly spatially sub-sampled in the case of spatially sparse content in the DCT basis. It is well adapted to periodic data.

This algorithms solves the following regularization problem:

$$\hat{\mathbf{x}} = \arg \min_{\mathbf{x} \in \mathbb{R}^{m \times n}} \frac{1}{2} \|(\mathbf{x} - \mathbf{y}) \cdot \Phi\|_F^2 + \lambda \|\mathbf{x}\Psi\|_1$$

where  $\mathbf{y}$  are the corrupted data,  $\Phi$  is a subsampling operator and  $\Psi$  is a 2D DCT operator.

**Caution:** It is strongly recommended to remove the mean before reconstruction. Otherwise, this value could be lost automatically by the algorithm in case of powerful high frequencies.

In the same way, normalizing the data is a good practice to have the parameter be low sensitive to data.

**These two operations are implemented in this function.**

#### Parameters

- **(m, n) numpy array (Y)** – An image which mean has been removed.
- **Lambda (float)** – Regularization parameter.
- **mask (optional, None, (m, n) numpy array)** – A sampling mask which is True if the pixel is sampled. Default is None for full sampling.
- **init (optional, None, (m, n, l) numpy array)** – The algorithm initialization. Default is None for random initialization.
- **Nit (optional, None, int)** – Number of iteration in case of inpainting. If None, the iterations will stop as soon as the functional no longer evolve. Default is None.
- **verbose (optional, bool)** – Indicates if information text is desired. Default is True.

#### Returns

- *(m, n) numpy array* – The reconstructed/denoised image.
- *dict* – A dictionary containing some extra info

---

**Note:** Infos in output dictionary:

- **E:** In the case of partial reconstruction, the cost function evolution over iterations.
  - **Gamma:** The array of kept coefficients (order is Fortran-style).
  - **nnz\_ratio:** the ratio `Gamma.size/(m*n)`.
-

### 3.5.3 system.restore.LS\_3D module

This module implements regularized least square restoration methods adapted to 3D data.

The two methods it gathers are

- **Smoothed SubSpace (3S) algorithm,**
- **Smoothed Nuclear Norm (SNN) algorithm.**

`system.restore.LS_3D.SSS` ( $Y$ ,  $\text{Lambda}$ ,  $\text{mask}=\text{None}$ ,  $\text{PCA\_transform}=\text{True}$ ,  $\text{PCA\_th}=\text{'auto'}$ ,  
 $\text{PCA\_info}=\text{None}$ ,  $\text{scale}=\text{1}$ ,  $\text{init}=\text{None}$ ,  $\text{Nit}=\text{None}$ ,  $\text{verbose}=\text{True}$ )

Smoothed SubSpace algorithm.

The 3S algorithm denoise or reconstructs a multi-band image possibly spatially sub-sampled in the case of spatially smooth images. It is well adapted to intermediate scale images.

This algorithm performs a PCA pre-processing operation to estimate:

- the data subspace basis  $\mathbf{H}$ ,
- the subspace dimension  $R$ ,
- the associated eigenvalues in decreasing order  $\mathbf{d}$ ,
- the noise level  $\hat{\sigma}$ .

After this estimation step, the algorithm solves the following regularization problem in the PCA space:

$$\hat{\mathbf{S}} = \arg \min_{\mathbf{S} \in \mathbb{R}^{m \times n \times R}} \frac{1}{2R} \|\mathbf{SD}\|_{\text{F}}^2 + \frac{\lambda}{2} \sum_{m=1}^R w_m |\mathbf{S}_{m,:}|_2^2$$

$$\text{s.t. } \frac{1}{R} |\mathbf{H}_{1:R}^T \mathbf{Y}_{\mathcal{I}(n)} - \mathbf{S}_{\mathcal{I}(n)}|_2^2 \leq \hat{\sigma}^2, \forall n \in \{1, \dots, m * n\}$$

where  $\mathbf{Y}$  are the corrupted data,  $\mathbf{D}$  is a spatial finite difference operator and  $\mathcal{I}$  is the set of all sampled pixels.

**Caution:** It is strongly recommended to perform PCA before running the algorithm core. This operation is integrated in this function.

In case this pre-processing step has already been done, set the `PCA_transform` parameter to `False` to disable the PCA step included in the `SSS` function. If `PCA_transform` is set to `False`, the `PCA_info` parameter is required.

#### Parameters

- **(m, n, 1) numpy array** ( $Y$ ) – A 3D multi-band image.
- **Lambda** (*float*) – Regularization parameter.
- **mask** (*optional, None, (m, n) numpy array*) – A sampling mask which is True if the pixel is sampled. Default is None for full sampling.
- **PCA\_transform** (*optional, bool*) – Enables the PCA transformation if True, otherwise, no PCA transformation is processed. Default is True.
- **PCA\_th** (*optional, int, str*) – The desired data dimension after dimension reduction. Possible values are ‘auto’ for automatic choice, ‘max’ for maximum value and an int value for user value. Default is ‘auto’.
- **PCA\_info** (*optional, dict*) – In case `PCA_transform` is `False`, some extra info should be given to `SSS`. The required keys for `PCA_info` are:

- 'd' which are the PCA eigenvalues.
- 'sigma' which is an estimate of the data noise std.
- **scale** (*optional, float*) – Scales the prox operator sphere radius. Should lay in ]0, +inf[. Default is 1.
- **init** (*optional, None, (m, n, l) numpy array*) – The algorithm initialization. Default is None for random initialization.
- **Nit** (*optional, None, int*) – Number of iteration in case of inpainting. If None, the iterations will stop as soon as the functional no longer evolve. Default is None.
- **verbose** (*optional, bool*) – Indicates if information text is desired. Default is True.

#### Returns

- (*m, n, l*) *numpy array* – The reconstructed/denoised multi-band image.
- *dict* – A dictionary containing some extra info

---

**Note:** Infos in output dictionary:

- E: in the case of partial reconstruction, the cost function evolution over iterations.
  - H : the basis of the chosen signal subspace
- 

#### References

Monier, E., Oberlin, T., Brun, N., Tencé, M., de Frutos, M., & Dobigeon, N. (2018). Reconstruction of Partially Sampled Multiband Images—Application to STEM-EELS Imaging. *IEEE Trans. Comput. Imag.*, 4(4), 585–598.

`system.restore.LS_3D.SNN` (*Y, Lambda, Mu, mask=None, PCA\_transform=True, PCA\_th='auto', init=None, Nit=None, verbose=True*)

Smoothed Nuclear Norm algorithm.

The SNN algorithm denoise or reconstructs a multi-band image possibly spatially sub-sampled in the case of spatially smooth images. It is well adapted to intermediate scale images.

This algorithm solves the following optimization problem:

$$\hat{\mathbf{X}} = \arg \min_{\mathbf{X} \in \mathbb{R}^{m \times n \times B}} \frac{1}{2} \|\mathbf{Y}_{\mathcal{I}} - \mathbf{X}_{\mathcal{I}}\|_{\text{F}}^2 + \frac{\lambda}{2} \|\mathbf{X}\mathbf{D}\|_{\text{F}}^2 + \mu \|\mathbf{X}\|_{*}$$

where  $\mathbf{Y}$  are the corrupted data,  $\mathbf{D}$  is a spatial finite difference operator and  $\mathcal{I}$  is the set of all sampled pixels.

This algorithm can perform a PCA pre-processing operation to estimate:

- the data subspace basis  $\mathbf{H}$ ,
- the subspace dimension  $R$ .

This is particularly usefull to reduce the data dimension and the execution time and to impose a data low-rank property.

**Caution:** It is strongly recommended to perform PCA before running the algorithm core. This operation is integrated in this function.

In case this pre-processing step has already been done, set the `PCA_transform` parameter to `False` to disable the PCA step included in the CLS function.

### Parameters

- **(m, n, l) numpy array (Y)** – A 3D multi-band image.
- **Lambda** (*float*) – Regularization parameter #1.
- **Mu** (*float*) – Regularization parameter #2.
- **mask** (*optional, None, (m, n) numpy array*) – A sampling mask which is True if the pixel is sampled. Default is None for full sampling.
- **PCA\_transform** (*optional, bool*) – Enables the PCA transformation if True, otherwise, no PCA transformation is processed. Default is True.
- **PCA\_th** (*optional, int, str*) – The desired data dimension after dimension reduction. Possible values are ‘auto’ for automatic choice, ‘max’ for maximum value and an int value for user value. Default is ‘auto’.
- **init** (*optional, None, (m, n, l) numpy array*) – The algorithm initialization. Default is None for random initialization.
- **Nit** (*optional, None, int*) – Number of iteration in case of inpainting. If None, the iterations will stop as soon as the functional no longer evolve. Default is None.
- **verbose** (*optional, bool*) – Indicates if information text is desired. Default is True.

### Returns

- (*m, n, l*) *numpy array* – The reconstructed/denoised multi-band image.
- *dict* – A dictionary containing some extra info

---

**Note:** Infos in output dictionary:

- **E**: in the case of partial reconstruction, the cost function evolution over iterations.
  - **H**: the basis of the chosen signal subspace
- 

### References

Monier, E., Oberlin, T., Brun, N., Tencé, M., de Frutos, M., & Dobigeon, N. (2018). Reconstruction of Partially Sampled Multiband Images—Application to STEM-EELS Imaging. *IEEE Trans. Comput. Imag.*, 4(4), 585–598.

## 3.5.4 pystem.restore.LS\_CLS module

This module implements regularized least square restoration methods adapted to 3D data.

The two methods it gathers are

- **Cosine Least Square (CLS) algorithm,**

- **Post-LS Cosine Least Square (Post\_LS\_CLS) algorithm.**

`system.restore.LS_CLS.CLS` (*Y*, *Lambda*, *mask=None*, *PCA\_transform=True*, *PCA\_th='auto'*,  
*init=None*, *Nit=None*, *verbose=True*)

Cosine Least Square algorithm

The CLS algorithm denoises or reconstructs a multi-band image possibly spatially sub-sampled in the case of spatially sparse content in the DCT basis. It is well adapted to periodic data.

This algorithm solves the following optimization problem:

$$\hat{\mathbf{X}} = \arg \min_{\mathbf{X} \in \mathbb{R}^{m \times n \times B}} \frac{1}{2} \|\mathbf{Y}_{\mathcal{I}} - \mathbf{X}_{\mathcal{I}}\|_{\mathbb{F}}^2 + \lambda \|\mathbf{X}\Psi\|_{2,1}$$

where  $\mathbf{Y}$  are the corrupted data,  $\mathbf{D}$  is a spatial finite difference operator and  $\mathcal{I}$  is the set of all sampled pixels.

This algorithm can perform a PCA pre-processing operation to estimate:

- the data subspace basis  $\mathbf{H}$ ,
- the subspace dimension  $R$ .

This is particularly useful to reduce the data dimension and the execution time and to impose a data low-rank property.

**Caution:** It is strongly recommended to perform PCA before running the algorithm core. This operation is integrated in this function.

In case this pre-processing step has already been done, set the **PCA\_transform** parameter to False to disable the PCA step included in the SSS function. If **PCA\_transform** is set to False, the **PCA\_info** parameter is required.

### Parameters

- **(m, n, l) numpy array** (*Y*) – A 3D multi-band image.
- **Lambda** (*float*) – Regularization parameter.
- **mask** (*optional, None, (m, n) numpy array*) – A sampling mask which is True if the pixel is sampled. Default is None for full sampling.
- **PCA\_transform** (*optional, bool*) – Enables the PCA transformation if True, otherwise, no PCA transformation is processed. Default is True.
- **PCA\_th** (*optional, int, str*) – The desired data dimension after dimension reduction. Possible values are ‘auto’ for automatic choice, ‘max’ for maximum value and an int value for user value. Default is ‘auto’.
- **init** (*optional, None, (m, n, l) numpy array*) – The algorithm initialization. Default is None for random initialization.
- **Nit** (*optional, None, int*) – Number of iteration in case of inpainting. If None, the iterations will stop as soon as the functional no longer evolve. Default is None.
- **verbose** (*optional, bool*) – Indicates if information text is desired. Default is True.

### Returns

- *(m, n, l) numpy array* – The reconstructed/denoised multi-band image.
- *dict* – A dictionary containing some extra info

---

**Note:** Infos in output dictionary:

- **E** : In the case of partial reconstruction, the cost function evolution over iterations.
  - **Gamma** : The array of kept coefficients (order is Fortran-style)
  - **nnz\_ratio** : the ratio  $\text{Gamma.size}/(m*n)$
  - **H**: the basis of the chosen signal subspace
- 

`system.restore.LS_CLS.Post_LS_CLS(Y, Lambda, mask=None, PCA_transform=True, PCA_th='auto', init=None, Nit=None, verbose=True)`

Post-Lasso CLS algorithm.

This algorithms consists in applying CLS to restore the data and determine the data support in DCT basis. A post-least square optimization is performed to reduce the coefficients bias.

#### Parameters

- **(m, n, l) numpy array** ( $Y$ ) – A 3D multi-band image.
- **Lambda** (*float*) – Regularization parameter.
- **mask** (*optional, None, (m, n) numpy array*) – A sampling mask which is True if the pixel is sampled. Default is None for full sampling.
- **PCA\_transform** (*optional, bool*) – Enables the PCA transformation if True, otherwise, no PCA transformation is processed. Default is True.
- **PCA\_th** (*optional, int, str*) – The desired data dimension after dimension reduction. Possible values are 'auto' for automatic choice, 'max' for maximum value and an int value for user value. Default is 'auto'.
- **init** (*optional, None, (m, n, l) numpy array*) – The algorithm initialization. Default is None for random initialization.
- **Nit** (*optional, None, int*) – Number of iteration in case of inpainting. If None, the iterations will stop as soon as the functional no longer evolve. Default is None.
- **verbose** (*optional, bool*) – Indicates if information text is desired. Default is True.

#### Returns

- *(m, n, l) numpy array* – The reconstructed/denoised multi-band image.
- *tuple* – A 2-tuple whose elements are the CLS and refitting information dictionaries.

---

**Note:** Infos in output dictionary:

- **E\_CLS** : In the case of partial reconstruction, the cost function evolution over iterations.
  - **E\_post\_ls** : In the case of partial reconstruction, the cost function evolution over iterations.
  - **Gamma** : The array of kept coefficients (order is Fortran-style)
  - **nnz\_ratio** : the ratio  $\text{Gamma.size}/(m*n)$
  - **H**: the basis of the chosen signal subspace
-

### 3.5.5 system.restore.DL\_ITKrMM module

This module implements the ITKrMM algorithm.

#### The ITKrMM algorithm

`system.restore.DL_ITKrMM.ITKrMM(Y, mask=None, PatchSize=5, K=128, L=1, S=20, Nit_lr=10, Nit=40, CLS_init=None, xref=None, verbose=True, PCA_transform=True, PCA_th='auto')`

ITKrMM restoration algorithm.

#### Parameters

- **Y** (*(m, n)* or *(m, n, l)* *numpy array*) – The input data.
- **mask** (*optional, None* or *(m, n)* *numpy array*) – The acquisition mask. Default is `None` for full sampling.
- **PatchSize** (*optional, int*) – The width (or height) of the patch. Default is 5.
- **K** (*optional, int*) – The dictionary dimension. Default is 128.
- **L** (*optional, int*) – The number of low rank components to learn. Default is 1.
- **S** (*optional, int*) – The code sparsity level. Default is 20.
- **Nit\_lr** (*optional, int*) – The number of iterations for the low rank estimation. Default is 10.
- **Nit** (*optional, int*) – The number of iterations. Default is 40.
- **CLS\_init** (*optional, dico*) – CLS initialization information. See Notes for details. Default is `None`.
- **xref** (*optional, (m, n)* or *(m, n, l)* *numpy array*) – Reference image to compute error evolution. Default is `None` for input Y data.
- **verbose** (*optional, bool*) – The verbose parameter. Default is `True`.
- **PCA\_transform** (*optional, bool*) – Enables the PCA transformation if `True`, otherwise, no PCA transformation is processed. Default is `True`.
- **PCA\_th** (*optional, int, str*) – The desired data dimension after dimension reduction. Possible values are `'auto'` for automatic choice, `'max'` for maximum value and an `int` value for user value. Default is `'auto'`.

#### Returns

- *(m, n)* or *(m, n, l)* *numpy array* – Restored data.
- *dict* – Additional informations. See Notes.

#### Notes

The algorithm can be initialized with CLS as soon as `CLS_init` is not `None`. In this case, `CLS_init` should be a dictionary containing the required `Lambda` key and eventually the `init` optional argument.

The output information keys are:

- `time`: Execution time in seconds.
- `lrc`: low rank component.

- dico: Estimated dictionary.
- E: Evolution of the error.

`system.restore.DL_ITKMM.ITKMM_matlab`(*Y*, *mask*, *PatchSize*=5, *K*=128, *L*=1, *S*=20, *Nit\_lr*=10, *Nit*=40, *CLS\_init*=None, *xref*=None, *verbose*=True, *PCA\_transform*=True, *PCA\_th*='auto')

ITKMM restoration algorithm with matlab code.

### Parameters

- **Y** (*(m, n)* or *(m, n, l)* numpy array) – The input data.
- **mask** (*optional*, None or *(m, n)* numpy array) – The acquisition mask. Default is None for full sampling.
- **PatchSize** (*optional*, *int*) – The width (or height) of the patch. Default is 5.
- **K** (*optional*, *int*) – The dictionary dimension. Default is 128.
- **L** (*optional*, *int*) – The number of low rank components to learn. Default is 1.
- **S** (*optional*, *int*) – The code sparsity level. Default is 20.
- **Nit\_lr** (*optional*, *int*) – The number of iterations for the low rank estimation. Default is 10.
- **Nit** (*optional*, *int*) – The number of iterations. Default is 40.
- **CLS\_init** (*optional*, *dico*) – CLS initialization information. See Notes for details. Default is None.
- **xref** (*optional*, *(m, n)* or *(m, n, l)* numpy array) – Reference image to compute error evolution. Default is None for input Y data.
- **verbose** (*optional*, *bool*) – The verbose parameter. Default is True.
- **PCA\_transform** (*optional*, *bool*) – Enables the PCA transformation if True, otherwise, no PCA transformation is processed. Default is True.
- **PCA\_th** (*optional*, *int*, *str*) – The desired data dimension after dimension reduction. Possible values are 'auto' for automatic choice, 'max' for maximum value and an int value for user value. Default is 'auto'.

### Returns

- *(m, n)* or *(m, n, l)* numpy array – Restored data.
- *dict* – Additional informations. See Notes.

### Notes

The algorithm can be initialized with CLS as soon as `CLS_init` is not None. In this case, `CLS_init` should be a dictionary containing the required `Lambda` key and eventually the `init` optional argument.

The output information keys are:

- `time`: Execution time in seconds.
- `lrc`: low rank component.
- `dico`: Estimated dictionary.
- `E`: Evolution of the error.

## The wKSVD algorithm

`system.restore.DL_ITKrMM.wKSVD_matlab` (*Y*, *mask*, *PatchSize=5*, *K=128*, *L=1*, *S=20*, *Nit\_lr=10*, *Nit=40*, *CLS\_init=None*, *xref=None*, *verbose=True*, *PCA\_transform=True*, *PCA\_th='auto'*)

wKSVD restoration algorithm with Matlab code.

### Parameters

- **Y** (*(m, n)* or *(m, n, l)* *numpy array*) – The input data.
- **mask** (*optional*, *None* or *(m, n)* *numpy array*) – The acquisition mask. Default is *None* for full sampling.
- **PatchSize** (*optional*, *int*) – The width (or height) of the patch. Default is 5.
- **K** (*optional*, *int*) – The dictionary dimension. Default is 128.
- **L** (*optional*, *int*) – The number of low rank components to learn. Default is 1.
- **S** (*optional*, *int*) – The code sparsity level. Default is 20.
- **Nit\_lr** (*optional*, *int*) – The number of iterations for the low rank estimation. Default is 10.
- **Nit** (*optional*, *int*) – The number of iterations. Default is 40.
- **CLS\_init** (*optional*, *dico*) – CLS initialization information. See Notes for details. Default is *None*.
- **xref** (*optional*, *(m, n)* or *(m, n, l)* *numpy array*) – Reference image to compute error evolution. Default is *None* for input *Y* data.
- **verbose** (*optional*, *bool*) – The verbose parameter. Default is *True*.
- **PCA\_transform** (*optional*, *bool*) – Enables the PCA transformation if *True*, otherwise, no PCA transformation is processed. Default is *True*.
- **PCA\_th** (*optional*, *int*, *str*) – The desired data dimension after dimension reduction. Possible values are 'auto' for automatic choice, 'max' for maximum value and an *int* value for user value. Default is 'auto'.

### Returns

- *(m, n)* or *(m, n, l)* *numpy array* – Restored data.
- *dict* – Additional informations. See Notes.

### Notes

The algorithm can be initialized with CLS as soon as *CLS\_init* is not *None*. In this case, *CLS\_init* should be a dictionary containing the required *Lambda* key and eventually the *init* optional argument.

The output information keys are:

- *time*: Execution time in seconds.
- *lrc*: low rank component.
- *dico*: Estimated dictionary.
- *E*: Evolution of the error.

## Patch manipulation functions

`system.restore.DL_ITKrMM.forward_patch_transform(ref, w)`

Transforms data from 2D/3D array to array whose shape is  $(w**2, N)$  where  $w$  is the patch width and  $N$  is the number of patches.

### Parameters

- **ref** ( $(m, n)$  or  $(m, n, l)$  numpy array) – The input image.
- **w** (*int*) – The width (or height) of the patch.

**Returns data** – The patches stacked version. Its shape is  $(w**2, N)$  where  $N$  is the number of patches if  $ref$  is 2D or  $(w**2*1, N)$  if  $ref$  is 3D.

**Return type**  $(w**2, N)$  or  $(w**2*1, N)$  numpy array

`system.restore.DL_ITKrMM.inverse_patch_transform(data, shape)`

Transforms data from array of the form  $(w**2, N)$  or  $(w**2*1, N)$  where  $w$  is the patch width,  $l$  is the number of bands (in the case of 3D data) and  $N$  is the number of patches into 2D/3D array.

### Parameters

- **data** ( $(w**2, N)$  or  $(w**2*1, N)$  numpy array) – The input data.
- **shape** ( $(m, n)$  or  $(m, n, l)$ ) – The image shape.

**Returns ref** – The input image.

**Return type**  $(m, n)$  or  $(m, n, l)$  numpy array

## CLS initialization function

`system.restore.DL_ITKrMM.CLS_init(Y, Lambda, K=128, S=None, PatchSize=5, mask=None, PCA_transform=False, PCA_th='auto', init=None, verbose=True)`

Dictionary learning initialization based on CLS restoration algorithm.

### Parameters

- **Y** ( $(m, n, l)$  numpy array) – A 3D multi-band image.
- **Lambda** (*float*) – Regularization parameter.
- **K** (*optional, int*) – The dictionary size. Default is 128.
- **S** (*optional, int*) – The code sparsity. Default is  $0.1*PatchSize*1$ .
- **PatchSize** (*optional, int*) – The patch size. Default is 5.
- **mask** (*optional, None, (m, n) boolean numpy array*) – A sampling mask which is True if the pixel is sampled and False otherwise. Default is None for full sampling.
- **PCA\_transform** (*optional, bool*) – Enables the PCA transformation if True, otherwise, no PCA transformation is processed. Default is False as it should be done in dico learning operator.
- **PCA\_th** (*optional, int, str*) – The desired data dimension after dimension reduction. Possible values are 'auto' for automatic choice, 'max' for maximum value and an int value for user value. Default is 'auto'.
- **init** (*optional, None, (m, n, l) numpy array*) – The algorithm initialization. Default is None for random initialization.

- **verbose** (*optional, bool*) – Indicates if information text is desired. Default is True.

**Returns**

- ( $K, l*PatchSize**2$ ) *numpy array* – The dictionary for dictionary learning algorithm.
- ( $K, l*PatchSize**2$ ) *numpy array* – The sparse code for dictionary learning algorithm.
- ( $m, n, l$ ) *numpy array* – CLS restored array.
- *dict* – Dictionary containing some extra info

---

**Note:** Infos in output dictionary:

- **E** : In the case of partial reconstruction, the cost function evolution over iterations.
  - **Gamma** : The array of kept coefficients (order is Fortran-style)
  - **nnz\_ratio** : the ratio  $Gamma.size/(m*n)$
  - **H**: the basis of the chosen signal subspace
- 

**The dictionary learning interface**

```
class system.restore.DL_ITKrMM.Dico_Learning_Executer (Y, mask=None, Patch-
Size=5, K=128, L=1,
S=20, Nit_lr=10,
Nit=40, CLS_init=None,
xref=None, verbose=True,
PCA_transform=True,
PCA_th='auto')
```

Class to define execute dictionary learning algorithms.

The following class is a common code for most dictionary learning methods. It performs the following tasks:

- reshapes the data in patch format,
- performs low-rank component estimation,
- launches the dictionary learning method,
- reshape output data,
- handle CLS initialization to speed-up computation.

**Variables**

- **Y** ( $(m, n)$  or  $(m, n, l)$  *numpy array*) – The input data.
- **Y\_PCA** ( $(m, n)$  or  $(m, n, PCA\_th)$  *numpy array*) – The input data in PCA space. Its value is Y if Y is 2D.
- **mask** ( $(m, n)$  *numpy array*) – The acquisition mask.
- **PatchSize** (*int*) – The width (or height) of the patch. Default is 5.
- **K** (*int*) – The dictionary dimension. Default is 128.
- **L** (*int*) – The number of low rank components to learn. Default is 1.
- **S** (*int*) – The code sparsity level. Default is 20.
- **Nit\_lr** (*int*) – The number of iterations for the low rank estimation. Default is 10.

- **Nit** (*int*) – The number of iterations. Default is 40.
- **CLS\_init** (*dico*) – CLS initialization information. See Note for details. Default is None.
- **xref** (*(m, n) or (m, n, l) numpy array*) – Reference image to compute error evolution. Default is None for input Y data.
- **verbose** (*bool*) – The verbose parameter. Default is True.
- **data** (*(PatchSize\*\*2, N) or (PatchSize\*\*2\*1, N) numpy array*) – The Y data in patch format. N is the number of patches.
- **mdata** (*(PatchSize\*\*2, N) or (PatchSize\*\*2\*1, N) numpy array*) – The mask in patch format. N is the number of patches.
- **init** (*(PatchSize\*\*2, K+L) or (PatchSize\*\*2\*1, K+L) numpy array*) – The initialization in patch format.
- **PCA\_operator** (*PcaHandler object*) – The PCA operator.
- **neam\_std** (*2-tuple*) – Tuple of size 2 which contains the data mean and std.

---

**Note:** The algorithm can be initialized with CLS as soon as CLS\_init is not None. In this case, CLS\_init should be a dictionary containing the required Lambda key and other optional arguments required for CLS (PCA\_transform, PCA\_th, init).

---

## The ITKrMM core

`system.restore.DL_ITKrMM.rec_lratom` (*data, masks=None, lrc=None, Nit=10, inatom=None, verbose=True*)  
 Recover new low rank atom equivalent to itkrmm with  $K = S = 1$ .

### Parameters

- **data** (*(d, N) numpy array*) – The (corrupted) training signals as its columns.
- **masks** (*(d, N) numpy array*) – Mask data as its columns. masks(..) in {0,1}. Default is masks = 1.
- **lrc** (*(d, n) numpy array*) – Orthobasis for already recovered low rank component. Default is None.
- **Nit** (*int*) – Number of iterations. Default is 10.
- **inatom** (*(d, ) numpy array*) – Initialisation that should be normalized. Default is None for random.
- **verbose** (*bool*) – If verbose is True, information is sent to the output. Default is True.

**Returns** **atom** – Estimated low rank component.

**Return type** (d, ) numpy array

`system.restore.DL_ITKrMM.OMPm` (*D, X, S, Masks=None*)  
 Masked OMP.

This is a modified version of OMP to account for corruptions in the signal.

Consider some input data  $\mathbf{X}$  (whose shape is  $(N, P)$  where  $N$  is the number of signals) which are masked by  $\mathbf{M}$ . Given an input dictionary  $\mathbf{D}$  of shape  $(K, P)$ , this algorithm returns the optimal sparse  $\hat{\mathbf{A}}$  matrix such that:

$$\hat{\mathbf{A}} = \arg \min_{\mathbf{A}} \frac{1}{2} \|\mathbf{MX} - \mathbf{M(AD)}\|_F^2$$

$$s.t. \max_k \|\mathbf{A}_{k,:}\|_0 \leq S$$

A slightly different modification of Masked OMP is available in “Sparse and Redundant Representations: From Theory to Applications in Signal and Image Processing,” the book written by M. Elad in 2010.

**Parameters**

- **D** ( $(K, P)$  *numpy array*) – The dictionary. Its rows MUST be normalized, i.e. their norm must be 1.
- **x** ( $(N, P)$  *numpy array*) – The masked signals to represent.
- **S** (*int*) – The max. number of coefficients for each signal.
- **Masks** (*optional, (N, P) numpy array or None*) – The sampling masks that should be 1 if sampled and 0 otherwise. Default is None for full sampling.

**Returns** sparse coefficient matrix.

**Return type**  $(N, K)$  sparse *coo\_matrix* array

`system.restore.DL_ITKrMM.itkrmm_core` (*data, masks=None, K=None, S=1, lrc=None, Nit=50, init=None, verbose=True, xref=None*)

Iterative Thresholding and  $K$  residual Means masked.

**Parameters**

- **data** ( $(d, N)$  *numpy array*) – The (corrupted) training signals as its columns.
- **masks** (*optional, None, (d, N) numpy array*) – The masks as its columns. `masks(..)` in  $\{0,1\}$ . Default is None for full sampling.
- **K** (*optional, None or int*) – Dictionary size. Default is None for  $d$ .
- **S** (*optional, int*) – Desired or estimated sparsity level of the signals. Default is 1.
- **lrc** (*optional, None or (d, L) numpy array*) – Orthobasis for low rank component. Default is None.
- **Nit** (*optional, int*) – Number of iterations. Default is 50.
- **init** (*optional, None or (d, K-L) numpy array*) – Initialisation, unit norm column matrix. Here,  $L$  is the number of low rank components. Default is None for random.
- **verbose** (*optional, optional, bool*) – The verbose parameter. Default is True.
- **xref** (*optional, None or (d, N) numpy array*) – True data or reference data to check convergence. Default is `data`.

**Returns**

- $(d, K)$  *numpy array* – Estimated dictionary
- *float* – Execution time in seconds.

**(Nit,)** *numpy array* Evolution of NMSE between current data and `xref`.

### 3.5.6 pystem.restore.DL\_BPFA module

This module implements the BPFA algorithm.

```
pystem.restore.DL_BPFA.BPFA_matlab(Y, mask, PatchSize=5, Omega=1, K=128, Nit=100,
                                     step=1, PCA_transform=True, PCA_th='auto', ver-
                                    bose=True)
```

Implements BPFA algorithm for python.

This function does not properly executes BPFA but it calls the Matlab BPFA code.

#### Parameters

- **Y** ( $(m, n)$  or  $(m, n, l)$  *numpy array*) – The input data.
- **mask** ( $(m, n)$  *numpy array*) – The acquisition mask.
- **PatchSize** (*int*) – The patch width. Default is 5.
- **Omega** (*int*) – The Omega parameter. Default is 1.
- **K** (*int*) – The dictionary dimension. Default is 128.
- **Nit** (*int*) – The number of iterations. Default is 100.
- **step** (*int*) – The distance between two consecutive patches. Default is 1 for full overlap.
- **PCA\_transform** (*optional, bool*) – Enables the PCA transformation if True, otherwise, no PCA transformation is processed. Default is True.
- **PCA\_th** (*optional, int, str*) – The desired data dimension after dimension reduction. Possible values are 'auto' for automatic choice, 'max' for maximum value and an int value for user value. Default is 'auto'.
- **verbose** (*bool*) – The verbose parameter. Default is True.

#### Returns

- $(m, n)$  or  $(m, n, l)$  *numpy array* – Restored data.
- *dict* – Additional informations. See Notes.

---

**Note:** The output information keys are:

- `time`: Execution time in seconds.
  - `Z`
  - `A`
  - `S`
-



## INDICES AND TABLES

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