
BASTet: Berkeley Analysis and Storage Toolkit

Release devel

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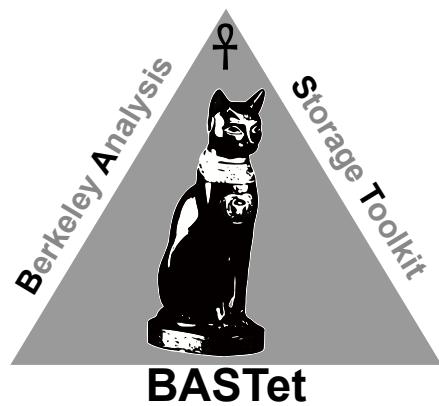
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**CHAPTER
ONE**

INTRODUCTION

BASTet has been originally developed as the analysis backend for the [OpenMSI](<https://openmsi.nerc.gov/>) science gateway.

A central goal of BASTet is to facilitate shareable and reproducible analysis and to bridge the gaps between the various stages in the typical life-cycle of new analysis methods, e.g., when transitioning from a research prototype to production or when integrating an analysis into more complex workflows or when sharing analysis results. BASTet provides users with an environment that makes it easy to develop and deploy analyses via OpenMSI by providing:

- standardized analysis interfaces that make analyses easily accessible to users and enable developers to build an accessible ecosystem of domain analytics,
- automatic provenance for reproducible analytics,
- standardized interfaces and a common format for storage, access, sharing and reuse of analysis results and raw MSI data
- support for integration of analyses to complex workflows, providing users a lightweight and easy-to-use entry-point to define and manage analysis workflows, and
- integrated tools and analytics to facilitate development and deployment.

While the design of BASTet has been motivated by the needs of OpenMSI, its core design and functionality are much more broadly applicable to other applications as well. Basket is implemented in Python using *NumPy* for data processing, *h5py* for HDF5-based data storage, and *mpi4py* for distributed parallel data processing.

CHAPTER
TWO

CONVERTING FILES AT NERSC AND MAKING THEM ACCESSIBLE

To convert a mass spectrometry imaging file, e.g., in img or bruckerflex format, to HDF5 do the following:

```
ssh cori.nersc.gov
cd /project/projectdirs/openmsi-devel/convert
source setupEnvironment.csh
python convertToOMSI.py <infile1> <output HDF5File>
```

Note if you use the bash shell then use `setupEnvironment.bash` instead.

Note, if you want to use the output file from `openmsi.nersc.gov` then the output file path should be:

```
/project/projectdirs/openmsi/omsi_data_private/<username>/<filename>
```

where `username` is the name of the primary user that owns the file.

2.1 Making a converted file accessible to OpenMSI (Private)

The conversion script will by default automatically try to register new files with the OpenMSI site and assign them private to a single user if the output file is placed in the OpenMSI private data location:

```
python convertToOMSI.py <infile1> /project/projectdirs/openmsi/omsi_data_private/<username>/<filename>
```

The `username` in the path will determine the user the file is assigned to. E.g: The filename will also be the name used in the listing on the site. In order to generate the HDF5 file without adding to the database, use the `--no-add-to-db` command line option, e.g.:

2.2 Changing file permissions:

Using the OpenMSI website the owner of the file can assign permissions to files online:

<https://openmsi.nersc.gov/openmsi/resources/filemanager?file=<filename>>

2.3 convertToOMSI: Usage and Options

NOTE: In order to view a current, complete list of conversions options use:

```
python convertToOMSI.py --help
```

```
python convertToOMSI.py --help
USAGE: Call "convertToOMSI [options] imgBaseFile1 imgBaseFile2 ... imgBaseFileN HDF5File"

This converter script takes the basename (i.e., path+basefilename) of a single
or multiple MSI files as input and converts them to HDF5. Each MSI file is
stored as a separate experiment in the output HDF5 file. If an input file
defines multiple regions, then those regions can either be stored as separate
datasets of the same experiment and/or merged to a single MSI dataset.
Using the various parameter settings described below, one can define how the
conversion should be performed, how the data should be stored in HDF5, and
indicate which analyses should be executed.

====HELPER OPTIONS====
--suggest-chunking : Iterate over all given input files and suggest a chunking strategy.
                    No data is converted when this option is given, i.e., no name for the
                    HDF5file should be given, but only input files should be listed.

====ERROR HANDLING OPTIONS====
--error-handling <options>: Define how errors should be handled. Options are:
    i) terminate-and-cleanup (default) : Terminate the conversion, delete the
        the HDF5 file and do not add the file to the database.
    ii) terminate-only, : Leave the generated HDF5 output file in place but do not
        add the file to the database.
    iii) continue-on-error: Ignore errors if possible and continue, even if this
        means that some data may be missing from the output.
--email <email1 email2 ...>: Send notification in case of both error or success to the email address
--email-success <email1 email2 ...>: Send notification in case of success to the given email address
--email-error <email1 email2 ...>: Send notification in case of error to the given email address.

====INPUT DATA OPTIONS====
Default input data options: --format auto --regions split+merge
--format <option>: Define which file format is used as input. By default the program tries to
                    automatically determine the input format. This option can be used to indicate
                    the format explicitly to in case the auto option fails. Available options are:
                    {'imzml_file': <class 'omsi.dataformat.imzml_file.imzml_file'>, 'bruckerflex_file': <class
--regions <option>: Some file formats (e.g., brucker) allow multiple regions to be imaged and stored
                    in a single file. This option allows one to specify how these regions should be
                    treated during file conversion. E.g., one may want to store i) each region as a
                    separate dataset in the output file (--regions split), ii) all regions combined
                    in a single dataset (--regions merge), or both (--regions split+merge)
                    Available options are:
                    ['split', 'merge', 'split+merge']

====FILE WRITE OPTIONS====
---FILE WRITE OPTIONS: Chunking---

Default HDF5 Chunking options: Enabled by default using --auto-chunking :
--auto-chunking : Automatically decide which chunking should be used. This option
                    automatically generates two copies of the data, one with a chunking
                    optimized for selection of spectra and another one optimized for
                    selection of ion image slices. All --chunking, --no-chunking, and
                    --optimized-chunking options are ignored if this parameter is given
--chunking <x y z> : Use chunking when writing the HDF5 file. (DEFAULT, x=4,y=4,z=2048)
--no-chunking : Disable chunking when writing the HDF5 file. Use in combination with
                    --no-compression since compression depends on chunking and will enable
                    it if compression is used.
```

```
--optimized-chunking <x y z> : Use this option to generate additional copies of the data
    with different chunked data layouts. Generating multiple copies of the
    data with different chunked data layouts can be help accelerate selective
    data read opeations. (DEFAULT OFF). We recommend a spectra-aligned chunking
    for the raw data, e.g., '--chunking 1 1 32768' and an image-aligned chunked
    secondary copy of the data, e.g., '--optimzied-chunking 20 20 100'.

---FILE WRITE OPTIONS: Compression---
HDF5 Compression: Default ON using (gzip, 4):
--compression: Enable compression using (gzip,4). NOTE: Compression requires the use of chunking.
--no-compression: Disable the use of compression.

====I/O OPTIONS===
--io <option>: Available options are: ['chunk', 'spectrum', 'all']
    i) all : Read the full data in memory and write it at once
    ii) spectrum : Read one spectrum at a time and write it to the file.
    iii) chunk : Read one chunk at a time and write it to the file.
    The io option applies only for the generation of subsequent chunkings
    and not the initial iteration over the file to generate the first convert.
    iv) spectrum-to-image: Default option when creating image chunk version from
        a spectrum-chunk MSI dataset. Read a block of spectra at a time to
        complete a set of images and then write the block of images at once.
--io-block-limit <MB>: When using spectrum-to-image io (default when using auto-chunking),
    what should the maximum block in MB that we load into memory. (Default=2000MB)

====DATABSE OPTIONS===
These options control whether the generated output file should be added to a server database
to manage web file access permissions
Default options are: --add-to-db --db-server http://openmsi.nersc.gov
--add-to-db : Explicitly add the output HDF5 file to the database. This option has no effect
    if --jobid is set as the file is added through the update of the job status
    in this case.
--no-add-to-db : Disable adding the file to the database.
--db-server : Specify the online server where the file should be registers. Default is
    http://openmsi.nersc.gov
--user : Name of the user that should be assigned as user. By default the user is
    determined automatically based on the file path.
--jobid : ID of the job. If set to 'auto' then the environment variable PBS_JOBID is used.
    NOTE: If job ID is set then we assume that the job has been scheduled via the
    the automated system and that the job is managed. As such the file will be added,
    to the database by updating the job status and NOT by explicitly adding the file.

====ANALYSIS OPTIONS===
NMF: Default ON: (nc=20, timeout=600, niter=2000, tolerance=0.0001, raw=False)
--nmf : Compute the nmf for all the input data files and store the results in the
    HDF5 file. NOTE: If global peak-finding (fpg) is performed, then
    nmf will be performed on the peak-cube, otherwise on the raw data
--no-nmf: Disable the execution of nmf
--nmf-nc <number>: Number of components to be computed by the NMF. (default nc=20)
--nmf-timeout <number>: Maximum time in seconds to be used for computing the NMF. (default timeout=600)
--nmf-niter <number>: Number of iterations (minimum is 2) (default niter=2000)
--nmf-tolerance <number>: Tolerance value for a relative stopping condition. (default tolerance=0.0001)
--nmf-raw <number>: Force execution of the NMF on the raw data. By default the results from
    the global peak finding (--fpg) are used to compute the NMF.

Global Peak Finding: Default ON:
```

```
--fpg : Compute the global peak finding for all input data files and save results
       in the HDF5 file (DEFAULT)
--no-fpg: Disable the global peak finding

Local Peak Finding: Default OFF:
--fpl : Compute the local peak finding for all input data files and save results
       in the HDF5 file
--no-fpl: Disable the local peak finding (DEFAULT)

TIC normalization:
--ticnorm : Compute tic normalization
--no-ticnorm : Disable computation of tic normaltization (DEFAULT)

---OTHER OPTIONS---

Generate Thumbnail image: Default OFF:
--thumbnail: Generate thumbnail image for the file based on, in order of availability:
    * The first three components of the NMF
    * The three most intense peaks from the global peak finding (fpg)
    * The three most intense peaks in the raw data that are at least 1 percent
      of the total m/z range apart.
--no-thumbnail: Do not generate a thumbnail image.

Generate XDMF header file for output file: Default OFF:
--xdmf: Write XDMF XML-based header-file for the output HDF5 file.
--no-xdmf: Do not generate a XDMF XML-based header for the HDF5 file.

====Metadata Options====

NOTE: Input datasets are numbers starting from 0 based on there order on the command line.

--methods : JSON describing the experimental methods
--methods# : JSON describing the experimental methods for input file number #
--instrument : JSON dictionary describing the instrument
--instrument# : JSON dictionary describing the instrument for input file number #
--notes : JSON dictionary with additional user notes about the data
--notes# : JSON dictionary with additional notes for input file number #
```

INTEGRATING NEW FILE FORMATS

3.1 Developing a file reader

In order to develop a new file reader we need to implement a corresponding class for the file format that inherits from `file_reader_base` (for formats that always contain a single region) or `file_reader_base_with_regions` (for formats that support multiple imaging regions in a single file). Both base classes are available in the `omsi.dataformat.file_reader_base` module. The developer then needs to implement the following functions:

```
from omsi.dataformat.file_reader_base import file_reader_base

class formatname_file(file_reader_base):

    # 1. Implement the init function which must accept basename and requires_slicing as inputs
    def __init__(self, basename=None, requires_slicing=True):
        """
        basename : Name of the file/folder to be opened
        requires_slicing: Boolean indicating whether the user requires array slicing via
            the __getitem__ function to work or not. This is an optimization, because many MSI
            data formats do not easily support arbitrary slicing of data but rather only
            iteration over spectra.
        """
        super(formatname_file, self).__init__(basename, requires_slicing) # 1.1 Call super __init__
        self.data_type = 'uint16' # 1.2 Define the data type used
        self.shape = [0, 0, 0] # 1.3 Define the shape of the dataset
        self.mz = 0 # 1.4 Define the m/z axis

    # 2. Implement __getitem__
    def __getitem__(self, key):
        # Implement array-based slicing for the format so that the data can be read
        # via [x,y,z]

    # 3. Implement close_file
    def close_file(self):
        # Function called to close any open files when deleting the object

    # 4. Implement is_valid_dataset
    @classmethod
    def is_valid_dataset(cls, name):
        # Given the name of a file or directory, determine whether the given
        # data defines a valid dataset for the current format
```

For file formats that support multiple regions the implementation is aside from a few additions the same. The main difference are:

1. Inherit from `file_reader_base_with_regions` instead of `file_reader_base`
2. Set the `self.region_dicts` and `self.select_region` attributes in the `__init__` function
3. Implement the `set_region_selection` function

```
from omsi.dataformat.file_reader_base import file_reader_base_with_regions

class formatname_file(file_reader_base):

    # 1. Implement the init function which must accept basename and requires_slicing as inputs
    def __init__(self, basename=None, requires_slicing=True):
        super(formatname_file, self).__init__(basename, requires_slicing)  # 1.1 Call super __init__
        self.data_type = 'uint16'  # 1.2 Define the data type used
        self.shape = [0, 0, 0]  # 1.3 Define the shape of the dataset
        self.mz = 0  # 1.4 Define the m/z axis
        self.region_dicts = []  # 1.5 Define a list of dicts where each dict describes
                               # the parameters of a region. In the simplest case
                               # of rectangular regions, a dict would specify the
                               # `origin` and `extends` of a region.
        self.select_region = None  # 1.6 Define the index of the selected region.
                               # Set to None to treat dataset as a whole (i.e.,
                               # merge all regions). If set to a region index,
                               # then the __getitem__ function is expected to
                               # behave as if the file consisted of just the
                               # selected region and the self.shape parameter
                               # must be set accordingly

    # 2-4: Implement the other functions of file_reader_base as described above.
    # Note, __getitem__ must consider the value of self.select_region and
    # treat any data requests as if they referred to the selected region
    # only. Depending on the data format this may require transformation
    # of the selection keys to locate the appropriate data

    # 5. Implement the set_region_selection function to allow a user to select a region
    def set_region_selection(self, region_index=None):
        """Define which region should be selected for local data reads.

        :param region_index: The index of the region that should be read. The shape of the
                            data will be adjusted accordingly. Set to None to select all regions and
                            treat the data as a single full 3D image.
        """
        # 5.1 Select all data
        if region_index is None:
            self.select_region = None  # 5.1.1 Set the region selection to None
            self.shape = self.full_shape  # 5.1.2 Define shape of the complete data
        # 5.2 Select a particular region
        elif region_index < self.get_number_of_regions():
            self.select_region = region_index  # 5.2.1 Set region index
            self.shape = ...  # 5.2.2 Define the 3D shape of the region
```

3.2 Integrating the file reader with OpenMSI

Integrating a new file reader with OpenMSI is simple:

1. Add the file reader module to the `omsi.dataformat.format` module and
2. Add the name of your module to the `__all__` variable in `omsi.dataformat.__init__.py`

Once these steps are complete, the `omsi.dataformat.file_reader_base` module will automatically detect the new format and make it available as part of the file conversion script `omsi.tools.convertToOMSI`. To check which formats are registered, simply do:

```
>>> from omsi.dataformat import *
>>> formats = file_reader_base.file_reader_base.available_formats()
>>> print formats
{'bruckerflex_file': <class 'omsi.dataformat.bruckerflex_file.bruckerflex_file'>,
 'img_file': <class 'omsi.dataformat.img_file.img_file'>}
```

Using this basic feature makes it possible to easily iterate over all available formats and the consistent interface described by the `file_format_base` module allows us to use all the formats in a consistent manner (avoiding special cases). E.g., if we want to read a file of an unknown format we can simply:

```
from omsi.dataformat import *
formats = file_reader_base.file_reader_base.available_formats()
filename = 'my_unknown_file'
filereader = None
formatname = None
for fname, fclass in formats.items():
    if fclass.is_valid_dataset(filename):
        filereader = fclass
        formatname = fname
if filereader is not None:
    print "Using "+str(formatname)+" to read the file"
    openfile = filereader(basename=filename, requires_slicing=True)
```


DEVELOPING A NEW ANALYSIS FOR BASTET

BASTet provides developers with two easy ways to integrate new analyses. First, the simplest and most basic solution is to wrap analysis functions using either the `@bastet_analysis` Python decorator or by explicitly wrapping a function via wrapped `funct = analysis.generic.from_function(my function)`. Second, to easily share and fully integrate an analysis with BASTet, we then create a new class that inherits from BASTet's base analysis interface class

4.1 Wrapping a function: The quick-and-dirty way

Sometimes developers just want to debug some analysis function or experiment with different variants of a code. At the same time, we want to be able to track the results of these kind of experiments in a simple fashion. The `omsi.analysis.generic()` provides us with such a quick-and-dirty solution. We say quick-and-dirty because it sacrifices some generality and features in favor for a very simple process.

Using the `omsi.analysis.generic.analysis_generic.from_function()` or `omsi.analysis.generic.bastet_analysis()` decorator, we can easily construct a generic `omsi.analysis.base.analysis_base` instance container object for a given function. We can then use this container object to execute our function, while tracking its provenance as well as save the results to file as we would with any other analysis object. This approach allows us to easily track, record, safe, share and reproduce code experiments with only minimal extra effort needed. Here we briefly outline the two main options to do this.

NOTE: Wrapping functions directly is not recommended for production workflows but is intended for development and debugging purposes only. This mechanism relies on that the library does the right thing in automatically determining input parameters, outputs, and their types and that we can handle all those types in the end-to-end process, from definition to storage. We do our best to make this mechanism work with a broad set of cases but we do not guarantee that the simple wrapping always work.

4.1.1 Option 1: Explicitly track specific executions of a function

Instead of calling our analysis function `f()` directly, we create an instance of `omsi.analysis.generic.analysis_generic()` via `g = analysis_generic.from_function(f)` which we then use instead of our function. To execute our function we can now either call `g.execute(...)` as usual or treat `g` as a function and call it directly `g(...)`

```
1 import numpy as np
2 from omsi.analysis.generic import analysis_generic
3
4 # Define some example function we want to wrap to track results
5 def mysum(a):
6     return np.sum(a)
7
8 # Create an analysis object for our function
```

```
9 g = analysis_generic.from_function(mysum)
10 g['a'] = np.arange(10)    # We can set all parameters prior to executing the function
11 g.execute()   # This is the same as: g(np.arange(10))
```

See `omsi.analysis.generic.analysis_generic.from_function()` for further details on additional optional inputs of the wrapping, e.g., to specify additional information about inputs and outputs.

4.1.2 Option 2: Implicitly track the last execution of a function

If we are only interested in recording the last execution of our function, then we can alternatively wrap our function directly using the `@bastet_analysis` decorator. The main difference between the two approaches is that using the decorator we only record the last execution of our function, while using the explicit approach of option 1, we can create as many wrapped instances of our functions as we want and track the execution of each independently.

```
1 import numpy as np
2 from omsi.shared.log import log_helper
3 log_helper.set_log_level('DEBUG')
4 from omsi.analysis.generic import bastet_analysis
5
6 # Define some example function and wrap it
7 @bastet_analysis
8 def mysum(a):
9     """Our own sum function"""
10    return np.sum(a)
11
12 # mysum['a'] = np.arange(10)
13 # As with the any wrapped function we can delay execution and set
14 # parameters before we actually run the analysis
15
16 # Execute the analysis
17 res = mysum(a=np.arange(10))  # Or we can set parameters and execute in the same call
```

See `omsi.analysis.generic.bastet_analysis()` for further details on additional optional inputs of the wrapping, e.g., to specify additional information about inputs and outputs.

4.1.3 Example 1: Defining and using wrapped functions

The code example shown below illustrates the “wrapping” of a simple example function `mysum(a)`, which simply uses `numpy.sum` to compute the sum of objects in an array. (NOTE: We could naturally also use `numpy.sum` directly, we use `mysum(a)` mainly to illustrate that this approach also works with functions defined in the interpreter.)

```
1 import numpy as np
2 from omsi.shared.log import log_helper
3 log_helper.set_log_level('INFO')
4 from omsi.analysis.generic import analysis_generic
5 from omsi.dataformat.omsi_file.main_file import omsi_file
6
7 # Define some example function we want to wrap to track results
8 def mysum(a):
9     return np.sum(a)
10
11 # Create an analysis object for our function
12 g = analysis_generic.from_function(mysum)
13
14 # Execute the analysis
```

```

15 res = g.execute(a=np.arange(10))
16 log_helper.log_var(__name__, res=res) # Logging the result
17
18 # Save the analysis to file
19 f = omsi_file('autowrap_test.h5', 'a')
20 e = f.create_experiment()
21 exp_index = e.get_experiment_index()
22 ana_obj, ana_index = e.create_analysis(g)
23 # Close the file
24 f.flush()
25 del f
26
27 # Restore the analysis from file
28 f = omsi_file('autowrap_test.h5', 'a')
29 e = f.get_experiment(exp_index)
30 a = e.get_analysis(ana_index)
31 g2 = a.restore_analysis()
32 res2 = g2.execute()
33 log_helper.log_var(__name__, res2=res2) # Logging the result
34 if res == res2:
35     log_helper.info(__name__, "CONGRATULATIONS---The results matched")
36 else:
37     log_helper.error(__name__, "SORRY---The results did not match")

```

When we run our script, we can see that we were able to successfully capture the execution of our function and recreate the analysis from file.

```

1 machine:dir username$ python autowrap_function.py
2 2015-09-29 15:21:32,729 - __main__ - INFO - res = 45
3 2015-09-29 15:21:32,778 - __main__ - INFO - res2 = 45
4 2015-09-29 15:21:32,778 - __main__ - INFO - CONGRATULATIONS---The results matched

```

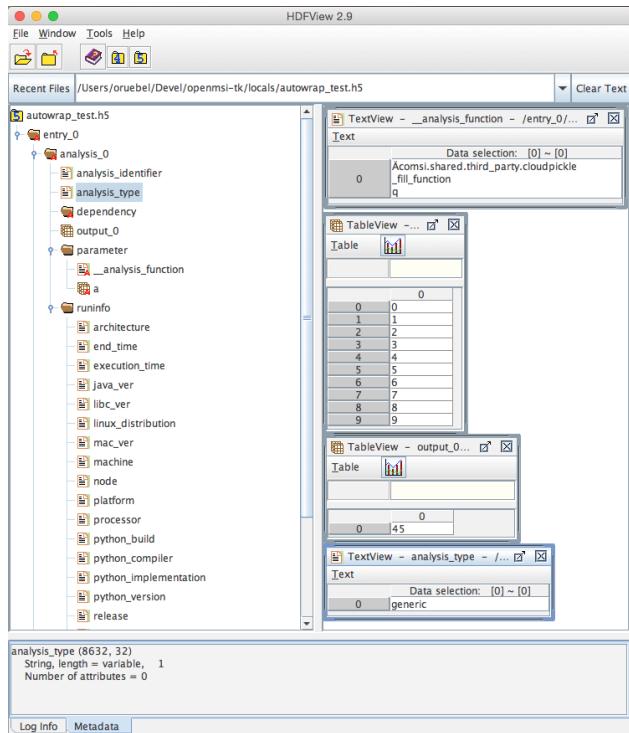
The figure below shows a view of the file generated by our wrapped function execution example shown above.

Note, we can use the wrapped function objects as usual in an analysis workflow to combine our functions with other analyses. For example, the simple example shown below shows how we can quickly define a simple filter to set all intensities that are less than 10 to a value of 0 before executing an analysis. We here first execute global peak finding to reduce the data, than apply a simple wrapped filter function to filter the data values, and then compute NMF on the filtered data.

```

1 from omsi.dataformat.omsi_file import *
2 from omsi.analysis.findpeaks.omsi_findpeaks_global import omsi_findpeaks_global
3 from omsi.analysis.multivariate_stats.omsi_nmf import omsi_nmf
4 from omsi.analysis.generic import analysis_generic
5 import numpy as np
6
7 f = omsi_file('/Users/oruebel/Devel/openmsi-data/msidata/20120711_Brain.h5', 'r')
8 d = f.get_experiment(0).get_msidata(0)
9
10 # Specify the analysis workflow
11 a1 = omsi_findpeaks_global()
12 a1['msidata'] = d
13 a1['mzdata'] = d.mz
14
15 # Wrap a simple function to filter all peaks with less than 10 counts
16 def f(a):
17     a[a<10] = 0
18     return a
19 a2 = analysis_generic.from_function(f)

```



```

20 a2['a'] = a1['peak_cube']      # Use the peak_cube from a1 as input for the filter
21
22 # Create an NMF for the filtered data
23 a3 = omsi_nmf()
24 a3['msidata'] = a2['output_0']  # Make the output of our analysis the input of the NMF
25 a3['numIter'] = 2
26
27 # Run our simple workflow, i.e.,: peak_finder --> our_filter --> nmf
28 a3.execute_recursive()

```

By default, the outputs are named and numbered using the schema `output_#`, i.e., in the above example we used `a2['output_0']` to access the output our wrapped function. To define user-defined names for the outputs of a wrapped function we can simply provide a list of strings to the input parameter `output_names` of the `analysis_generic.from_function(...)`.

4.2 Writing a new analysis class for BASTet – Part 1: Overview

The OpenMSI Toolkit includes a basic template for implementing new analyses as part of OpenMSI. The template is located in `omsi.templates.omsi_analysis_template.py`. The template provides step-by-step instructions on how to implement a new analysis. Simply search top-to-bottom for `EDIT_ME` markers to find locations that need to be edited and what changes need to be made.

The implementation of a new analysis is divided into three main steps. We here provide a brief overview of these steps. A detailed walk-through the required implementation is provided in the following sections.

Step 1) Basic integration of your analysis with OpenMSI (Required)

The basic integration is simple and should requires only minimal additional effort. The basic integration with the OpenMSI provides:

- full integration of the analysis with the OpenMSI file format and API
- full support for OpenMSI's data provenance capabilities
- full integration with analysis drivers (e.g, the command line driver) enabling direct execution of the analysis with automatic handling of user input specification, help, etc.
- basic integration of the analysis with the website, in that a user will be able to browse the analysis in the online file browser. The basic integration automatically provides full support for the qmetadata and qcube URL data access patterns. The basic integration provides limited support for the qslice, qspectrum, and qmz patterns, in that it automatically exposes all dependencies of the analysis that support these patterns but it does not expose the data of the analysis itself. This is part of step 2.

Step 2) Integrating your analysis with the OpenMSI web-based viewer (Recommended)

Once the basic integration is complete, you may want integrate your analysis fully with the OpenMSI online viewer, in order to make your analysis easily accessible to the OpenMSI user community. This step requires the implementation of the qslice, qspectrum, and qmz URL patterns for the analysis. This step completes the integration with the OpenMSI framework itself.

Step 3) Making your analysis self-sufficient (Recommended)

This step makes your analysis “self-sufficient” in that it allows you to execute your analysis from the command-line. This step is usually very simple as we can just use BASTet’s integrated analysis driver to do the job for us.

4.2.1 Some important features of analysis_base

`omsi.analysis.analysis_base` is the base class for all omsi analysis functionality. The class provides a large set of functionality designed to facilitate i) storage of analysis data in the omsi HDF5 file format and ii) integration of new analysis capabilities with the OpenMSI web API and the OpenMSI web-based viewer (see Viewer functions below for details), iii) support for data provenance, and iv) in combination with the `omsi_analysis_driver` module enable the direct execution of analysis, e.g, from the command line

Slicing

`analysis_base` implements basic slicing to access data stored in the main member variables. By default the data is retrieved from `__data_list` by the `__getitem__(key)` function, which implements the `[..]` operator, i.e., the function returns `__data_list[key]['data']`. The key is a string indicating the name of the parameter to be retrieved. If the key is not found in the `__data_list` then the function will try to retrieve the data from `__parameter_list` instead. By adding “parameter/key” or “dependency/key” one may also explicitly retrieve values from the `__parameter_list` and `__dependency_list`.

Important Member Variables

- `analysis_identifier` defines the name for the analysis used as key in search operations.
- `__data_list` defines a list of `omsi.analysis.analysis_data.analysis_data` objects to be written to the HDF5 file. Derived classes need to add all data that should be saved for the analysis in the omsi HDF5 file to this dictionary. See `omsi.analysis.analysis_data` for details.
- `parameters` List of `parameter_data` to be written to the HDF5 file. Derived classes need to add all parameter data that should be saved for the analysis in the omsi HDF5 file to this dictionary using the provided `add_parameter(...)` function. See `omsi.analysis.analysis_data` and `add_parameter(..)` function of `analysis_base` for details.

- `data_names` is a list of strings of all names of analysis output datasets. These are the target names for `__data_list`. **NOTE** Names of parameters specified in `parameters` and `data_names` should be distinct.

I/O functions

These functions can be optionally overwritten to control how the analysis data should be written/read from the omsi HDF5 file. Default implementations are provided here, which should be sufficient for most cases.

- `write_analysis_data`: By default all data is written by `omsi.dataformat.omsi_file.analysis.omsi_file_analysis`. By implementing this function we can implement the write for the main data (i.e., what is stored in `self.__data_list`) ourselves. In practice (at least in the serial case) this should not be needed. However, overwriting the function can be useful when implementing an analysis using MPI and we want to avoid gathering the data on rank the root rank (usually rank 0).
- `add_custom_data_to_omsi_file`: The default implementation is empty as the default data write is managed by the `omsi_file_experiment.create_analysis()` function. Overwrite this function, in case that the analysis needs to write data to the HDF5 omsi file beyond what the defualt omsi data API does.
- `read_from_omsi_file`: The default implementation tries to reconstruct the original data as far as possible, however, in particular in case that a custom `add_custom_data_to_omsi_file` funtion has been implemented, the default implementation may not be sufficien. The default implementation reconstructs: i) `analysis_identifier` and reads all custom data into ii) `__data_list`. Note, an error will be raised in case that the analysis type specified in the HDF5 file does not match the analysis type specified by `get_analysis_type()`. This function can be optionally overwritten to implement a custom data read.

Web API Functions

Several convenient functions are used to allow the OpenMSI online viewer to interact with the analysis and to visualize it. The default implementations provided here simply indicate that the analysis does not support the data access operations required by the online viewer. Overwrite these functions in the derived analysis classes in order to interface them with the viewer. All viewer-related functions start with `v__...`.

NOTE: the default implementation of the viewer functions defined in `analysis_base` are designed to take care of the common requirement for providing viewer access to data from all depencies of an analysis. In many cases, the default implementation is often sill called at the end of custom viewer functions.

NOTE: The viewer functions typically support a `viewerOption` parameter. `viewerOption=0` is expected to refer to the analysis itself.

- `v_qslice`: Retrieve/compute data slices as requested via qslice URL requests. The corrsponding view of the DJANGO data access server already translates all input parameters and takes care of generating images/plots if needed. This function is only responsible for retrieving the data.
- `v_qspectrum`: Retrieve/compute spectra as requested via qspectrum URL requests. The corrsponding view of the DJANGO data access server already translates all input parameters and takes care of generating images/plots if needed. This function is only responsible for retrieving the data.
- `v_qmz`: Define the m/z axes for image slices and spectra as requested by qspectrum URL requests.
- `v_qspectrum_viewer_options`: Define a list of strings, describing the different viewer options available for the analysis for qspectrum requests (i.e., `v_qspectrum`). This feature allows the analysis developer to define multiple different visualization modes for the analysis. For example, when performing a data reduction (e.g., PCA or NMF) one may want to show the raw spectra or the loadings vector of the projection in the spectrum view (`v_qspectrum`). By providing different viewer options we allow the user to decide which option they are most interested in.
- `v_qslice_viewer_options`: Define a list of strings, describing the different viewer options available for the analysis for qslice requests (i.e., `v_qslice`). This feature allows the analysis developer to define multiple

different visualization modes for the analysis. For example, when performing a data reduction (e.g., PCA or NMF) one may want to show the raw spectra or the loadings vector of the projection in the spectrum view (v_qspectrum). By providing different viewer options we allow the user to decide which option they are most interested in.

Executing, saving, and restoring an analysis object

Using the command-line driver we can directly execute analysis as follows:

```
python omsi/analysis/omsi_analysis_driver <analysis_module_class> <analysis_parameters>
```

E.g. to execute a non-negative matrix factorization (NMF) using the *omsi.analysis.multivariate_stats.omsi_nmf* module we can simply:

```
python omsi/analysis/omsi_analysis_driver.py multivariate_stats/omsi_nmf.py  
--msidata "test_brain_convert.h5:/entry_0/data_0"  
--save "test_ana_save.h5"
```

Any analysis based on the infrastructure provided by *analysis_base* is fully integrated with OpenMSI file API provided by “*omsi.dataformat.omsi_file*”. This means the analysis can be directly saved to an OMSI HDF5 file and the saved analysis can be restored from file. In OMSI files, analyses are generally associated with experiments, so that we use the *omsi.dataformat.omsi_file.omsi_file_experiment* API here.

```
1 # Open the MSI file and get the desired experiment  
2 from omsi.dataformat.omsi_file import *  
3 f = omsi_file( filename, 'a' )  
4 e = f.get_experiment(0)  
5  
6 # Execute the analysis  
7 d = e.get_msidata(0)  
8 a = omsi_myanalysis()  
9 a.execute(msidata=d, integration_width=10, msidata_dependency=d)  
10  
11 # Save the analysis object.  
12 analysis_object, analysis_index = exp.create_analysis( a )  
13  
14 # This single line is sufficient to store the complete analysis to the omsi file.  
15 # By default the call will block until the write is complete. Setting the  
16 # parameter flushIO=False enables buffered write, so that the call will  
17 # return once all data write operations have been scheduled. Here we get  
18 # an omsi.dataformat.omsi_file.omsi_file_analysis  
19 # object for management of the data stored in HDF5 and the integer index of the analysis.  
20  
21 # To restore an analysis from file, i.e., read all the analysis data from file  
22 # and store it in a corresponding analysis object we can do the following.  
23 # Similar to the read_from_omsi_file(...) function of analysis_base  
24 # mentioned below, we can decide via parameter settings of the function,  
25 # which portions of the analysis should be loaded into memory  
26 a2 = analysis_object.restore_analysis()  
27  
28 # If we want to now re-execute the same analysis we can simply call  
29 a2.execute()  
30  
31 # If we want to rerun the analysis but change one or more parameter settings,  
32 # then we can simply change those parameters when calling the execute function  
33 d2 = e.get_msidata(1) # Get another MSI dataset  
34 a2.execute(msidata=d2) # Execute the analysis on the new MSI dataset  
35
```

```
36 # The omsi_file_analysis class also provides a convenient function that allows us
37 # to recreate, i.e., restore and run the analysis, in a single function call
38 a3 = analysis_object.recreate_analysis()
39
40 # The recreate_analysis(...) function supports additional keyword arguments
41 # which will be passed to the execute(...) call of the analysis, so that we
42 # can change parameter settings for the analysis also when using the
43 # recreate analysis call.
44
45 # If we know the type of analysis object (which we can also get from file), then we
46 # naturally also restore the analysis from file ourselves via
47 a4 = omsi_myanalysis().read_from_omsi_file(analysisGroup=analysis_object, \
48                                         load_data=True, \
49                                         load_parameters=True, \
50                                         load_runtime_data=True, \
51                                         dependencies_omsi_format=True )
52 # By setting load_data and/or load_parameters to False, we create h5py instead of
53 # numpy objects, avoiding the actual load of the data. CAUTION: To avoid the accidental
54 # overwrite of data we recommend to use load_data and load_parameters as False only
55 # when the file has been opened in read-only mode 'r'.
56
57 # Rerunning the same analysis again
58 a4.execute()
```

4.3 Writing a new analysis class for BASTet – Part 2: Analysis Template

In this section we describe the basic development of a new analysis using the analysis template provided by BASTet.

4.3.1 Step 1) Basic integration

The simple steps outlined below provide you now with full integration of your analysis with the OpenMSI file format and API and full support for OpenMSI's data provenance capabilities. It also provides basic integration of your analysis with the OpenMSI website, in that a user will be able to browse your analysis in the online file browser. The basic integration also automatically provides full support for the qmetadata and qcube URL data access patterns, so that you can start to program against your analysis remotely. The basic integration provides limited support for the qslice, qspectrum, and qmz patterns, in that it automatically exposes all dependencies of the analysis that support these patterns but it does not expose the data of your analysis itself. This is part of step 2. Once you have completed the basic integration your final analysis code should look something like this:

```
1 class omsi_mypeakfinder(analysis_base) :
2
3     def __init__(self, name_key="undefined"):
4         """Initialize the basic data members"""
5
6         super(omsi_mypeakfinder, self).__init__()
7
8         self.analysis_identifier = name_key
9         # Define the names of the outputs generated by the analysis
10        self.data_names = [ 'peak_cube' , 'peak_mz' ]
11
12        # Define the input parameters of the analysis
13        dtypes = self.get_default_dtypes()
```

```

14     groups = self.get_default_parameter_groups()
15     self.add_parameter(name='msidata',
16                         help='The MSI dataset to be analyzed',
17                         dtype=dtypes['ndarray'],
18                         group=groups['input'],
19                         required=True)
20     self.add_parameter(name='mzdata',
21                         help='The m/z values for the spectra of the MSI dataset',
22                         dtype=dtypes['ndarray'],
23                         group=groups['input'],
24                         required=True)
25     self.add_parameter(name='integration_width',
26                         help='The window over which peaks should be integrated',
27                         dtype=float,
28                         default=0.1,
29                         group=groups['settings'],
30                         required=True)
31     self.add_parameter(name='peakheight',
32                         help='Peak height parameter',
33                         dtype=int,
34                         default=2,
35                         group=groups['settings'],
36                         required=True)
37
38
39 def execute_analysis(self) :
40     """
41     # Copy parameters to local variables. This is purely for convenience and is not mandatory.
42     # NOTE: Input parameters are automatically record (i.e., we don't need to do anything special)
43     msidata = self['msidata']
44     mzdata = self['mzdata']
45     integration_width = self['integration_width']
46     peakheight = self['peakheight']
47
48     # Implementation of my peakfinding algorithm
49
50     ...
51
52     # Return the result.
53     # NOTE: We need to return the output in the order we specified them in self.data_names
54     # NOTE: The outputs will be automatically recorded (i.e., we don't need to do anything special)
55     return peakCube, peakMZ
56     self['peak_cube'] = peakCube
57
58     ...
59
60 # Defining a main function is optional. However, allowing a user to directly execute your analysis
61 # from the command line is simple, as we can easily reuse the command-line driver module
62 if __name__ == "__main__":
63     from omsi.analysis.omsii_analysis_driver import cl_analysis_driver
64     cl_analysis_driver(analysis_class=omsi_mypeakfinder).main()

```

1.1 Creating a new analysis skeleton

- Copy the analysis template to the appropriate location where your analysis should live (NOTE: The analysis template may have been updated since this documentation was written). Any new analysis should be located in a submodule of the `omsi.analysis`. module. E.g., if you implement a new peak finding algorithm, it

should be placed in omsi/analysis/findpeaks. For example:

```
cp omsi/templates/omsi_analysis_template.py openmsi-tk/omsi/analysis/findpeaks/omsi_mypeakfinder.py
```

- Replace all occurrences of omsi_analysis_template in the file with the name of your analysis class, e.g., omsi_mypeakfinder. You can do this easily using “Replace All” feature of most text editors or on most Unix systems (e.g., Linux or MacOS) on the commandline via:

```
cd openmsi-tk/omsi/analysis/findpeaks
sed -i.bak 's/omsi_analysis_template/omsi_mypeakfinder/' omsi_mypeakfinder.py
rm omsi_mypeakfinder.py.bak
```

- Add your analysis to the `__init__.py` file of the python module where your analysis lives. In the `__init__.py` file you need to add the name of your analysis class to the `all__` list and add a import of your class, e.g., `from omsi_mypeakfinder import *`. For example:

```
1 all__ = [ "omsi_mypeakfinder", "omsi_findpeaks_global" , ... ]
2 from omsi_findpeaks_global import *
3 from omsi_findpeaks_local import *
4 ...
```

- The analysis template contains documentation on how to implement a new analysis. Simply search for `EDIT_ME` to locate where you should add code and descriptions of what code to add.

1.2 Specifying analysis inputs and outputs

In the `__init__` function specify the names of the input parameters of your analysis as well as the names of the output data generated by your analysis. Note, the `__init__` function should have a signature that allows us to instantiate the analysis without having to provide any inputs. E.g.,

```
1 def __init__(self, name_key="undefined"):
2     """Initialize the basic data members"""
3
4     super(omsi_mypeakfinder, self).__init__()
5     self.analysis_identifier = name_key
6
7     # Define the names of the outputs
8     self.data_names = ['peak_cube', 'peak_mz']
9
10    # Define the input parameters
11    dtypes = self.get_default_dtypes()      # List of default data types. Build-in types are
12                                         # available as well but can be safely used directly as well
13    groups = self.get_default_parameter_groups() # List of default groups to organize parameters. We
14                                         # to use the 'input' group for all input data to be
15                                         # as this will make the integration with OpenMSI eas
16    self.add_parameter(name='msidata',
17                       help='The MSI dataset to be analyzed',
18                       dtype=dtypes['ndarray'],
19                       group=groups['input'],
20                       required=True)
21    self.add_parameter(name='mzdata',
22                       help='The m/z values for the spectra of the MSI dataset',
23                       dtype=dtypes['ndarray'],
24                       group=groups['input'],
25                       required=True)
26    self.add_parameter(name='integration_width',
27                       help='The window over which peaks should be integrated',
28                       dtype=float,
```

```

29         default=0.1,
30         group=groups['settings'],
31         required=True)
32     self.add_parameter(name='peakheight',
33                         help='Peak height parameter',
34                         dtype=int,
35                         default=2,
36                         group=groups['settings'],
37                         required=True)

```

1.3: Implementing the execute_analysis function

1.3.1 Document your execute_analysis function. OpenMSI typically uses Sphynx notation in the doc-string. The doc-string of the execute_analysis(..) function and the class are used by the analysis driver modules to provide a description of your analysis as part of the help and will also be included in the help string generated by the `get_help_string()` inherited via `analysis_base` function.

```

1 def execute_analysis(self) :
2     """This analysis computes global peaks in MSI data...
3 """

```

1.3.2 Implement your analysis. For convenience it is often useful to assign the your parameters to local variables, although, this is by no means required. Note, all values are stored as 1D+ numpy arrays, however, are automatically converted for you, so that we can just do:

```
integration_width = self['integration_width']
```

1.3.4 Return the outputs of your analysis in the same order as specified in the `self.data_names` you specified in your `__init__` function (here `['peak_cube', 'peak_mz']`):

```
return peakCube, peakMZ
```

Results returned by your analysis will be automatically saved to the respective output variables. This allows users to conveniently access your results and it enables the OpenMSI file API to save your results to file. We here automatically convert single scalars to 1D numpy arrays to ensure consistency. Although, the data write function can handle a large range of python built_in types by automatically converting them to numpy for storage in HDF5, we generally recommend to convert use numpy directly here to save your data.

With this you have now completed the basic integration of your analysis with the OpenMSI framework.

4.3.2 Step 2) Integrating the Analysis with the OpenMSI Web API:

Once the analysis is stored in the OMSI file format, integration with `qmetadata` and `qcube` calls of the web API is automatic. The `qmetadata` and `qcube` functions provide general purpose access to the data so that we can immediately start to program against our analysis.

Some applications—such as the OpenMSI web-based viewer—utilize the simplified, special data access patterns `qslice`, `qspectrum`, and `qmz` in order to interact with the data. The default implementation of these function available in `oms1.analysis.analysis_base` exposes the data from all dependencies of the analysis that support these patterns. For full integration with the web API, however, we need to implement this functionality in our analysis class. The `qmz` pattern in particular is relevant to both the `qslice` and `qspectrum` pattern and should be always implemented as soon as one of the two patterns is defined.

2.1 Implementing the qslice pattern

```
1  class omsi_myanalysis(analysis_base) :
2      ...
3
4      @classmethod
5      def v_qslice(cls , anaObj , z , viewer_option=0) :
6          """Implement support for qslice URL requests for the viewer
7
8          anaObj: The omsi_file_analysis object for which slicing should be performed.
9          z: Selection string indicating which z values should be selected.
10         viewer_option: An analysis can provide different default viewer behaviors
11             for how slice operation should be performed on the data.
12             This is a simple integer indicating which option is used.
13
14         :returns: numpy array with the data to be displayed in the image slice
15             viewer. Slicing will be performed typically like [::,zmin:zmax].
16
17         """
18
19         from omsi.shared.omsidata_selection import *
20         #Implement custom analysis viewer options
21         if viewer_option == 0 :
22             dataset = anaObj[ 'labels' ] #We assume labels was a 3D image cube of labels
23             zselect = selection_string_to_object(z)
24             return dataset[ : , : , zselect ]
25
26         #Expose recursively the slice options for any data dependencies. This is useful
27         #to allow one to trace back data and generate complex visualizations involving
28         #multiple different data sources that have some form of dependency in that they
29         #led to the generation of this analysis. This behavior is already provided by
30         #the default implementation of this function ins analysis_base.
31         elif viewer_option >= 0 :
32             #Note, the base class does not know out out viewer_options so we need to adjust
33             #the vieweoOption accordingly by subtracting the number of our custom options.
34             return super(omsi_myanalysis,cls).v_qslice( anaObj , z , viewer_option-1 )
35             #Invalid viewer_option
36         else :
37             return None
38
39     @classmethod
40     def v_qslice_viewer_options(cls , anaObj ) :
41         """Define which viewer_options are supported for qspectrum URL's"""
42         #Get the options for all data dependencies
43         dependent_options = super(omsi_findpeaks_global,cls).v_qslice_viewer_options(anaObj)
44         #Define our custom viewer options
45         re = ["Labels"] + dependent_options
46         return re
```

NOTE: We here convert the selection string to a python selection (i.e., a list, slice, or integer) object using the `omsi.shared.omsidata_selection.check_selection_string(...)`. This has the advantage that we can use the given selection directly in our code and avoids the use of a potentially dangerous `eval`, e.g., `return eval("dataset[:, :, %s]" %(z,))`. While we can also check the validity of the selection string using `omsi.shared.omsidata_selection.check_selection_string(...)`, it is recommended to convert the string to a valid python selection to avoid possible attacks.

2.2 Implementing the qspectrum pattern

```

1  class omsi_myanalysis(analysis_base) :
2      ...
3      @classmethod
4      def v_qspectrum( cls, anaObj , x , y , viewer_option=0 ) :
5          """Implement support for qspectrum URL requests for the viewer.
6
7          anaObj: The omsi_file_analysis object for which slicing should be performed
8          x: x selection string
9          y: y selection string
10         viewer_option: If multiple default viewer behaviors are available for a given
11             analysis then this option is used to switch between them.
12
13         :returns: The following two elemnts are expected to be returned by this function :
14
15             1) 1D, 2D or 3D numpy array of the requested spectra. NOTE: The spectrum axis,
16                 e.g., mass (m/z), must be the last axis. For index selection x=1,y=1 a 1D array
17                 is usually expected. For indexList selections x=[0]&y=[1] usually a 2D array
18                 is expected. For range selections x=0:1&y=1:2 we one usually expect a 3D array.
19                 This behavior is consistent with numpy and h5py.
20
21             2) None in case that the spectra axis returned by v_qmz are valid for the
22                 returned spectrum. Otherwise, return a 1D numpy array with the m/z values
23                 for the spectrum (i.e., if custom m/z values are needed for interpretation
24                 of the returned spectrum).This may be needed, e.g., in cases where a
25                 per-spectrum peak analysis is performed and the peaks for each spectrum
26                 appear at different m/z values.
27
28         Developer Note: h5py currently supports only a single index list. If the user provides
29         an index-list for both x and y, then we need to construct the proper merged list and
30         load the data manually, or, if the data is small enough, one can load the full data
31         into a numpy array which supports mulitple lists in the selection. This, however, is
32         only recommended for small datasets.
33
34     """
35
36     data = None
37     customMZ = None
38     if viewer_option == 0 :
39         from omsi.shared.omsi_data_selection import *
40         dataset = anaObj[ 'labels' ]
41         if (check_selection_string(x) == selection_type['indexlist']) and \
42             (check_selection_string(y) == selection_type['indexlist']) :
43             #Assuming that the data is small enough, we can handle the multiple list
44             #selection case here just by loading the full data use numpy to do the
45             #subselection. Note, this version would work for all selection types but
46             #we would like to avoid loading the full data if we don't have to.
47             xselect = selection_string_to_object(x)
48             yselect = selection_string_to_object(y)
49             data = dataset[:,xselect,yselect,:]
50             #Since we already confirmed that both selection strings are index lists we could
51             #also just do an eval as follows.
52             #data = eval("dataset[:,%s,%s, :]" %(x,y))
53     else :
54         xselect = selection_string_to_object(x)
55         yselect = selection_string_to_object(y)
56         data = dataset[xselect,yselect,:]
```

```
57     #Return the spectra and indicate that no customMZ data values (i.e. None) are needed
58     return data, None
59
60     #Expose recursively the slice options for any data dependencies. This is useful
61     #to allow one to trace back data and generate complex visualizations involving
62     #multiple different data sources that have some form of dependency in that they
63     #led to the generation of this analysis. This behavior is already provided by
64     #the default implementation of this function in analysis_base.
65     elif viewer_option >= 0 :
66         #Note, the base class does not know about viewer_options so we need to adjust
67         #the viewerOption accordingly by subtracting the number of our custom options.
68         return super(omsi_findpeaks_global,cls).v_qspectrum( anaObj , x , y, viewer_option-1)
69
70     return data , customMZ
71
72     @classmethod
73     def v_qspectrum_viewer_options(cls , anaObj ) :
74         """Define which viewer_options are supported for qspectrum URL's"""
75         #Get the options for all data dependencies
76         dependent_options = super(omsi_findpeaks_global,cls).v_qspectrum_viewer_options(anaObj)
77         #Define our custom viewer options
78         re = ["Labels"] + dependent_options
79         return re
```

2.3 Implementing the qmz pattern

```
1  class omsi_myanalysis(analysis_base) :
2      ...
3
4      @classmethod
5      def v_qmz(cls, anaObj, qslice_viewer_option=0, qspectrum_viewer_option=0) :
6          """Implement support for qmz URL requests for the viewer.
7
7           Get the mz axes for the analysis
8
9           anaObj: The omsi_file_analysis object for which slicing should be performed.
10          qslice_viewer_option: If multiple default viewer behaviors are available for
11              a given analysis then this option is used to switch between them
12              for the qslice URL pattern.
13          qspectrum_viewer_option: If multiple default viewer behaviors are available
14              for a given analysis then this option is used to switch between
15              them for the qspectrum URL pattern.
16
17          :returns: The following four arrays are returned by the analysis:
18
19              - mzSpectra : 1D numpy array with the static mz values for the spectra.
20              - labelSpectra : String with label for the spectral mz axis
21              - mzSlice : 1D numpy array of the static mz values for the slices or
22                  None if identical to the mzSpectra array.
23              - labelSlice : String with label for the slice mz axis or None if
24                  identical to labelSpectra.
25              - valuesX: The values for the x axis of the image (or None)
26              - labelX: Label for the x axis of the image
27              - valuesY: The values for the y axis of the image (or None)
28              - labelY: Label for the y axis of the image
29              - valuesZ: The values for the z axis of the image (or None)
30              - labelZ: Label for the z axis of the image
31
32
```

```

33     Developer Note: Here we need to handle the different possible combinations
34     for the different viewer_option patterns. It is in general safe to populate
35     mzSlice and labelSlice also if they are identical with the spectrum settings,
36     however, this potentially has a significant overhead when the data is transferred
37     via a slow network connection, this is why we allow those values to be None
38     in case that they are identical.
39
40     """
41     #The four values to be returned
42     mzSpectra = None
43     labelSpectra = None
44     mzSlice = None
45     labelSlice = None
46     peak_cube_shape = anaObj[ 'labels' ].shape #We assume labels was a 3D image cube of labels
47     valuesX = range(0, peak_cube_shape[0])
48     labelX = 'pixel index X'
49     valuesY = range(0, peak_cube_shape[1])
50     labelY = 'pixel index Y'
51     valuesZ = range(0, peak_cube_shape[2]) if len(peak_cube_shape) > 3 else None
52     labelZ = 'pixel index Z' if len(peak_cube_shape) > 3 else None
53
54     #Both qslice and qspectrum here point to our custom analysis
55     if qspectrum_viewer_option == 0 and qslice_viewer_option==0: #Loadings
56         mzSpectra = anaObj[ 'labels' ][:,:]
57         labelSpectra = "Labels"
58     #Both viewer_options point to a data dependency
59     elif qspectrum_viewer_option > 0 and qslice_viewer_option>0 :
60         mzSpectra, labelSpectra, mzSlice, labelSlice = \
61             super(omsi_findpeaks_global,cls).v_qmz( anaObj, \
62                   qslice_viewer_option-1 , qspectrum_viewer_option-1)
63     #Only the a qslice options point to a data dependency
64     elif qspectrum_viewer_option == 0 and qslice_viewer_option>0 :
65         mzSpectra = anaObj[ 'peak_mz' ][:,:]
66         labelSpectra = "m/z"
67         tempA, tempB, mzSlice, labelSlice, valuesX, labelX, valuesY, labelY, valuesZ, labelZ
68             super(omsi_findpeaks_global,cls).v_qmz( anaObj, \
69                   qslice_viewer_option-1 , 0)
70     #Only the qspectrum option points to a data dependency
71     elif qspectrum_viewer_option > 0 and qslice_viewer_option==0 :
72         mzSlice = anaObj[ 'peak_mz' ][:,:]
73         labelSlice = "m/z"
74         # Ignore the spatial axes and slice axis as we use our own
75         mzSpectra, labelSpectra, tempA, tempB, vX, vY, lX, lY, vZ, lZ = \
76             super(omsi_findpeaks_global,cls).v_qmz( anaObj, \
77                   0 , qspectrum_viewer_option-1)
78
79     return mzSpectra, labelSpectra, mzSlice, labelSlice, valuesX, labelX, valuesY, labelY, va

```

4.3.3 Step 3) Making your analysis self-sufficient

Making your analysis self sufficient is trivial. If you used the analysis template provided by the toolkit, then you have already completed this step for free. In order to allow a user to run our analysis from the command line we need a main function. We here can simply reuse the command line driver provided by the toolkit. Using the command line driver we can run the analysis via:

```
python omsi/analysis/omsi_analysis_driver.py finpeaks.omsi_mypeakfinder  
--msidata "test_brain_convert.h5:/entry_0/data_0"  
--mzdata "test_brain_convert.h5:/entry_0/data_0/mz"  
--save "test_ana_save.h5"
```

To now enable us to execute our analysis module itself we simply need to add the following code (which is already part of the template)

```
1 if __name__ == "__main__":  
2     from omsi.analysis.omsi_analysis_driver import cl_analysis_driver  
3     cl_analysis_driver(analysis_class=omsi_mypeakfinder).main()
```

With this we can now directly execute our analysis from the command line, get a command-line help, specify all our input parameters on the command line, and save our analysis to file. To run the analysis we can now do:

```
python omsi/analysis/findpeaks/omsi_findpeaks_global.py  
--msidata "test_brain_convert.h5:/entry_0/data_0"  
--mzdata "test_brain_convert.h5:/entry_0/data_0/mz"  
--save "test_ana_save.h5"
```

This will run our peak finder on the given input data and save the result to the first experiment in the test_ana_save.h5 (the output file will be automatically created if it does not exist).

The command line driver also provides us a well-formatted help based on the our parameter specification and the doc-string of the analysis class and its execute_analysis(...) function. E.g:

```
1 >>> python omsi/analysis/findpeaks/omsi_findpeaks_global.py --help  
2  
3 usage: omsi_findpeaks_global.py [-h] [--save SAVE] --msidata MSIDATA --mzdata  
4 MZDATA [--integration_width INTEGRATION_WIDTH]  
5 [--peakheight PEAKHEIGHT]  
6 [--slwindow SLWINDOW]  
7 [--smoothwidth SMOOTHWIDTH]  
8  
9 class description:  
10  
11     Basic global peak detection analysis. The default implementation  
12     computes the peaks on the average spectrum and then computes the peak-cube data,  
13     i.e., the values for the detected peaks at each pixel.  
14  
15     TODO: The current version assumes 2D data  
16  
17 execution description:  
18  
19         Execute the global peak finding for the given msidata and mzdata.  
20  
21 optional arguments:  
22     -h, --help                  show this help message and exit  
23     --save SAVE                 Define the file and experiment where the analysis  
24                                         should be stored. A new file will be created if the  
25                                         given file does not exists but the directory does. The  
26                                         filename is expected to be of the form:  
27                                         <filename>:<entry_#> . If no experiment index is  
28                                         given, then experiment index 0 (i.e, entry_0) will be  
29                                         assumed by default. A validpath may, e.g, be  
30                                         "test.h5:/entry_0" or jus "test.h5" (default: None)  
31  
32  
33
```

```

34 analysis settings:
35     Analysis settings
36
37     --integration_width INTEGRATION_WIDTH
38             The window over which peaks should be integrated
39             (default: 0.1)
40     --peakheight PEAKHEIGHT
41             Peak height parameter (default: 2)
42     --slwindow SLWINDOW Sliding window parameter (default: 100)
43     --smoothwidth SMOOTHWIDTH
44             Smooth width parameter (default: 3)
45
46 input data:
47     Input data to be analyzed
48
49     --msidata MSIDATA      The MSI dataset to be analyzed (default: None)
50     --mzdata MZDATA        The m/z values for the spectra of the MSI dataset
51             (default: None)
52
53 how to specify ndarray data?
54 -----
55 n-dimensional arrays stored in OpenMSI data files may be specified as
56 input parameters via the following syntax:
57     -- MSI data: <filename>.h5:/entry_#/data_#
58     -- Analysis data: <filename>.h5:/entry_#/analysis_#/<dataname>
59     -- Arbitrary dataset: <filename>.h5:<object_path>
60 E.g. a valid definition may look like: 'test_brain_convert.h5:/entry_0/data_0'
61 In rear cases we may need to manually define an array (e.g., a mask)
62 Here we can use standard python syntax, e.g, '[1,2,3,4]' or '[[1, 3], [4, 5]]'
63
64 This command-line tool has been auto-generated using the OpenMSI Toolkit

```

4.4 Writing a new analysis class for BASTet – Part 3: Customizing core features

4.4.1 Custom data save

In most cases the default data save and restore functions should be sufficient. However, the `analysis_base` API also supports implementation of custom HDF5 write. To extend the existing data write code, simple implement the following function provided by `analysis_base`.

```

1 def add_custom_data_to_omsi_file(self , analysisGroup) :
2     """This function can be optionally overwritten to implement a custom data write
3     function for the analysis to be used by the omsi_file API.
4
5     Note, this function should be used only to add additional data to the analysis
6     group. The data that is written by default is typically still written by the
7     omsi_file_experiment.create_analysis() function, i.e., the following data is
8     written by default: i) analysis_identifier ,ii) get_analysis_type,
9     iii)_data_list, iv) __parameter_list , v) __dependency_list. Since the
10    omsi_file_experiment.create_analysis() functions takes care of setting up the
11    basic structure of the analysis storage (included the subgroups for storing
12    parameters and data dependencies) this setup can generally be assumed to exist
13    before this function is called. This function is called automatically at the
14    end omsi_file_experiment.create_analysis() (i.e, actually

```

```
15     omsi_file_analysis.__populate_analysis__(...)) so that this function does not need
16     to be called explicitly.
17
18     Keyword Arguments:
19
20     :param analysisGroup: The omsi_file_analysis object of the group for the
21         analysis that can be used for writing.
22
23     """
24
25     pass
```

4.4.2 Custom analysis restore

Similarly in order implement custom data restore behavior we can overwrite the default implementation of `omsi.analysis.analysis_base.analysis_base.read_from_omsi_file()`. In this case one will usually call the default implementation via `super(omsi_myanalysis, self).read_from_omsi_file(...)` first and then add any additional behavior.

4.4.3 Custom analysis execution

Analysis are typically executed using the `omsi.analysis.analysis_base.analysis_base.execute()` function we inherit from `py:class:omsi.analysis.analysis_base.analysis_base`. The `execute()` function controls many pieces, from recording and defining input parameters and outputs to executing the actual analysis. We, therefore, for NOT recommend to overwrite the `execute(..)` function, but rather to customize specific portions of the execution. To do this, `execute()` is broken into a number of functions which are called in a specific order. In this way we can easily overwrite select functions to customize a particular feature without having to overwrite the complete `execute(..)` function.

Customizing setting of parameters

First, the `execute` function uses `omsi.analysis.analysis_base.analysis_base.update_analysis_parameters()` to set all parameters that have been passed to `execute` accordingly. The default implementation of `update_analysis_parameters(..)`, hence, simply calls `self.set_parameter_values(...)` to set all parameter values. We can customize this behavior simply by overwriting the `update_analysis_parameters(...)` function.

Customizing setting of default settings

Second, the `execute` function uses the `omsi.analysis.analysis_base.analysis_base.define_missing_parameter` function to set any required parameters that have not been set by the user to their respective values. Overwrite this function to customize how default parameter values are determined/set.

Customizing the recording of runtime information

The recording of runtime information is performed using the `omsi.shared.run_info_data.run_info_dict()` data structure. This data structure provides a series of functions that are called in order, in particular:

- `omsi.shared.run_info_data.run_info_dict.clear()` : This function is called first to clear the runtime dictionary. This is the same as the standard `dict.clear`.

- `omsi.shared.run_info_data.run_info_dict.record_preeexecute()` : This function is called before the `execute_analysis` function is called and records basic system information,
- `omsi.shared.run_info_data.run_info_dict.record_postexecute()` : This function is called after the `execute_analysis` function has completed to record additional information, e.g, the time and duration of the analysis,
- `omsi.shared.run_info_data.run_info_dict..runinfo_clean_up()` : This function is called at the end to clean up the recorded runtime information. By default, `runinfo_clean_up()` removes any empty entries, i.e., key/value pairs where the value is either None or an empty string.

We can customize any of these function by implementing a derived class of `omsi.shared.run_info_data.run_info_dict()` where we can overwrite the functions. In order to use our derived class we can then assign our object to `omsi.analysis.analysis_base.analysis_base.run_info()`. This design allows us to modularly use the runtime information tracking also for other tasks, not just with our analysis base infrastructure.

Customizing the analysis execution

The analysis is completely implemented in the `omsi.analysis.analysis_base.analysis_base.execute_analysis()` function, which we have to implement in our derived class, i.e, running the analysis is fully custom anyways.

Customizing the recording of analysis outputs

Finally (i.e., right before returning analysis results), `execute(..)` uses the `omsi.analysis.analysis_base.analysis_base.record_execute_analysis_outputs()` function to save all analysis outputs. Analysis outputs are stored in the `self._data_list` variable. We can save analysis outputs simply by slicing and assignment, e.g., `self[output_name] = my_output`. By overwriting `record_execute_analysis_outputs(...)` we can customize the recording of data outputs.

DEFINING AND EXECUTING ANALYSIS WORKFLOWS

Figure *Illustration of an example workflow for image normalization*, illustrates the basic steps of using analysis workflows, i.e.,:

1. Create the analysis tasks
2. Define the analysis inputs
3. Execute

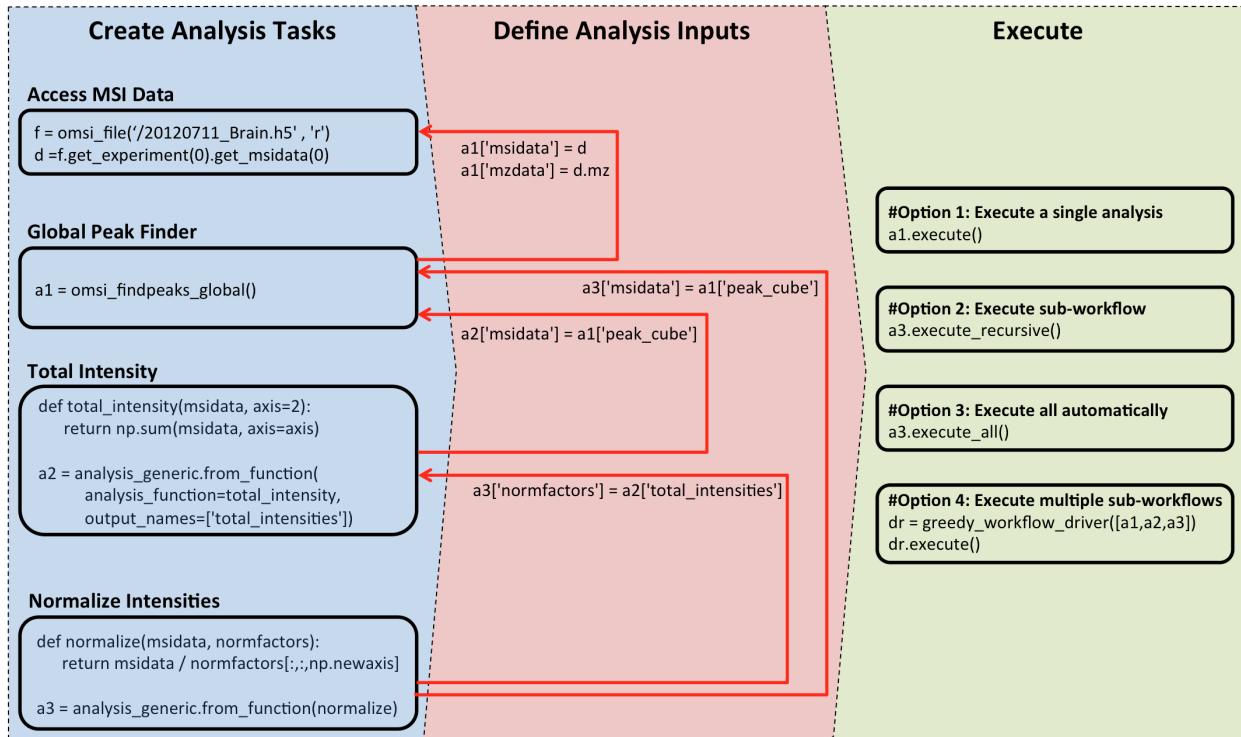


Fig. 5.1: Illustration of an example workflow for image normalization

In the following we will use a simple analysis—workflow in which we compute a peak-cube from a raw MSI dataset and then compute an NMF from the peak cube—to illustrate the main steps involved for performing complex analysis workflows.

5.1 Step 1: Create the analysis tasks:

First we need to create our main analysis objects.

```
1 from omsi.dataformat.omsi_file import *
2 from omsi.analysis.findpeaks.omsi_findpeaks_global import omsi_findpeaks_global
3 from omsi.analysis.multivariate_stats.omsi_nmf import omsi_nmf
4
5 # Open a file to get some MSI data
6 f = omsi_file('/Users/oruebel/Devel/openmsi-data/msidata/20120711_Brain.h5', 'r')
7 d = f.get_experiment(0).get_msidata(0)
8
9 # Specify the analysis workflow
10 # Create a global peak finding analysis
11 a1 = omsi_findpeaks_global()          # Create the analysis
12 # Create an NMF that processes our peak cube
13 a2['numIter'] = 2                   # Set input to perform 2 iterations only
```

5.2 Step 2: Define analysis inputs:

We can define the input parameters of analysis simply using standard dict-like assignment. Any dependencies between analysis tasks or OpenMSI files are created automatically for us.

```
1 # Define the inputs of the global peak finder
2 a1['msidata'] = d                  # Set the input msidata
3 a1['mzdata'] = d.mz                # Set the input mz data
4 # Define the inputs of the NMF
5 a2['msidata'] = a1['peak_cube']    # Set the input data to the peak cube
6 a2['numIter'] = 2                  # Set input to perform 2 iterations only
```

NOTE: So far we have only specified our workflow. We have not executed any analysis yet, nor have we loaded any actual data yet.

5.3 Step 3: Execute

Finally we need to execute our analyses. For this we have various options, depending on which parts of our workflow we want to execute.

5.3.1 Executing a single analysis

To execute a single analysis, we can simply call the `execute()` function of our analysis. Note, the `execute` may raise and `AnalysisReadyError` in case that the inputs of the analysis are not ready. E.g.:

```
1 a2.execute()      # Will fail with ``AnalysisReadyError``
```



```
1 a1.execute()      # Will successfully execute a1
```

5.3.2 Executing a single sub-workflow

To execute a single analysis including any missing dependencies, we can simply call the `execute_recursive()` function. E.g.:

```
1 a2.execute_recursive() # Will successfully execute a1
```

The above will execute a1 as well as a2 since a2 depends on a1.

NOTE: Recursive execution will only execute other analyses that are actually needed to complete our analysis and analysis results of dependent analyses that have been executed before will be reused. E.g., if we would call a2.execute_recursive() again, then only a2 would be executed again.

NOTE: When executing multiple dependent analyses, then the execution is typically controlled by a workflow executor py:meth:*omsi.workflow.executor*. By default, `execute_recursive(..)` will automatically create a default driver. If we want to customize the driver to be used then we can simply assign a driver to the analysis before-hand by setting the py:var:*omsi.analysis.base.analysis_base.driver*' instance variable.

5.3.3 Executing all analyses

To run all analyses that have been created—*independent* of whether they depend on each other or not—we can simply call `omsi.analysis.base.analysis_base.execute_all()`.

```
1 a1.execute_all() # Execute all analyses
```

The above will execute any analysis that have not up-to-date. NOTE: In contrast to py:meth:*omsi.analysis.base.analysis_base.execute* and py:meth:*omsi.analysis.base.analysis_base.execute_recursive*, this is a class-level method and not an object-method. Again, the function uses a workflow driver, which we can customize by providing as driver as input to the function.

5.3.4 Executing multiple sub-workflows

To explicitly execute a subset of analyses (and all their dependencies) we can explicitly define a driver for the workflow we want to execute:

```
1 from omsi.workflow.driver.greedy_executor import greedy_executor
2 driver = greedy_executor() # Create a driver
3 driver.add_analysis(a1) # Add one ore more analyses
4 driver.add_analysis(a2)
5 driver.execute() # Execute the workflow and its dependencies
```



```
1 driver2 = greedy_executor()
2 driver2.add_analysis_all() # Add all analyses
3 driver2.execute() # Execute all analyses
```

5.4 Example: Normalizing an image

The goal of this example is to 1) illustrate the general concepts of how we can define analysis workflows and 2) illustrate the use of simple wrapped functions in combination with integrated analytics to create complex analysis workflows. The example shown below defines a basic image normalization workflow in which we:

1. Compute a reduced peak cube from an MSI image using the global peak finding analysis provided by BASTet
2. Use a simple wrapped function to compute the total intensity image for the peak cube dataset computed in step 1
3. use a simple wrapped function to normalize the peak cube computed in step 1 using the total intensity image computed in step 2

This is the same workflow as shown in Figure *Illustration of an example workflow for image normalization*.

```

1 # Illustration of the basic image normalization workflow defined below:
2 #
3 # +-----+-----+-----+
4 # | a1 | a2 | a3 |
5 # +---+---+---+---+---+---+
6 # | msidata | peak_cube | msidata | total_intensities | norm_factors | output
7 # | | | | | | |
8 # | mzdata | | | axis=2 | | |
9 # +-----+-----+-----+-----+-----+-----+
10 # | | | | | | |
11 # | | | | | | |
12 # +-----+-----+-----+

```

```

1 import numpy as np
2 from omsi.shared.log import log_helper
3 log_helper.set_log_level('DEBUG')
4 from omsi.analysis.findpeaks.omsi_findpeaks_global import omsi_findpeaks_global
5 from omsi.dataformat.omsi_file.main_file import omsi_file
6 from omsi.analysis.generic import analysis_generic
7
8 # Define a simple function to compute the total intensity image
9 def total_intensity(msidata, axis=2):
10     import numpy as np
11     return np.sum(msidata, axis=axis)
12
13 # Define a simple function to normalize an MSI data cube by per-spectrum normalization factors
14 def normalize_intensities(msidata, normfactors):
15     import numpy as np
16     return msidata / normfactors[:, :, np.newaxis]
17
18 # Get an example MSI image
19 f = omsi_file('/Users/oruebel/Devel/openmsi-data/msidata/20120711_Brain.h5', 'r')
20 d = f.get_experiment(0).get_msidata(0)
21
22 # Define the global peak finder
23 a1 = omsi_findpeaks_global()
24 a1['msidata'] = d
25 a1['mzdata'] = d.mz
26
27 # Define compute of total intensity image
28 a2 = analysis_generic.from_function(analysis_function=total_intensity,
29                                     output_names=['total_intensities'])
30 a2['msidata'] = a1['peak_cube']
31
32 # Define the normalization of the peak cube
33 a3 = analysis_generic.from_function(normalize_intensities)
34 a3['msidata'] = a1['peak_cube']
35 a3['normfactors'] = a2['total_intensities']
36
37 # To run the workflow we now have several basic options
38 #
39 # 1) a3.execute_recursive() : Recursively execute the last analysis and all its dependencies (i.e.,
40 # 2) a1.execute_all() : Tell any analysis to execute all available analyses (i.e., a1, a2, a3)
41 # 3) Create our own workflow driver to control the execution of the analyses
42 # 4) Manually call execute on a1, a2, and a3 in order of their dependencies
43
44 # Execute the workflow

```

45 a3.execute_recursive()

WORKFLOW TOOLS

Similar to the `omsi.workflow.driver.cl_analysis_driver` (and the corresponding tool `omsi.tools.run_analysis`) for running single analysis tasks, BASTet provides basic tools for executing complete workflows via the concept of workflow drivers. Users may implement their own drivers using the appropriate base classes `omsi.workflow.driver.base`.

Some basic drivers and tools are already available with BASTet, e.g., the `omsi.workflow.driver.cl_workflow_driver` module (and the corresponding tool `omsi.tools.run_workflow`) defines a driver for driving and executing one or multiple workflows defined via workflow scripts, directly from the command-line.

6.1 Workflow Scripts

Workflow scripts are regular python scripts that include the i) creation of the analysis objects, and ii) full or partial definition of analysis parameters but usually **NOT** the actual execution of any of the analyses. Following our example from earlier, we may simply save the following code in python source file, e.g, `normalize_image.py`.

```
1 import numpy as np
2 from omsi.analysis.findpeaks.omsi_findpeaks_global import omsi_findpeaks_global
3 from omsi.dataformat.omsi_file.main_file import omsi_file
4 from omsi.analysis.generic import analysis_generic
5
6 # Define a simple function to compute the total intensity image
7 def total_intensity(msidata, axis=2):
8     import numpy as np
9     return np.sum(msidata, axis=axis)
10
11 # Define a simple function to normalize an MSI data cube by per-spectrum normalization factors
12 def normalize_intensities(msidata, normfactors):
13     import numpy as np
14     return msidata / normfactors[:, :, np.newaxis]
15
16 # Define the global peak finder
17 a1 = omsi_findpeaks_global()
18
19 # Define compute of total intensity image
20 a2 = analysis_generic.from_function(analysis_function=total_intensity,
21                                     output_names=['total_intensities'])
22 a2['msidata'] = a1['peak_cube']
23
24 # Define the normalization of the peak cube
25 a3 = analysis_generic.from_function(normalize_intensities)
```

```

26 a3['msidata'] = a1['peak_cube']
27 a3['normfactors'] = a2['total_intensities']

```

When using our command-line tool, all parameters that are not defined for any of the analyses are automatically exposed via command-line options. In contrast to our previous example, we here, e.g., do not set the input msidata and mzdata parameters for our global peak finder (a1). In this way, we can now easily set the input file we want to process directly via the command line. In cases where we want to expose a parameter via the command line but still want to provide a good default setting for the user, we can set the default value of a parameter via, e.g., `a1.get_parameter_data_by_name('peakheight')['default'] = 3.`

To execute our above example from the command line we can now simply do the following:

```

python run_workflow.py --script normalize_image.py
    --ana_0:msidata $HOME/20120711_Brain.h5:/entry_0/data_0
    --ana_0:mzdata $HOME/20120711_Brain.h5:/entry_0/data_0/mz

```

In order to avoid collisions between parameters with the same name for different analyses, the tool prepends the unique analysis_identifier to each parameter. Since we did not set any explicit analysis_identifier (e.g., via `'a1.analysis_identifier='a1'`), the tool automatically generated unique identifiers (i.e., ana_0, ana_1, and ana_3 for our 3 analyses). To view all available command line option we can simply call the script with `--help`. If one or more workflow scripts are given (here via separate `--script` parameters), then all unfilled options of those workflows and the corresponding analyses will be listed as. E.g.

```

1 newlappy:tools oruebel$ python run_workflow.py --script normalize_image.py --help
2 usage: run_workflow.py --script SCRIPT [--save SAVE] [--profile]
3                               [--memprofile]
4                               [--loglevel {INFO,WARNING,CRITICAL,ERROR,DEBUG,NOTSET}]
5                               --ana_0:msidata ANA_0:MSIDATA --ana_0:mzdata
6                               ANA_0:MZDATA
7                               [--ana_0:integration_width ANA_0:INTEGRATION_WIDTH]
8                               [--ana_0:peakheight ANA_0:PEAKHEIGHT]
9                               [--ana_0:slwindow ANA_0:SLWINDOW]
10                              [--ana_0:smoothwidth ANA_0:SMOOTHWIDTH]
11                              [--ana_1:axis ANA_1:AXIS]
12                              [--reduce_memory_usage REDUCE_MEMORY_USAGE]
13                              [--synchronize SYNCHRONIZE] [-h]
14
15 Execute analysis workflow(s) based on a given set of scripts
16
17 required arguments:
18   --script SCRIPT           The workflow script to be executed. Multiple scripts
19                                may be added via separate --script arguments (default:
20                                None)
21
22 optional arguments:
23   --save SAVE               Define the file and experiment where all analysis
24                                results should be stored. A new file will be created
25                                if the given file does not exists but the directory
26                                does. The filename is expected to be of the form:
27                                <filename>:<entry_#>. If no experiment index is
28                                given, then experiment index 0 (i.e., entry_0) will be
29                                assumed by default. A validpath may, e.g, be
30                                "test.h5:/entry_0" or just "test.h5" (default: None)
31   --profile                 Enable runtime profiling of the analysis. NOTE: This
32                                is intended for debugging and investigation of the
33                                runtime behavior of an analysis. Enabling profiling
34                                entails certain overheads in performance (default:
35                                False)

```

```

36  --memprofile          Enable runtime profiling of the memory usage of
37  analysis. NOTE: This is intended for debugging and
38  investigation of the runtime behavior of an analysis.
39  Enabling profiling entails certain overheads in
40  performance. (default: False)
41  --loglevel {INFO,WARNING,CRITICAL,ERROR,DEBUG,NOTSET}
42  Specify the level of logging to be used. (default:
43  INFO)
44  -h, --help             show this help message and exit
45
46 ana_0:omsi.analysis.findpeaks.omsi_findpeaks_global:analysis settings:
47   Analysis settings
48
49   --ana_0:integration_width ANA_0:INTEGRATION_WIDTH
50     The window over which peaks should be integrated
51     (default: 0.1)
52   --ana_0:peakheight ANA_0:PEAKHEIGHT
53     Peak height parameter (default: 2)
54   --ana_0:slwindow ANA_0:SLWINDOW
55     Sliding window parameter (default: 100)
56   --ana_0:smoothwidth ANA_0:SMOOTHWIDTH
57     Smooth width parameter (default: 3)
58
59 ana_0:omsi.analysis.findpeaks.omsi_findpeaks_global:input data:
60   Input data to be analyzed
61
62   --ana_0:msidata ANA_0:MSIDATA
63     The MSI dataset to be analyzed (default: None)
64   --ana_0:mzdata ANA_0:MZDATA
65     The m/z values for the spectra of the MSI dataset
66     (default: None)
67
68 ana_1 : generic:
69   --ana_1:axis ANA_1:AXIS
70
71 optional workflow executor options:
72   Additional, optional settings for the workflow execution controls
73
74   --reduce_memory_usage REDUCE_MEMORY_USAGE
75     Reduce memory usage by pushing analyses to file each
76     time they complete, processing dependencies out-of-
77     core. (default: False)
78   --synchronize SYNCHRONIZE
79     Place an MPI-barrier at the beginning of the execution
80     of the workflow. This can be useful when we require
81     that all MPI ranks are fully initialized. (default:
82     False)
83
84 how to specify ndarray data?
85 -----
86 n-dimensional arrays stored in OpenMSI data files may be specified as
87 input parameters via the following syntax:
88   -- MSI data: <filename>.h5:/entry_#/data_#
89   -- Analysis data: <filename>.h5:/entry_#/analysis_#/<dataname>
90   -- Arbitrary dataset: <filename>.h5:<object_path>
91 E.g. a valid definition may look like: 'test_brain_convert.h5:/entry_0/data_0'
92 In rear cases we may need to manually define an array (e.g., a mask)
93 Here we can use standard python syntax, e.g, '[1,2,3,4]' or '[[1, 3], [4, 5]]'
```

94

95 This command-line tool has been auto-generated by BASTet (Berkeley Analysis & Storage Toolkit)

DEVELOPER NOTES

7.1 Building the online documentation

The sources for the sphinx docs are part of the doc/ folder and can be build locally as usual via, e.g., make html. This will build the documentation locally only as part of the doc/_build folder.

The online documentation is hosted via GitHub pages and are part of the gh-pages branch. The sphinx docs build scripts are conveniently set up to simply the update of the online documentation as part of the regular development process. However, before we can do this we need to do the following simple setup first:

- cd to your local copy of the BASTet repo (i.e., where the /omsi and /doc folder are located)
- cd ..
- mkdir bastet_docs
- cd bastet_docs
- git clone https://github.com/oruebel/BASTet.git html
- git checkout -b gh-pages remotes/origin/ghpages

Once we have created and setup our bastet_docs repo for the gh-pages branch we can now build the online documentation as usual from the doc folder of our development repo via the following commands:

- make htmlpublic : Rebuild the html docs locally and then copy the docs to the ../../bastet_docs repo with the gh-pages branch. This will only make local changes without committing or publishing anything.
- make latexpdfpublic : Rebuild the latex and pdf and then copy the pdf to the ../../bastet_docs repo with the gh-pages branch. This will only make local changes without committing or publishing anything.
- make updatepublic : Once you have confirmed that the docs are correct, you can rebuild the html and pdf docs for publications using this command. The command also commits and pushes all changes to the docs back to GitHub for publication, so that they become immediately available online.

OMSI DATA FORMAT

The following discusses the specification and use of OMSI mass spectrometry imaging data files.

8.1 Data Layout

Experiment Information

- */entry_# (HDF5 group)* : Each /entry# groups stores data for a single imaging experiment. Data from multiple related experiments may be stored in different /entry_# groups within the same file. To link data from related experiments that are stored in separate HDF5 files, one could create a master-file in which the /entry_# are softlinks to the corresponding groups in the external HDF5 files
 - */entry_#/experiment_identifier (String dataset)* : For each experiment a user-defined identifier name —which should be unique— is stored. This can be used to search for a particular experiment based on its name.

MSI Data

- */entry_#/data_# (HDF5 dataset)* : Multiple original images may be stored for each imaging experiment. The OMSI format manages the data associated with each dataset in a separate group. For a standard MSI dataset this group contains the following datasets:
 - * */entry_#/data_#/data_# (3D dataset)* : Each data group may contain multiple copies of the same data. This is to allow for optimizations of the data layout for different selective read operations. This is important to enable fast data access to spectra and images via the web. By default the omsi format uses 3D arrays to store the spectral imaging data because:
 - This allows the use of chunking in HDF5 to optimize data access for slicing operations in all dimensions. 1D and 2D layout allow for optimization only for a limited set of selection operations.
 - When using, e.g., a 1D data array to store the data, one would also need to store the resolution and order of the different dimensions to make sure that one can interpret and read the data correctly.
 - * */entry_#/data_#/format (String dataset)* : Simple string dataset describing the internal layout type of the dataset. While the most common data layout is to store the data in a single 3D array, other data layouts are supported as well, e.g., to enable more efficient storage for sparse MSI datasets.
 - * */entry_#/data_#/mz (1D dataset)* : The m/z values associated with the data.

Instrument Information

- */entry_#/instrument (HDF5 group)* : For each experiment a group with additional data about the instrument is stored. The example shown above defines a name for the instrument but we could define a larger list of optional instrument information that we would like to store here. The CXIDB format allows multiple instruments for each experiment. To assign data uniquely to an instrument the data is stored in the corresponding instrument group. However, to ease access to the data, CXIDB defines soft-links to the data

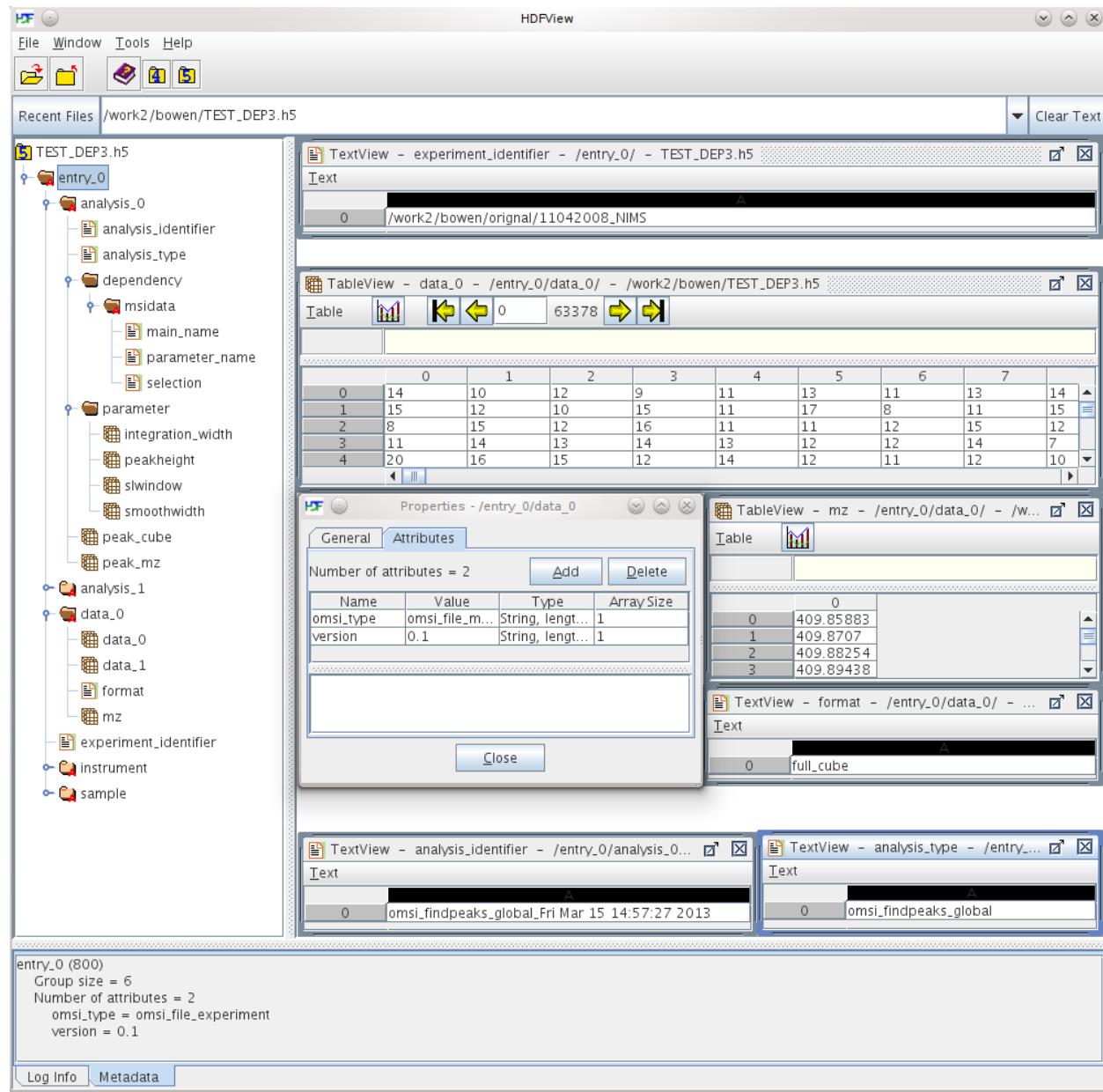


Fig. 8.1: Illustration of an example HDF5 file using the OpenMSI data format.

in the /entry_# group for the experiment as well. Allowing multiple instruments for a single experiment makes the format very complicated and is unnecessary in most cases. In the OMSI format defined here, one can still store data from related experiments in a single file, simply by creating separate entry_# group.

- * /entry_#/instrument/name (*String dataset*) : The name of instrument used
- * /entry_#/instrument/mz (*ID dataset*) : The mz data of the instrument

Sample Information

- /entry_#/sample (*HDF5 group*) : For each experiment a group with additional data about the sample used in the experiment is stored. The example shown below only defines a name for the sample but we could define a larger list of optional instrument information that we would like to store here. The proposed format here makes a similar simplification compared to the CXIDB format as in the case of the instrument. For each experiment —represented by a /entry_# group— only a single sample may be used. Data from related samples may be stored in the proposed format in separate /entry_# groups representing different experiments.
 - * /entry_#/sample/name (*String dataset*) : Name of the sample imaged.

Data Analysis Results

- /entry_#/analysis_# (*HDF5 group*) : Multiple derived analysis results may be stored in the proposed format in analysis_# groups associated with the experiment they were created from. Similar to the experiment a user-defined analysis-identifier string should be given to each analysis to allow searches for analysis results by name. Which data needs to be stored for an analysis will depend on the analysis. The omsi python API specifies some base classes to ease integration of analysis algorithms with the API and the HDF5 data format. Further formalizations may be specified to ease support of specific types of analysis results —e.g., clustering results— via the OpenMSI web-interface.
 - * /entry_#/analysis_#/analysis_identifier (*String dataset*) : For each analysis a user-defined identifier name —which should be unique— is stored. This can be used to search for a particular experiment based on its name.
 - * /entry_#/analysis_#/analysis_type (*String dataset*) : String describing the type of analysis. This should be high-level category, e.g., peak_finding_local, peak_finding_global, clustering etc. We will define a set of these categories that should be used. Having high-level categories for different algorithms that store their data in the same fashion will help later on with analyzing and visualizing the results from different algorithms that essentially produce the same output.
 - * /entry_#/analysis_#/... (*Arbitrary HDF5 dataset*) : In the example shown in *Illustration of an example HDF5 file using the OpenMSI data format*. above, we have an example /entry_0/analysis_0/peakcube. The name for the output datasets from the analysis is currently not restricted. A set of name convention will however be defined by the omsi_analysis associated with the indicated analysis_type to ensure that the data can be handled gracefully. Otherwise, if an unknown analysis type is given then all datasets in the /entry_#/analysis_#/ group that are not part of the standard are assumed to be analysis datasets.
 - * /entry_#/analysis_#/parameter (*HDF5 Group*) : Group containing additional datasets with input parameters of the analysis
 - /entry_#/analysis_#/parameter/... (*Arbitrary HDF5 datasets*) : Datasets defining input parameters of the analysis
 - * /entry_#/analysis_#/dependency (*HDF5 Group*) : Group containing additional datasets specifying dependencies of the analysis.
 - /entry_#/analysis_#/dependency/... (*HDF5 Group*) : Each dependency is defined in a separate group containing the following required datasets

- `/entry_#/analysis_#/dependency/.../main_name` (*String dataset*) : Path to the HDF5 object the analysis depends on.
 - `/entry_#/analysis_#/dependency/.../parameter_name` (*String dataset*) : Name of the analysis parameter that has the dependency.
 - `/entry_#/analysis_#/dependency/.../selection` (*String dataset*) : Optional Numpy selection string, indicating the subset of the data used.
- * `/entry_#/analysis_#/runinfo/` (*HDF5 Group*) : Group containing all runtime information data, e.g., start, stop and execution times, system and OS metadata etc.

Attributes

HDF5 attributes are used by the OMSI file format only to store format related information but not to store any data. Currently the following attributes are associated with the different high level groups:

- `omsi_type` (*String*) : Attribute indicating the `omsi_file` API object to be used to manage the given group. If the attribute is not present then the API decides which API object to use base on the name conventions described above.
- `version` (*String*) : Attribute indicating the version of the API class that should be used to represent this group.

8.2 Accessing OMSI data files

The `omsi.dataformat.omsi_file` module provides a convenient python-based API for reading and writing OMSI data files. The class also provides a convenient function for generating a XML-format XMDF header for the OMSI HDF5 file. Using the XMDF header file, the HDF5 data can be loaded in VisIt using VisIt's XMDF file reader. OMSI data files are valid HDF5 data files and can be accessed via the standard HDF5 libraries.

- **C/C++:**
 - More information about HDF5 can be found here: <http://www.hdfgroup.org/HDF5/>
- **Python:**
 - H5Py is a python interface to the HDF5 library. More detailed information can be found here: <http://h5py.alfven.org/docs-2.0/>
- **MATLAB:**
 - MATLAB provides both high-level and low-level access functions to HDF5. For more details see <http://www.mathworks.com/help/techdoc/ref/hdf5.html>
 - Simple example usin the high-level API:

```
file='~/Data/Imaging/DoubleV.hdf5'
h5disp(file)
mz=h5read(file,'/entry_0/instrument/mz');
[m m]=min(abs(mz-746.22))
tic
y=h5read(file,'/entry_0/data_0',[m 1 1],[1 250 160]);
toc
imagesc(squeeze(y))
axis equal
axis tight
```

- Simple example using the low-level API:

```
file='~/Data/Imaging/DoubleV.hdf5'
plist = 'H5P_DEFAULT';
fid = H5F.open(file);
gid = H5G.open(fid,'/entry_0');
dset_id = H5D.open(fid,'/entry_0/data_0');
dims = [160 250 1];
offset = [0 0 mx]
block = dims;
mem_space_id = H5S.create_simple(3,dims,[]);
file_space_id = H5D.get_space(dset_id);
H5S.select_hyperslab(file_space_id,'H5S_SELECT_SET',offset,[],[],block);
tic
data = H5D.read(dset_id,'H5ML_DEFAULT',mem_space_id,file_space_id,plist);
toc
H5D.close(dset_id);
H5F.close(fid);
data=squeeze(data);
imagesc(data)
axis equal
axis tight
```

- **Using HDF5 at NERSC**

- Overview of python at NERSC: <http://www.nersc.gov/users/software/development-tools/python-tools/>
- HDF5 modules are installed on most machines at NERSC:

```
module load hdf5
module load python
python
>>> import h5py
>>> import numpy
```

8.3 Convert Mass Spectrometry Imaging Data to OMSI (HDF5) format

See section *Converting Files at NERSC and Making them Accessible* for details.

- `omsi.tools.convertToOMSI` : This python script, which is available via the OMSI software toolkit, provides functionality for converting img files to HDF5. The script takes a single or multiple img files as input and writes them to a single HDF5 file. The data of each img file is stored in a separate /entry_#/data_# object. The script also supports execution of a number of different analysis, such as, peak finding or nmf, directly during the data conversion. For up-to-date information about the usage of the script see `python imgToHDF5 --help`. A summary of the main command-line options of the tool are available below.
- `omsi.dataformat.omsi_file` : Module containing a set of python class for reading and writing HDF5 data files for the proposed OMSI HDF5 data layout.
- `omsi.dataformat.img_file` : Simple python class for reading img data files.
- `omsi.dataformat.bruckerflex_file` : Simple python class for reading bruckerflex files.

HDF5 I/O PERFORMANCE

Analysis and visualization of mass spectrometry imaging (MSI) data is often based on selected subsets of the data, e.g., single or multiple spectra or m/z data slices. It is, therefore, crucial that we are able to quickly access select subsets of the data. In the context of web-based applications —such as the OpenMSI Viewer— this is particularly crucial in order to enable interactive data analysis and to provide a satisfactory user experience. The tests described here focus on characterizing and optimizing the performance of data access operations performed in serial on OMSI HDF5 files. While we here focus on the performance of serial data accesses, the optimizations described here are fundamental to optimizing parallel data access as well.

In the following, we first identify a select set of target compute platforms (Section [Test Platforms](#)) and define a set of representative use cases in order to evaluate the performance of different data layouts (Section [Test Cases](#)). We then discuss the basic layout of the MSI data (Section [Dataset Layout](#)) and establish the baseline performance using the default contiguous data layout (Section [Baseline Performance](#)). Afterwards, we explore further optimization of the data layout using HDF5’s data chunking (Section [Chunking: Part 1](#)) and data compression (Section [Compression](#)) capabilities. We conclude this study with a discussion of lessons-learned in Section [Discussion](#).

9.1 Test Platforms

All tests were performed on two main compute systems: i) login node of `hopper.nersc.gov` (short `hopper`) and ii) `portal-auth.nersc.gov` (short `portal`). On `hopper` we utilized the LUSTRE-based `/scratch` file system, as well as the global GPFS-based `/project` file system. On `portal` we can only access the `/project` file system. We chose these systems because: i) `hopper` is our candidate system for performing large-scale parallel analysis of MSI data and ii) `portal` is our target system for providing web-based access to MSI data.

9.1.1 `hopper.nersc.gov`

The `hopper` system has 12 login nodes with 4 quad-core AMD 2.4 GHz Opteron 8378 processors (16 cores total) each on 8 of the login nodes and 4 8-core AMD 2.0 GHz Opteron 6128 processors (32 cores total) each on 4 of the login nodes. Each login node has 128 GB of memory. The login nodes are external to the main Cray XE6 system. All tests were performed using `hopper` login nodes.

Scratch: There are two Lustre file systems on `hopper` —mounted as `/scratch` and `/scratch2` (in the following we use `/scratch2`)— with the following setup:

- 13 LSI 7900 disk controllers (Each disk controller is served by 2 I/O Object Storage Servers (OSSs))
- Each OSS host 6 OSTs (Object Storage Target) (simplified speaking a software abstraction of a physical disk)
- Fiber Channel 8 connectivity from OSSs to the LSI disk controllers
- Infiniband connects the Lustre router nodes in the 3d torus through a QDR switch to the OSSs

- In total each `/scratch` file system has 156 OSTs which is the lowest layer with which users need to interact. When a file is created in `/scratch` it is by default “striped” or split across two different OSTs. Striping is a technique to increase I/O performance. Instead of writing to a single disk, striping to two disks allows the user to potentially double read and write bandwidth. In the following experiments we use the default stripping settings but depending on file size, larger stripe settings may be advantageous. Using the `/scratch` file system for temporary storage of MSI data files can be advantageous when performing complex I/O intensive analysis.

Global `/project` : This is a large (1606 TB), permanent, medium-performance GPFS-based file system. We utilized the `/project` file system in the context of the OpenMSI project for permanent storage of MSI data.

9.1.2 `portal-auth.nersc.gov`

The `portal` system is used at NERSC for any data services that require public access from the Internet (such as Science Gateways) and as such also hosts the OpenMSI webpage and science gateway. The system consists of 2 quad-core AMD Opteron 2378 processors (8 cores total) with 24GB of memory. This system has only access to the `/project` file system.

9.2 Test Cases

In order to evaluate the performance of different data layouts, we designed a set of test-cases modeling the most common data access patterns in the analysis of MSI data. One particular focus of this study is to optimize the performance of the file format for web-based access to the data required for OpenMSI’s online data viewing, analysis and exploration functionality. In this context it is most important that we are able to quickly access select subsets of the data, in particular, image slices, spectra or subcubes of the data. These type of data access patterns, however, are very common also for a large range of data analyses, e.g., peak finding on individual spectra, data clustering and many others. In contrast to analysis performed with direct access to the compute system, the abilities for data caching are typically much more limited in a web-based setting due to the fact that: i) http accesses are stateless, i.e., a file is typically reopend for each incoming request and closed again afterwards and ii) access patterns to the data are much more irregular with multiple users working with different datasets and/or different subsets of the data at the same time. While the median performance for repeated data selection operations on the same open file is often very important for data analysis, in a web-based setting the maximum time for the first access to the data is often much more important. In the following we report for each selection test case the median time (indicating the sustained performance on an open file) and the maximum time (indicating the selection performance after the first opening of the file). We usually repeat each selection test case 50 times for each data layout using randomized selection parameters.

9.2.1 Case 1: m/z Slice Selection

This test case models the selection of a series of z-slices of the data (i.e., slices in a mass range), and extracts a set of consecutive, full images of the data. This type of operation is required in the OpenMSI viewer when updating channels in the image viewer itself. It is also a common operation in many other analyses, e.g, when analyzing the distribution for a particular peak across the image.

- **Randomized Selection Parameters:** `zmin`
- **Dependent Selection Parameters:** `zmax = zmin+25`
- **Extracted Dataset:** $100 \times 100 \times 25 = 250,000$ records = $500,000$ bytes = 0.5MB

9.2.2 Case 2: Spectra Selection

This test case models the selection of a 5×5 set of full spectra. In the OpenMSI viewer, access to single and multiple neighboring spectra is required when updating the spectrum plot’s. This is also a typical operation for many analyses

that operate on a per spectrum basis, e.g., peak finding for a single spectrum.

- **Randomized Selection Parameters:** `xmin , ymin`
- **Dependent Selection Parameters:** `xmax = xmin+5 , ymax = ymin+5`
- **Extracted Dataset:** $5 \times 5 \times 100,000 = 200,000$ records = 2,500,000 bytes = 5MB

9.2.3 Case 3: 3D Subcube Selection

This selection models the general access to consecutive sub-pieces of the data, e.g., when accessing data from a particular spatial region of the data related to a particular set of m/z data values. This type of operation is required, e.g., when analyzing the data of a cluster of pixels with a particular set of peaks of interest.

- **Randomized Selection Parameters:** `xmin , ymin, zmin`
- **Dependent Selection Parameters:** `xmax = xmin+5 , ymax = ymin+5, zmax = zmin+1000`
- **Extracted Dataset:** $5 \times 5 \times 1,000 = 25,000$ records = 50,000 bytes = 0.05 MB

9.2.4 Case 4: Data Write

As described above, the aim of this study is to optimize the performance of selective data read operations (termed hyperslap selections in HDF5). In contrast to the data read, data write is a one-time cost during the file conversion step and is, therefore, less critical to the operation of OpenMSI. A reduced write performance may, therefore, be acceptable in lieu of an increase in read performance as long as an acceptable write performance is maintained. During selection performance tests, the data write is repeated only 3 times for each data layout (i.e., once for each of the three selection test cases). For selected cases (indicated in the plot titles) we ran dedicated data write tests with 10 repeats. We here typically report the average times for data write.

9.2.5 Case 5: File Size

The size of data files is important to this study as different file layouts may have different space requirements (e.g., due to padding and additional metadata). While reduction of the size of data files is not the main objective of this work, it is important to avoid unnecessary overheads in file size and, hence, storage cost. The size of files reported in this study have been determined using the Python command `os.stat(filename).st_size`.

9.2.6 Test Data

For this study we use a $100 \times 100 \times 100,000$ test dataset. The dataset is stored as a 3D array of UInt (16bit) data values using the OMSI HDF5 format described in Chapter [OMSI Data Format](#). Data write and hyperslap performance are independent of the data values being written/read, so to test the baseline write-performance, we simply assign to each data element the index of the corresponding data chunk. For test cases that utilize data compression, we use a donor MSI data file to fill the file with realistic data. We may replicate data from the donor file in case that the testfile is larger than the donor file. In case that a donor file is used, we read the donor data into memory prior to writing of the test dataset. For each test case (i.e., data layout + selection case) we generate a new test data file to reduce/eliminate effects of data caching. The newly generated file is then opened and the current selection (i.e., hyperslap selection) is repeated 50 times using randomized selection parameters.

Raw data files used in this study are:

- **Dataset A:** (default donor file)
 - **Name:** 11042008_NIMS.h5

- **Dimensions:** $227 \times 108 \times 63, 378$
- **Raw Data Size:** 3.2GB
- **File Size:** 3.3GB (including results from global peak finding and nmf)
- **Dataset B:**
 - **Name:** 2012_0403_KBL_platename.h5 (DoubleV)
 - **Dimensions:** $160 \times 250 \times 116, 152$
 - **Raw Data Size:** 9.3GB
 - **File Size:** 9.5GB (including results from global peak finding and nmf)

9.3 Dataset Layout

A single (2D) MSI dataset defines a 3D data volume with the spatial coordinates x, y and the m/z (mass) as third dimension (z). In raw block-of-uint format (e.g., in the IMG format) the data is often stored in a 1D linearized fashion: $spectrum_{0,0}, spectrum_{0,1}, \dots, spectrum_{l,m}$. While such a layout is well-suited for accessing single full spectra, access to single image z-slices requires $l * m$ seek operations and traversal of the complete dataset (with l, m being the number of pixels in x, y , respectively). Selection of spectra and z-slices of the data are orthogonal selection operations, i.e., a 1D data layout can always just optimize one of the two access operations but not both. Similarly, a 2D data layout can be defined to enable easy access to full spectra as well as full z-slices, but does not easily support to optimize access to 3D subsets of the data. We, therefore, store MSI data as a 3D array in HDF5 to: i) be able to optimize and find a good performance compromise for selection of spectra, z-slices as well as 3D subcubes of the data and ii) because the 3D array reflects the true dimensionality of the data.

HDF5 can represent array datasets with as many as 32 dimensions. However, in the file the data is linearized in order to store it as part of the 1-dimensional stream of data that is the low-level file. The data layout determines in which way the multidimensional dataset is mapped to the serial file. The simplest way to accomplish this is to flatten the dataset (similar to how arrays are stored in memory) and to store the entire dataset into a monolithic block on disk. We here use this, so-called, contiguous layout as baseline for our performance tests (see Section [Baseline Performance](#)).

Chunking provides an alternative to the contiguous layout. In contrast to storing the data in a single block in the HDF5 file, using chunking the data is split into multiple chunks. Each chunk of a dataset is allocated separately and stored at independent locations throughout the HDF5 file. The chunks of a dataset can then be read/written independently, enabling independent parallel I/O and potentially improving performance when operating on a subset of the dataset. Data chunks may be stored in arbitrary order and position within the HDF5 file. HDF5 uses a B-tree to map a chunks N-dimensional address to a physical file addresses. The size of the B-tree directly depends on the number of chunks allocated for a dataset. The more chunks are allocated for a dataset: i) the larger overhead for traversal of the B-tree, ii) the higher the potential contention for the metadata cache, and iii) the larger the number of I/O operations. An introduction to data chunking in HDF5 is provided at <http://www.hdfgroup.org/HDF5/doc/Advanced/Chunking/>. The performance of different chunking strategies for storing MSI data is evaluated in Section [Chunking: Part 1](#).

Use of chunking also enables the use of HDF5 I/O filters. We here investigate the use of compression filters. I/O filters are applied in HDF5 to each chunk individually, and entire chunks are processed at once. I/O filters enabled for a dataset are executed every time a chunk is loaded or flushed to disk. Choosing proper settings for the chunking (and chunk cache) are, therefore, critical for the performance of filtered datasets. The potential use of gzip compression for improving file size and hyperslab selection of MSI datasets is evaluated in Section [Compression](#).

Chunking and HDF5 I/O filters (e.g., data compression) are implemented transparently in HDF5, i.e., the API functions for reading/writing chunked/compressed datasets are the same ones used to read/write datasets with an uncompressed, contiguous layout. The layout (i.e., chunking scheme and compression options) is defined via a single function call to set up the layout on a property list before the dataset is created.

9.3.1 Baseline Performance

The goal of this section is to establish a baseline for the performance of the basic HDF5 contiguous data layout (i.e., without chunking). The baseline performance for the three selection test cases are shown in Figures i) *Baseline performance for the slice selection test case*, ii) *Baseline performance for the spectra selection test case*, and iii) *Baseline performance for the subcube selection test*. The bar plots show the minimum (blue), median (blue+red), average (blue+red+green), and maximum (blue+red+green+lilac) times for retrieving the selected data. We observe that hopper using /scratch provides much better performance for selection of spectra and 3D subcubes of the data. For the z-slice selection we observe that hopper achieves good median and average selection performance, whereas the performance of the z-slice selection on portal is generally poor. In all cases, we observe poor worst-case (maximum) times for the z-slice selection case.

For serial data write performance we observe that /project provides better write performance. However, for parallel write operations, the LUSTRE-based /scratch file system is expected to outperform /project.

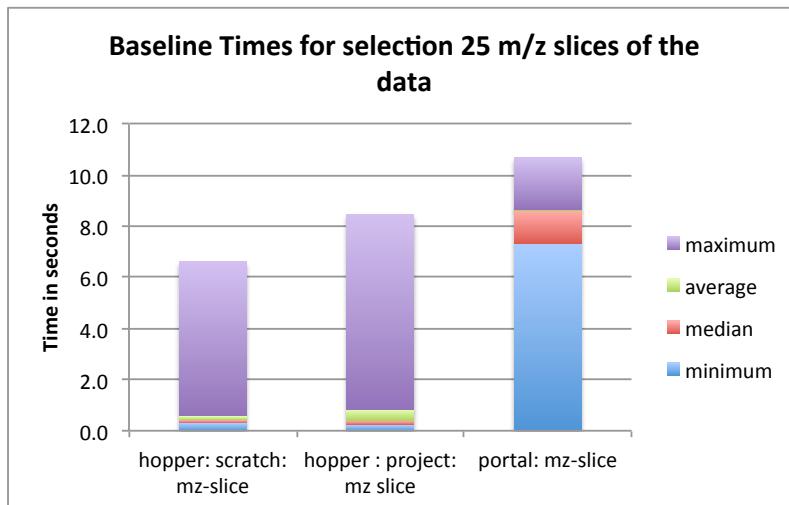


Fig. 9.1: Baseline performance for the slice selection test case

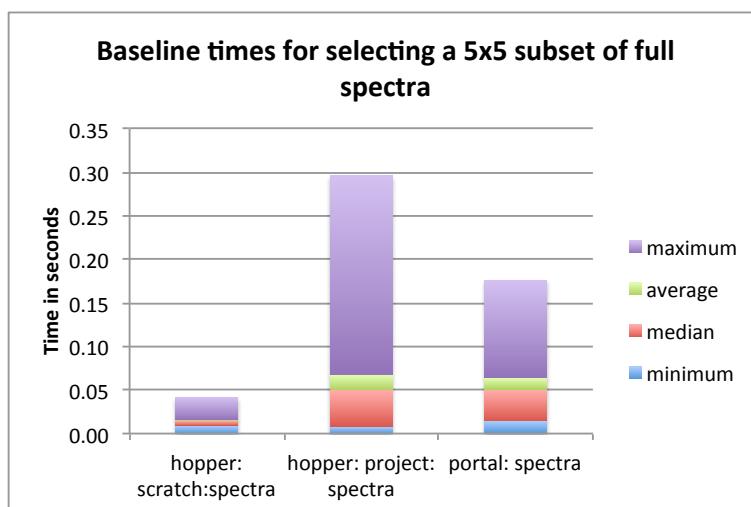


Fig. 9.2: Baseline performance for the spectra selection test case

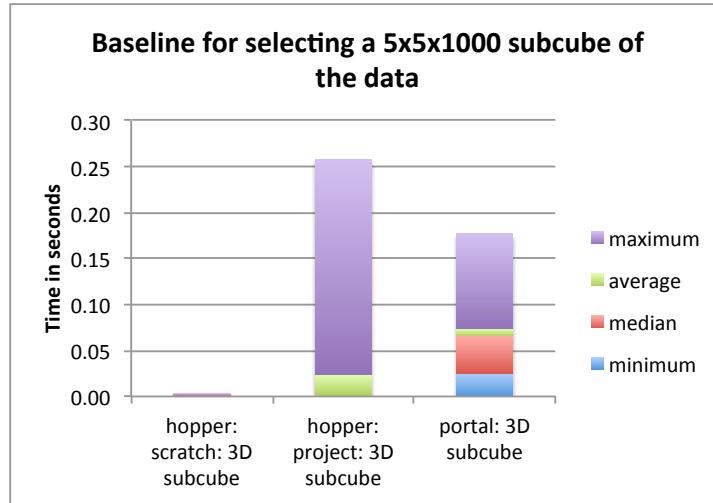


Fig. 9.3: Baseline performance for the subcube selection test

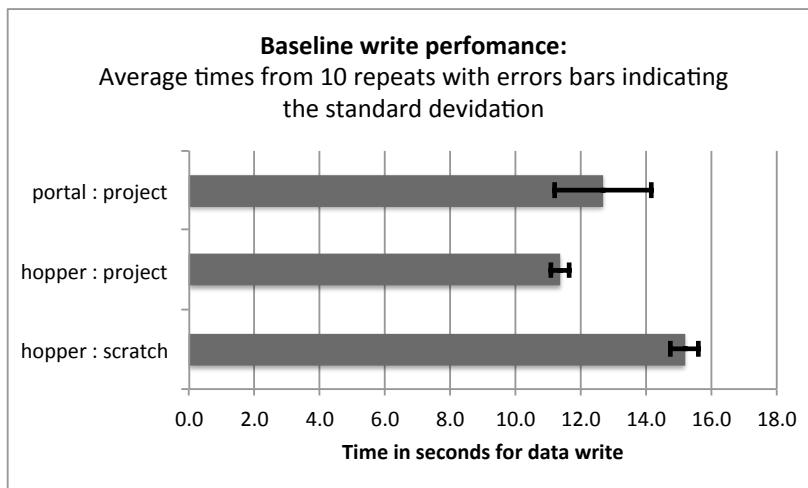


Fig. 9.4: Baseline performance for data write

9.4 Chunking: Part 1

Use of a chunked data layout has many potential advantages. In particular, use of chunking enables independent data I/O operations on individual chunks of the data so that chunking: i) can reduce the amount of data that needs to be read during hyperslab selections, ii) enables parallel independent I/O on a single file, and iii) enables the use of data compression (discussed later in Section [Compression](#)). The goal of this section is to evaluate the use of chunking to improve I/O performance. Due to the amount of additional metadata and overhead associated with finding chunks, one should avoid the use of too small chunks. At the same time, use of too large chunks should be avoided, because the entire chunk must be read from disk (and decompressed) before performing any operations. When operating on small subsets of the data (and if the cache is too small to hold the chunk), the use of too large chunks can result in large performance penalties. In addition, if the chunk is too large to be held in memory, the operating system may have to page memory to disk, slowing down the entire system.¹

Choosing a good chunking strategy for MSI data is complicated because: i) the data has a very unconventional shape, with the m/z dimension being three to four orders of magnitude larger than the spatial x/y dimensions and ii) orthogonal data access operations (access to spectra vs. z-slices) are required with good first-time-access performance.

To account for these properties we use odd chunk sizes of $m \times m \times n$ with $n \gg m$. Finding a good compromise for choosing a good chunking is challenging. Larger chunk sizes m in x, y are expected to improve z-slice selections but also increase the overhead for spectra selections. Similarly, large chunk sizes n in z (m/z) are expected to improve spectra selections while increasing the overhead for z-slice selections. The goal of this first set of experiments is to find a chunking that provides a good compromise in performance for all three selection test cases.

In the following we compare the performance of a range of different chunking strategies of the form $m \times m \times n$ with $m \in \{1, 2, 4, 8, 16, 32\}$ and $n \in \{128, 256, 512, 1024, 2048, 4096, 8192\}$ using hopper using /scratch. We first evaluate the effects of the different data layouts on file size (Section [File Size](#)) and write performance (Section [Data Write](#)). We then compare the performance for performing the three selection test cases (Section [Selection Performance](#)). We conclude this chunked layout study with an evaluation of the overall performance of the different chunked data layouts to identify the best-performing data layouts (Section [Selection Performance](#))

9.4.1 File Size

The use of chunking effects the size of data files in two main ways. First, storing the additional metadata required for chunking —such as the B-tree used for indexing of data chunks— increases file size. Second, the use of chunking may result in allocation of additional empty data (padding) in case that the chunks do not align with the data. This can result in substantial data overheads. A simple example illustrates this problem. When storing a simple 1D dataset with 101 elements using a chunk size of 100, then we need to allocate two chunks, one chunk to store the first 100 elements and a second chunk to store the last element. In this case we allocated space for 200 elements in order to store 101 elements, nearly twice the amount of storage needed for the raw data. For multi-dimensional data arrays —here 3D— the storage overheads due to padding can increase even faster. It is, therefore, important that we consider the potential storage overhead when evaluating the use of data chunking.

Figure [File sizes using different chunking strategies](#) illustrates the effects of chunking on the size of data files. The baseline curve indicates the file size using a contiguous data layout. We observe that the file with a chunking of $1 \times 1 \times 128$ is much larger than the other files with a $1 \times 1 \times n$ chunked layout. No padding is applied in the spatial dimensions x, y . When using a z chunk size of 128, 782 chunks are required per spectrum, resulting in a total of 7,820,000 chunks. Due to padding in the z dimension, 96 100×100 slices remain empty. However, this accounts for only $100 * 100 * 96 * 2\text{Bytes} = 1,920,000\text{Bytes} = 1.92\text{MB}$. In comparison, the $1 \times 1 \times 2048$ dataset is much smaller while requiring a much larger z padding of 352 slices (i.e., $\approx 7.04\text{MB}$). The reason for the larger file size for the $1 \times 1 \times 128$ chunking illustrates the large overhead for storing the metadata required for the large number of chunks.

We also observe that the file size increases significantly when using chunk sizes in x, y of $8 \times 8 \times n$ or larger. This behavior is due to the padding required in the spatial dimensions. For example, when using a chunking of

¹ See also <http://www.hdfgroup.org/HDF5/doc/Advanced/Chunking/>

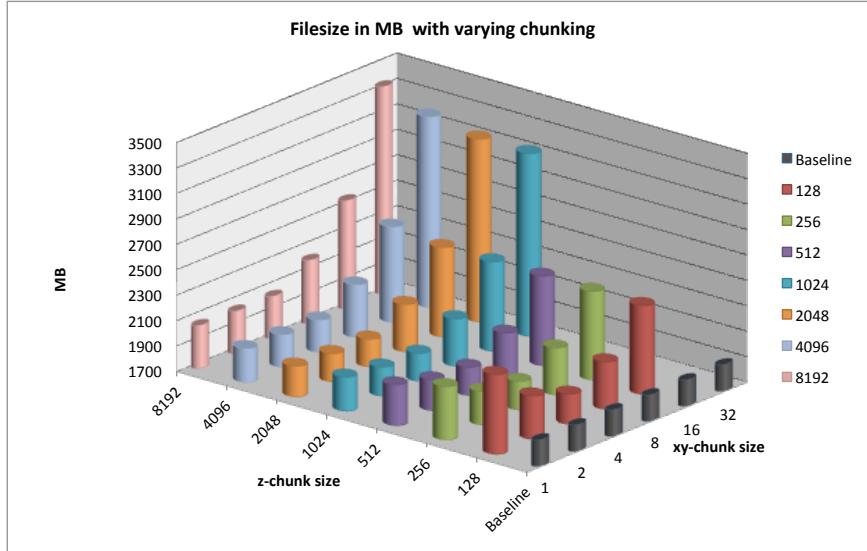


Fig. 9.5: File sizes using different chunking strategies

$32 \times 32 \times n$ we requires 4 chunks in the x and y dimension (i.e., $4 * 32 = 128$ elements). This means, in order to store the $100 \times 100 \times 100,000$ test dataset, we allocate space for at least $128 \times 128 \times 100,000$ records (additional padding may be required in the z dimension). This means that we allocate at least an additional amount of space of $(28 * 128 * 100,000) + (28 * 100 * 100,000)$ records = 638,400,000*2 Bytes = 1,276,800,000 Bytes = 1276.8 MB. This example illustrates that a bad choice for the chunking can result in substantially larger data files. Since in the case of MSI data, the x , y dimensions of the data are much smaller than the z (mz , mass) dimension, it is important that we keep the padding required in x and y as small as possible, whereas padding in the z dimension typically has a much smaller effect on the size of the data.

9.4.2 Data Write

Traditionally, MSI data is often written one-spectrum-at-a-time. Figure [Write performance using one-spectrum-at-a-time I/O using different chunk sizes \(hopper using /scratch\)](#) illustrates the write performance for the different data layouts using a one-spectrum-at-a-time write strategy. It is not surprising that we observe a significant decrease in performance with increasing chunk sizes m in the x and y dimensions, as each data chunk is modified $m * m$ times. For chunkings of $m \times m \times 32$ with $m \in \{1024, 2048, 4096, 8192\}$ the write performance improves possibly due to higher HDF5 chunk-cache hit rates. The write performance data points for data layouts with a chunking of $128 \times 128 \times 32$, $256 \times 256 \times 32$, and $512 \times 512 \times 32$ are missing as we terminated the tests due to the very poor one-spectrum-at-a-time write performance in those cases.

To achieve optimal data write performance, it is important that we reduce the number of times each chunk is modified. Figure [Write performance using different data write strategies and chunk sizes \(hopper using /project\)](#) compares the write performance for $m \times m \times 2048$ chunked data layout using a one-spectrum-at-a-time, $m \times m$ -spectra-at-a-time, and chunk-at-a-time data write strategy. Using the latter two strategies ensures that each chunk is modified only once. We observe that the chunk-at-a-time write strategy quickly outperforms the other write strategies as the chunk size increases (and the total number of chunks decreases). It is not surprising that the contiguous baseline layout outperforms the chunked layouts in a serial setting. However, the chunked layouts efficiently support parallel data write operations. Using a chunk-at-a-time write strategy, independent parallel tasks can be utilized to write the different chunks.

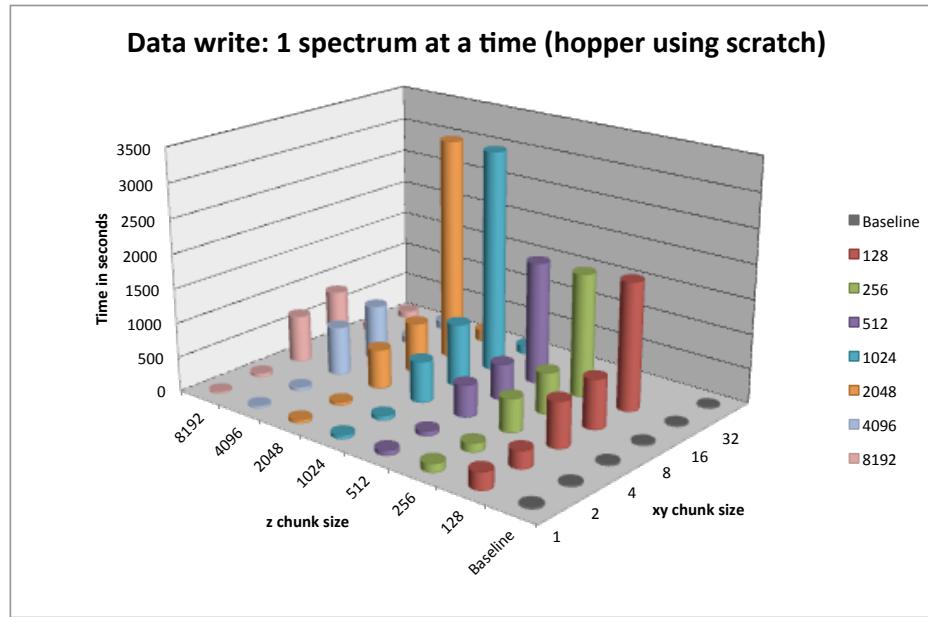


Fig. 9.6: Write performance using one-spectrum-at-a-time I/O using different chunk sizes (hopper using /scratch)

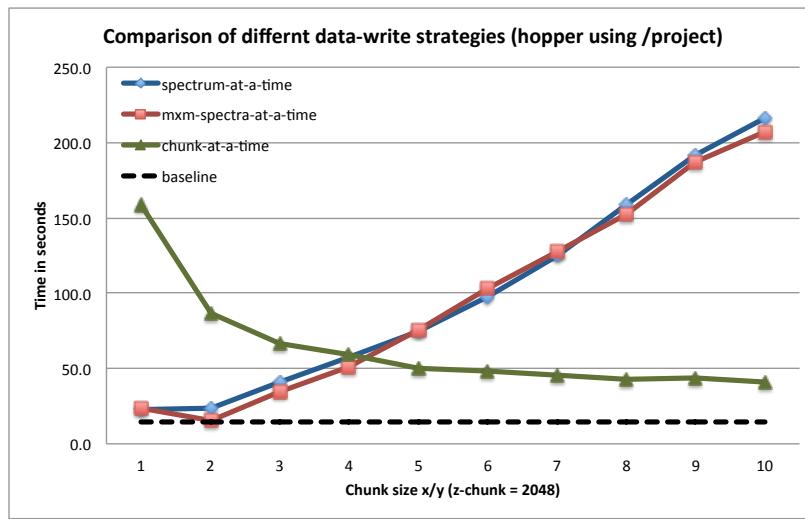


Fig. 9.7: Write performance using different data write strategies and chunk sizes (hopper using /project)

9.4.3 Selection Performance

In this section we evaluate the selection performance of the different chunked data layouts for the three selection test cases: i) selection of a random set of 25 consecutive z-slices, ii) selection of a random 5×5 set of full spectra, and iii) selection of a random $5 \times 5 \times 1000$ subcube of the data. Figure *Performance results for z-slice selection using varying chunk sizes (hopper using /scratch)*² shows the results for the z-slice hyperslab selection. We observe that data layouts with a chunking of $m \times m \times n$ with $m \in \{4, 8, 16\}$ and $n \in \{128, 256, 512, 1024, 2048, 4096\}$ show the best z-slice selection performance. For the mentioned chunking strategies we observe in general best performance for larger values in m and smaller values of n . This behavior is likely due to the reduced amount of data and number of chunks that need to be loaded to fulfill the selection of complete slices in z .

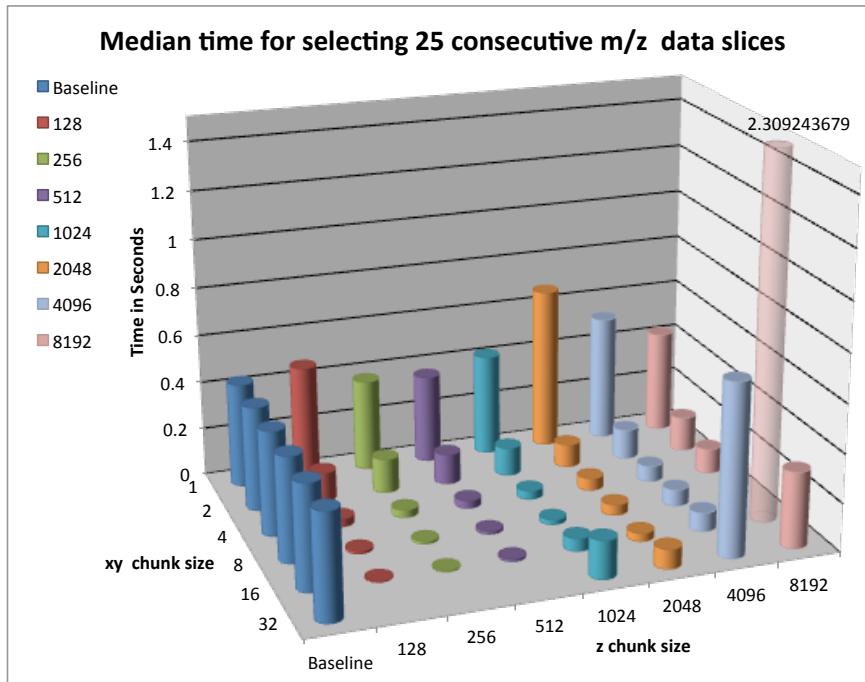


Fig. 9.8: Performance results for z-slice selection using varying chunk sizes (hopper using /scratch)

For the spectra selections (see Figure *Performance results for spectra selection using varying chunk sizes (hopper using /scratch)*) we observe in most cases a decrease in the median performance compared to the baseline contiguous data layout. This behavior is likely due to the fact that the data is flattened in a z-column order in the contiguous layout, so that a full spectrum can be read via a single seek and contiguous read operation. In contrast, using a chunked data layout requires for the test dataset, loading $100,000/n$ chunks. However, we observe that data layouts with a chunk size in z of 1024 and larger, still provide good performance for the selection of full spectra. In this case, small chunk sizes in x, y of 2 or 4, work well for the test case of loading a 5×5 set of spectra, as the number of chunks that need to be loaded remains constant. For data layouts with a x,y chunking of 8×8 , the 5×5 spectra selection can fit into a single x,y chunk, however, it is still likely that the 5×5 selection crosses multiple chunk boundaries, requiring the load of a large number of chunks. For x, y chunk sizes of 16 or 32, the 5×5 spectra selection is more likely to fit in a single chunk in x,y , explaining the better performance of those data layouts.

Figure *Performance results for 3D subcube selection using varying chunk sizes (hopper using /scratch)*² summarizes the results for the selection of a $5 \times 5 \times 1000$ data subcube. We observe that using chunking generally improves the performance of the selection. In particular, using chunking decreases the time for initial data access compared to the baseline contiguous data layout.

² Bars shown transparently indicate that the bars exceed the maximum value shown in the plot. The real value for those bars are indicated via additional text labels.

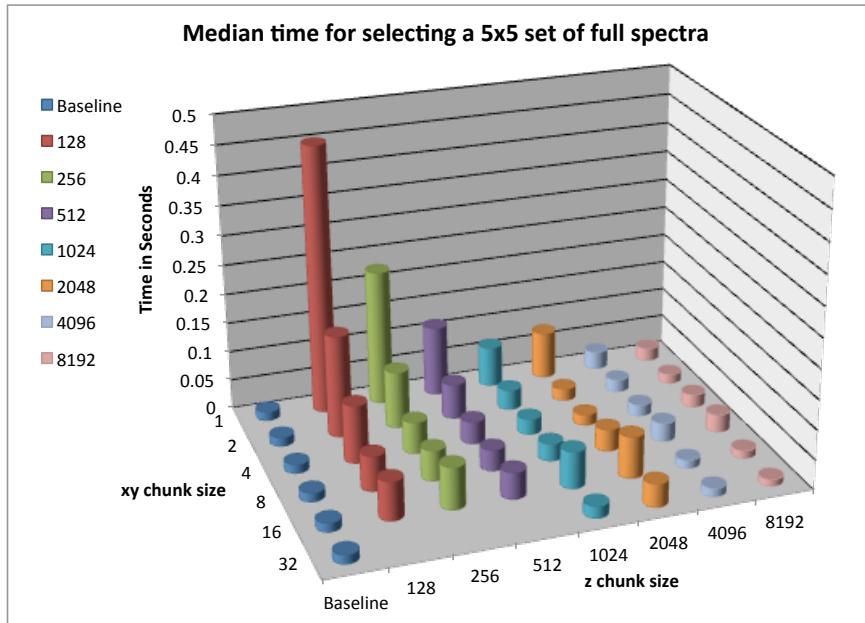


Fig. 9.9: Performance results for spectra selection using varying chunk sizes (hopper using /scratch)

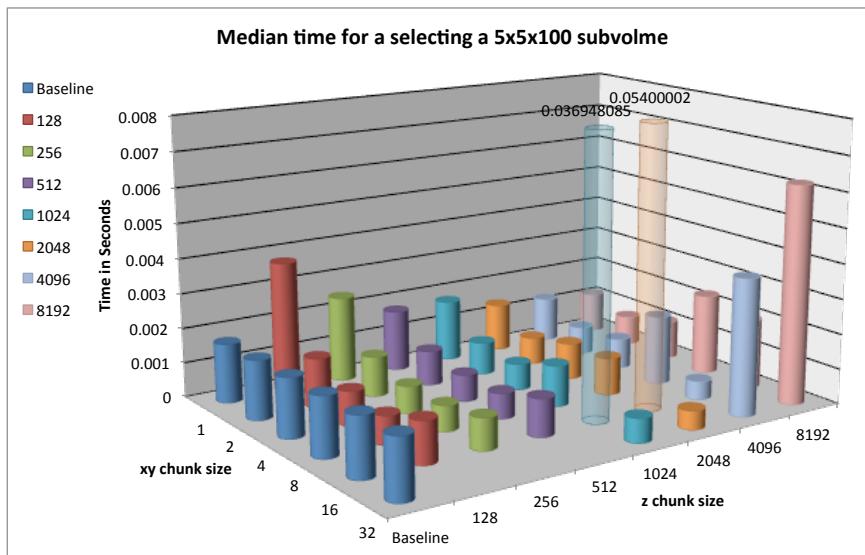


Fig. 9.10: Performance results for 3D subcube selection using varying chunk sizes (hopper using /scratch)

When comparing the selection performance plots, we observe that — even though the amount of data that is retrieved is only 0.5MB in z-slice selection case compared to 5MB in the spectra selection case— the performance for z-slice selection case is generally lower than for the spectra selection case. The reason for this behavior is that while the z-slice selection returns less data, the number of I/O (seek) operations required and the amount of data that needs to be loaded to fulfill the selection is larger. E.g, using a chunking of $4 \times 4 \times 2048$ each chunk requires $4 * 4 * 2048 * 2\text{Byte} = 65536\text{Byte} = 64\text{kB}$. To retrieve a 5×5 set of spectra, HDF5 needs to load $2 * 2 * 49$ Chunks = $196 * 64 \text{ kB} = 12.25 \text{ MB}$, whereas in order retrieve 25 z-slices (without crossing a z-chunk boundary), HDF5 needs to load $25 * 25$ Chunks = 625 Chunks = 39.0625 MB, i.e, more than three times the data (and that even though the 4×4 x,y chunking does not align well with the 5×5 spectra selection). Similary, in the contiguous data layout, we can load a single spectrum using a single seek and contiguous read operation, whereas in order to load complete a z-slice we requires $m * m$ ($= 100 * 100 = 10,000$ for the test data) seek and load operations.

9.4.4 Summary

To illustrate the overall performance of the different dataset layouts and to identify the “best” layouts, we define the following set of minimum performance criteria a data layout should fulfill:

- The median time for the z-slice selection test case should be $< 0.1 \text{ s}$
- The median time for the spectra selection test case should be $< 0.05 \text{ s}$
- The median time for the 3D subcube selection test case should be $< 0.002 \text{ s}$
- The total file size should be $< 2100 \text{ MB}$ (limiting the overhead in the test case to a maximum of $\approx 200\text{MB}$)
- (We do not take the write performance results shown in Figure *Write performance using one-spectrum-at-a-time I/O using different chunk sizes (hopper using /scratch)* into account in the total score here as a chunk-at-a-time write strategy likely improve the write performance significantly)

Based on these criteria we can determine an overall performance score by evaluating how many of the criteria a particular data layout fulfills (with 4=best (passes all criteria) and 0=worst (does not pass any of the criteria)). We observe a cluster of 8 data layouts that satisfy the four performance conditions.

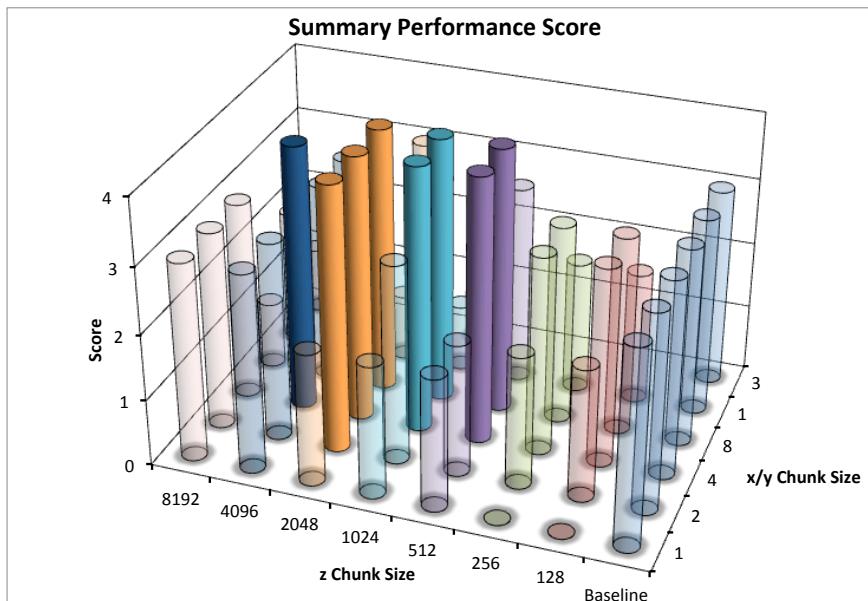


Fig. 9.11: Summary performance score using various different chunk sizes (hopper using /scratch)

Figure *Summary performance score using various different chunk sizes (hopper using /scratch)* summarizes the performance scores for the different data layouts. Bars with the maximum score of 4 are plotted opaque whereas all other bars are plotted transparently. We observe a cluster of 8 layouts with a performance score of 4. While the overall performance score used here is simple in nature, it illustrates well which data layouts achieve overall the best performance. Overall, the performance experiments indicate that the largest z chunk size for which we observe good performance in our experiments across a large range of x/y chunk sizes is 2048. We, therefore, chose a z chunk size of 2048 for further experiments.

So far our experiments have focused on hopper using the `/scratch` file system. In order to evaluate the performance of the permanent data storage system `/project` and the web-hosting system `portal` we performed a series of follow-up tests using a fixed z-chunking of 2048 on `portal` as well as on hopper using `/project` (more details are provided in the next section). We generally observed that the `/project` file system provided better serial write performance while the overall performance for selection was not as good as for `/scratch`. While the performance of ‘‘hopper using `/project` was still acceptable, the performance (and in particular the worst-case maximum times) were poor using `/portal` (see, e.g., Figure *Performance results for z-slice selection (portal using compression)* shown later). We, therefore, next extended our evaluation to also include data compression as an option to possibly improve data I/O performance and storage requirements.

9.5 Chunking: Part 2

In part 1 of the chunking study we were interesting in finding chunked data layouts that provide a good compromise for all three selection use-cases. In part 2 we focus on chunked data layouts that are designed to optimize single selection operations.

9.5.1 Image-aligned Chunking

Figure *Comparison of the performance of the default chunking with a chunked layout that is better-aligned with the ion-images to improve the performance the z-slice selection*. shows the performance of the z-slice selection in the OpenMSI client when optimizing the chunked data layout to align with the selection of m/z images. Using an image-aligned chunking of $50 \times 80 \times 100$, only 10 chunks containing 100 image slice need to be read in order to retrieve a single image slice, wheras, using the default chunking of $4 \times 4 \times 2048$, HDF5 needs to load 2,520 chunks containing 2048 image slices. The figure shows the performance we achieve in the OpenMSI client using the same data stored without compression using the two different chunked layouts. Using the default chunking it takes $\approx 20s$ to compute the ion-images compared to just $\approx 0.5s$ using the image-aligned chunking. However, not surprisingly, the performance of the orthogonal operation of selecting full spectra decreases significantly (here from 45ms to 8.1s) when optimizing the chunking to improve the selection of z-slices.

Further improvement in performance could be achieved by using a (m/z, x ,y) or (m/z, y, x) layout of the data rather than the commen (x, y, m/z). By transposing the image cube (making m/z the first dimension of the 3D cube) the data will be linearized on disk as $ionimage_0, ionimage_1, \dots, ionimage_n$ rather than $spectrum_{0,0}, spectrum_{0,1}, \dots, spectrum_{l,m}$. Linearizing the data in image order improves locality of data and reduces the number of seek operations required when loading ion-image. Currently, reordering of data dimensions is not yet supported by HDF5 as a transparent data layout optimization, but rather needs to be performed manually by the user. To remain ease of usability of the OpenMSI file format we, therefore, chose to use a consistent ordering of dimensions in all cases.

9.6 Compression

The primary goal of data compression is to reduce the size of data by providing a more compact encoding of the data. In many cases, compression is used as means to reduce the size of data stored on disk. However, while additional compute time overheads are incurred due to the time required for compression/decompression of the data during

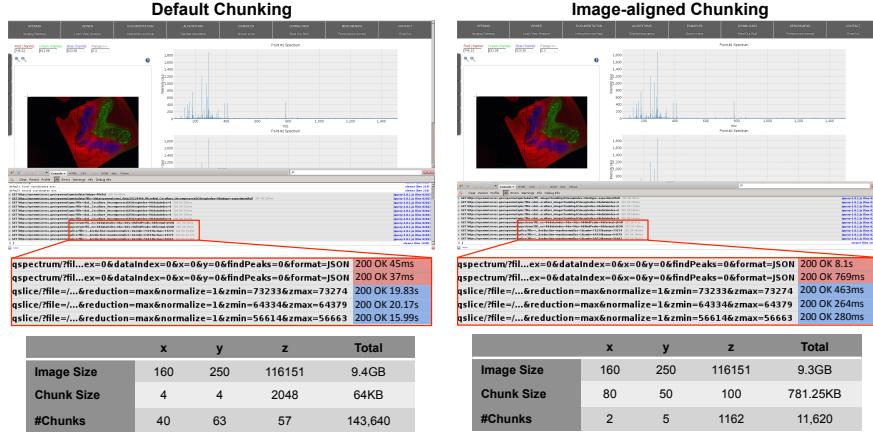


Fig. 9.12: Comparison of the performance of the default chunking with a chunked layout that is better-aligned with the ion-images to improve the performance the z-slice selection.

write/read, compression may also improve the read and/or write performance, as less data needs to be transferred and/or written to disk. This is in particular the case in I/O bound systems (e.g., due to network bottlenecks etc.).

Use of data compression in HDF5 relies on the use of chunking and, hence, shares the same overheads and advantages and disadvantages. Compression is applied to each chunk of the data. The overall compression ratio achieved, therefore, inherently relies on the use of a good chunking strategy. Data compression is implemented via I/O filters in HDF5, which are applied transparently during data read and write operations, i.e., after enabling compression when generating the dataset, data read/write operations are performed using the same API calls whether the data is stored in raw or compressed form.

HDF5/h5py typically provides three main compression algorithms: i) `gzip`, standard HDF5 deflate compression available with most HDF5 installations, ii) `szip`, third-party compression algorithm optionally available with HDF5 (i.e., it may not be available on all systems), iii) LZF is a stand-alone compression filter for HDF5 available via h5py but may not be available in many other standard (non-Python) installations of HDF5. In the context of OpenMSI it is important that we are able to transfer and use data at different institutes, compute systems and using a larger range of API's for accessing HDF5 data (e.g., matlab, HDF5 C API, h5py etc.). We, therefore, chose the standard `gzip` compression filter as it is typically available with most systems (in contrast to LZF and `szip`). The `gzip` filter provides an additional `aggression` parameter. The `aggression` parameter is a number between [0, 9] to indicate the trade-off between speed and compression ratio (zero is fastest, nine is best ratio). Unless indicated otherwise, we here generally set the `aggression` parameter to 4 for all tests to achieve a balance of compression ratio and speed.

9.6.1 Compression Ratio

Using a chunking of $4 \times 4 \times 2,048$, we achieve for dataset *A* a compression ratio of ≈ 2.9 , reducing the data from 3.3GB (including ≈ 100 MB of data for nmf and global peak-finding) to 1.2GB (while only the MSI data is stored in compressed form). Using the same setup, we achieve for dataset *B* a compression ratio of ≈ 6.3 , reducing the dataset from 9.5GB to 1.5GB (again with nmf and global peak-finding results included in the file and stored uncompressed in both cases). An overview of the file sizes using compression and compression ratios achieved using the $100 \times 100 \times 100,000$ test dataset (using dataset *A* as donor MSI dataset) are summarized in Figure [Compression ratios using different chunk sizes](#). The compression ratios we achieve are on the order of 2.9 to 3.8 in all cases (comparable to the compression ratio we have seen for the donor dataset *A*).

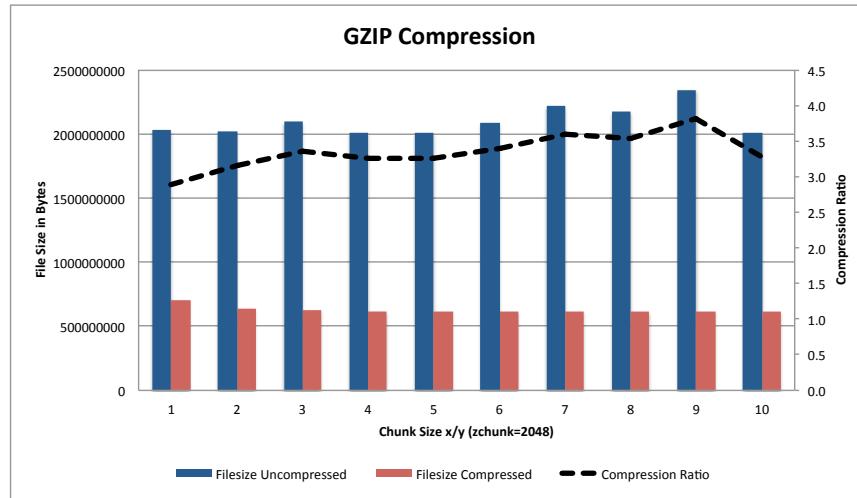


Fig. 9.13: Compression ratios using different chunk sizes

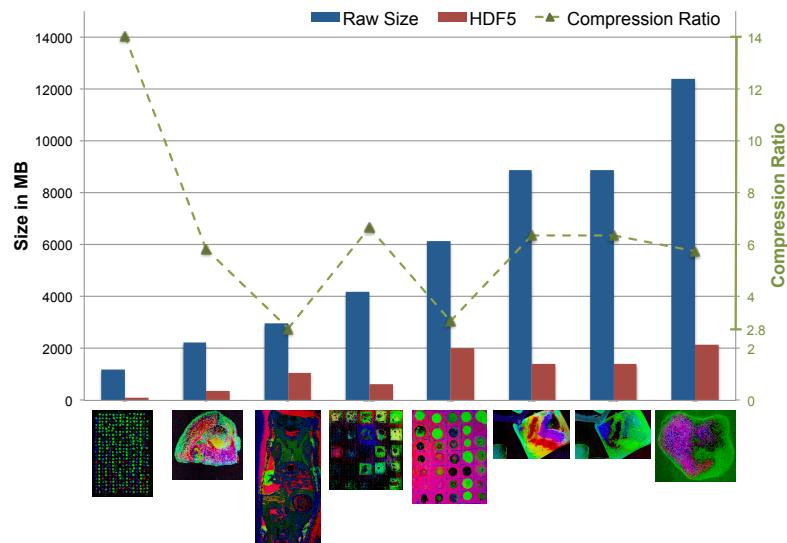


Fig. 9.14: Compression performance on a select set of real MSI datasets.

9.6.2 Data Write

Figure [Serial write performance using compression](#) compares the write performance results with and without using compression for data layouts with a chunking of $m \times m \times 2048$ with $m \in [1, 10]$. As expected, we observe a general decrease in the write performance when using compression. As mentioned earlier, when using compression it is important that we use a chunk-aligned data write strategy as the compression filter needs to be executed each time a chunk is loaded and/or modified. We, therefore, use the chunk-at-a-time write strategy when writing HDF5 datasets with compression enabled.

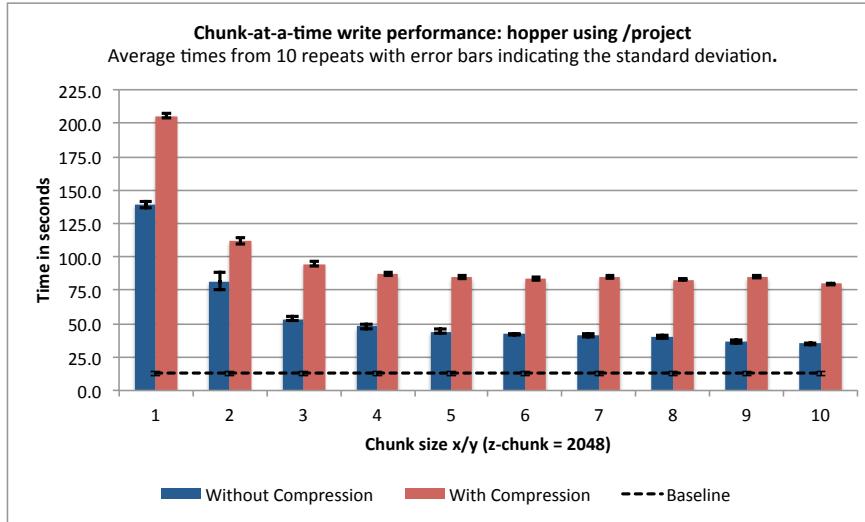


Fig. 9.15: Serial write performance using compression

9.6.3 Selection Performance

In this section we evaluate the selection performance of the different $m \times m \times 2048$ chunked data layouts (with $m \in [1, 10]$) for `portal` and `hopper` using `/project` and `/scratch`. For `portal` we observe that using compression can significantly improve the median selection time for the z-slice selection test case (see Figure [Performance results for z-slice selection \(portal using compression\)](#)). In particular, using compression significantly reduces and stabilizes the worst-case maximum time for selecting z-slices of the data³. This is especially important in the context of a web-based application, such as, OpenMSI's online data viewer. For the other two selection test cases we observe that we can achieve similar performance for the spectra and 3D subcube selection test cases on `portal` with and without compression (see Figures [Performance results for spectra selection \(portal using compression\)](#) and [Performance results for 3D subcube selection \(portal using compression\)](#))

The selection performance results for `hopper` using `/project` and `/scratch` and with and without using compression are shown in Figures: i) [Performance results for z-slice selection \(hopper using compression\)](#), ii) [Performance results for spectra selection \(hopper using compression\)](#), and [Performance results for subcube selection \(hopper using compression\)](#). As baseline we use the performance of the contiguous data layout on `hopper` using `/project`. In contrast to `portal`, we observe on `hopper` a general decrease (of up to 1 order of magnitude) in the selection performance when using compression compared to when storing the data in raw, uncompressed form. Compared to the

³ **Author comment:** Depending on when the test were run we have seen significant (approximately 1 order of magnitude) differences in the median selection times on `portal`, however, the maximum appeared to not improve between different reruns of the experiments. Using compression, the results on `portal` have been much more stable and, in particular, the maximum times were much better. This indicates that: i) system load, on a highly utilized system like `portal`, has a significant impact on the performance and ii) compression can significantly improve performance the selection performance on I/O bound systems and stabilized the performance results.

baseline contiguous data layout we, however, still observe an improvement in many cases even when using compression. Generally it appears that the use of compression may have stronger negative effect on the selection performance when operating on the `/scratch` filesystem then when using `/project`⁴.

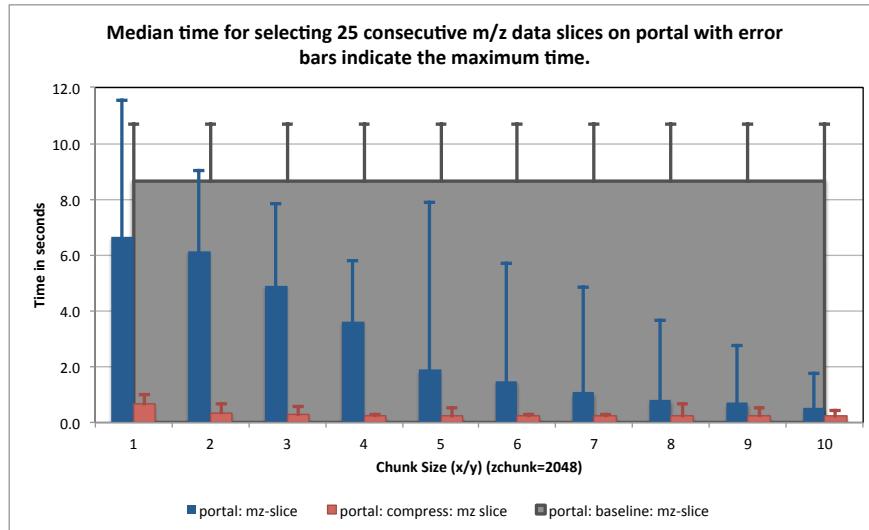


Fig. 9.16: Performance results for z-slice selection (`portal` using compression)

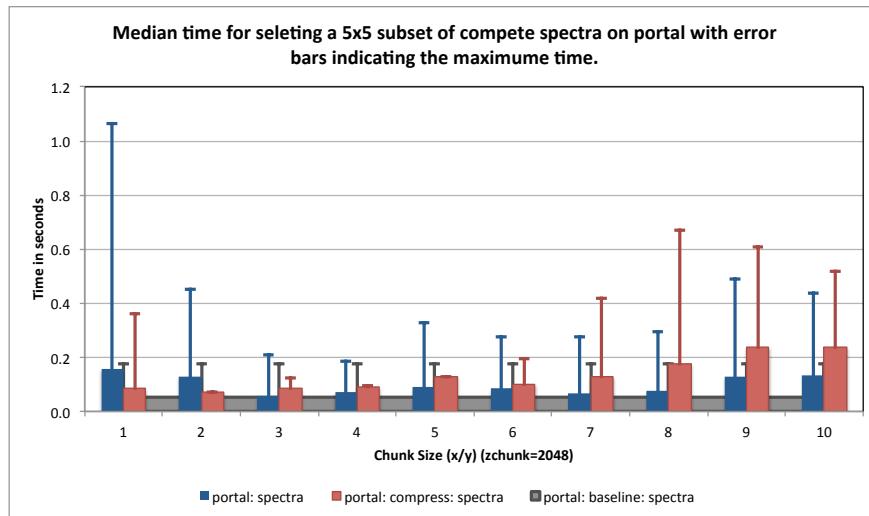


Fig. 9.17: Performance results for spectra selection (`portal` using compression)

9.6.4 Aggression Parameter Study

So far we have focused on the performance using `gzip` with `aggression = 4`, assuming that a medium aggression value provides a good balance of compression ratio and speed.⁵ The goal of this section is to determine the influence

⁴ **Author comment:** Note, `/scratch` is a parallel, LUSTRE-based file system, whereas `/project` is based on GPFSS. Also `hopper` may have a higher bandwidth connection to the `/scratch` file system than `/project`. Overall, accesses to `/project` is likely to be more I/O bound than access to `/scratch`.

⁵ The `aggression` parameter is a number between [0, 9] to indicate the tradeoff between speed and compression ratio (0=fastest, 9=best ratio).

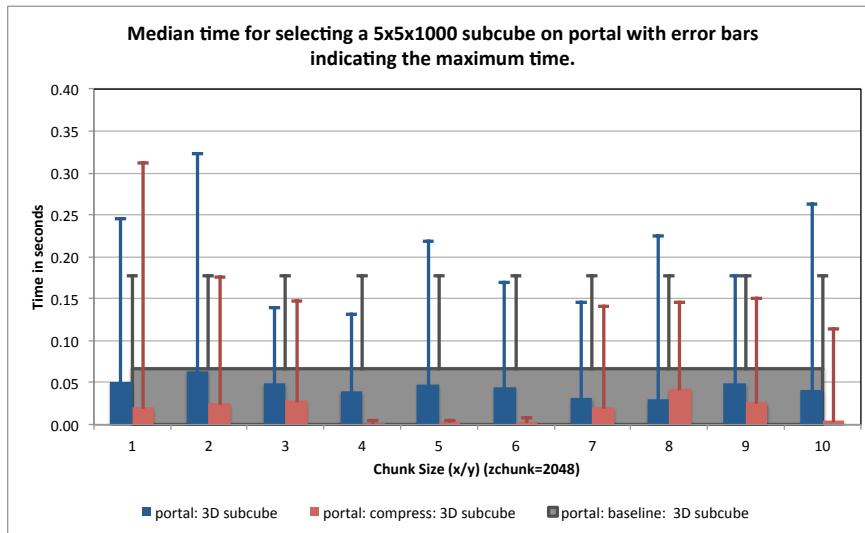


Fig. 9.18: Performance results for 3D subcube selection (portal using compression)

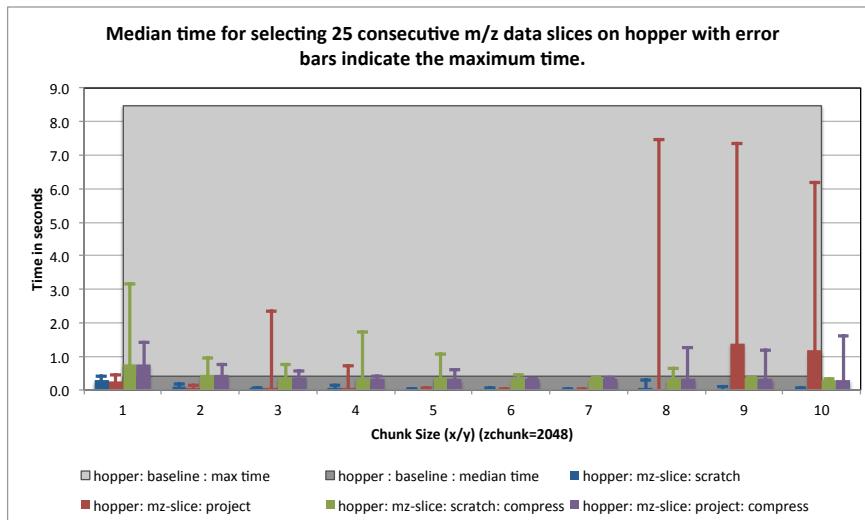


Fig. 9.19: Performance results for z-slice selection (hopper using compression)

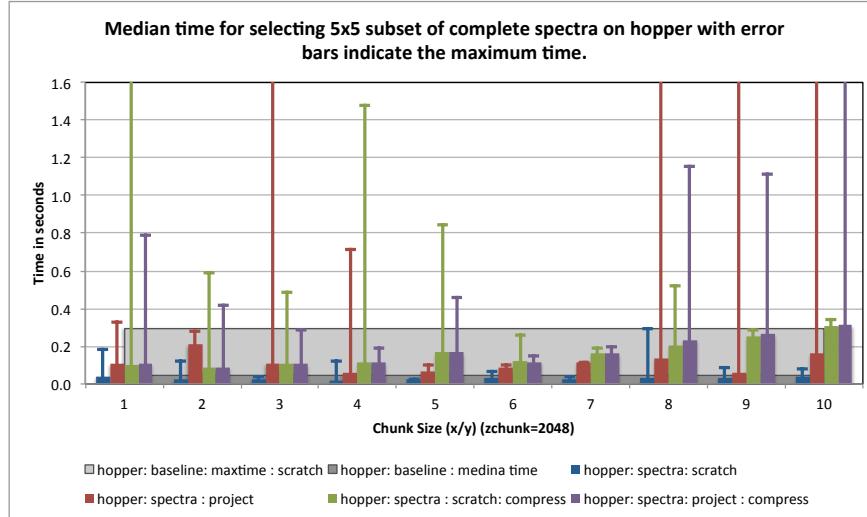


Fig. 9.20: Performance results for spectra selection (hopper using compression)

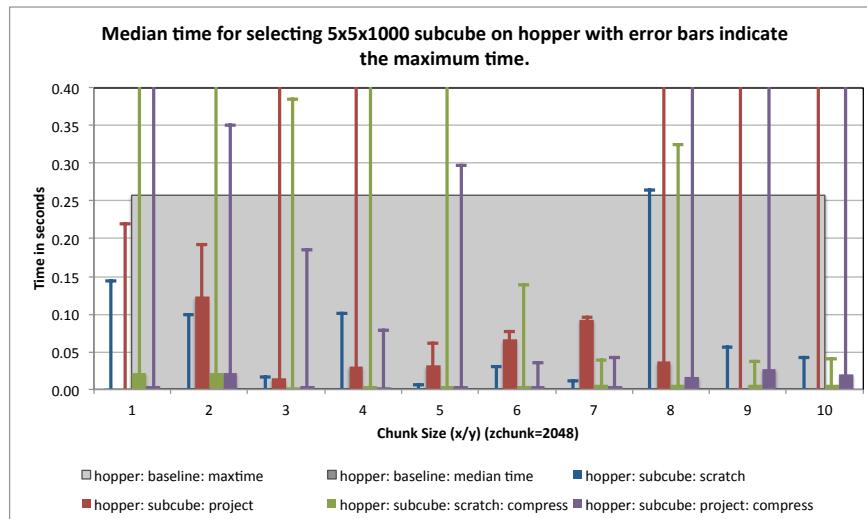


Fig. 9.21: Performance results for subcube selection (hopper using compression)

of the *aggression* setting on the overall performance. Figure [File size and write performance using varying gzip aggression settings](#) shows that the data compression we achieve for the test $100 \times 100 \times 100,000$ dataset (using dataset A as donor dataset) are comparable for all $\text{aggression} \in [1, 8]$ settings (we did not evaluate an aggression setting of 9 as the write performance was very poor). For the data write, we observe that the performance is acceptable for $\text{aggression} \in [1, 5]$ and decreases significantly for $\text{aggression} > 5$.

For the selection test cases, the performance results are consistent with the results from the previous tests. On *portal*, the performance of the z-slice selection improves significantly when using compression, while the spectra and subcube selection show comparable performance with and without compression (see Figure [Selection performance results using varying gzip aggression settings \(portal\)](#)). For *hopper*, we again observe a general strong decrease in the selection performance when enabling compression (while, although much slower, the overall selection performance is still acceptable) (see Figures [Selection performance results using varying gzip aggression settings \(hopper using /project\)](#) and [Selection performance results using varying gzip aggression settings \(hopper using /scratch\)](#)⁶).

Overall, we find that for the data layouts tested here, increasing the aggression parameter above 1 does not have a large impact on the compression ratio and selection performance, whereas high aggression values may significantly decrease the data write performance. In the context of MSI data, low aggression values of $\text{aggression} \in [1, 4]$ may, therefore, be preferable when using gzip compression.

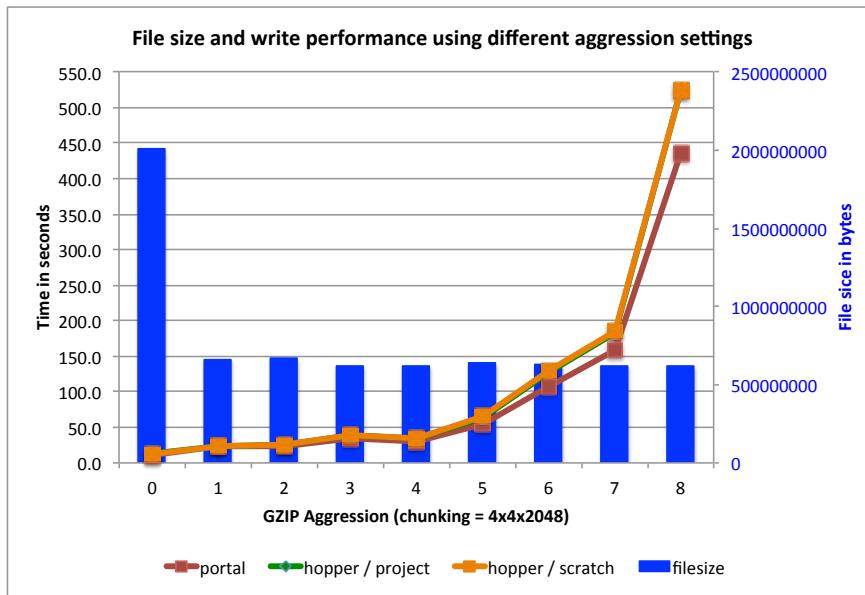


Fig. 9.22: File size and write performance using varying gzip aggression settings

9.7 Local Scalability: Multi-processing

Next we tested the local scalability using Python’s multiprocessing capabilities (i.e., on a single *hopper* login node and *portal*, and not across multiple compute nodes). We again use a $100 \times 100 \times 100,000$ test dataset (using A as donor dataset) and we regenerate the dataset for each experiment (i.e., file layout + system). We repeat each computation 50 times on the same file and report the average times and standard deviations. For this test we select 20,000 z slices (i.e., 20% of the data) and compute the variance of the data values across the slices, i.e.:

- `numpy.var(data[:, :, zstart : (zstart + 20001)])` with $zstart$ being selected randomly ($zstart \in [0, 79999]$)

⁶ Bars shown transparently indicate that the bars exceed the maximum value shown in the plot. The real value for those bars are indicated via additional text labels.

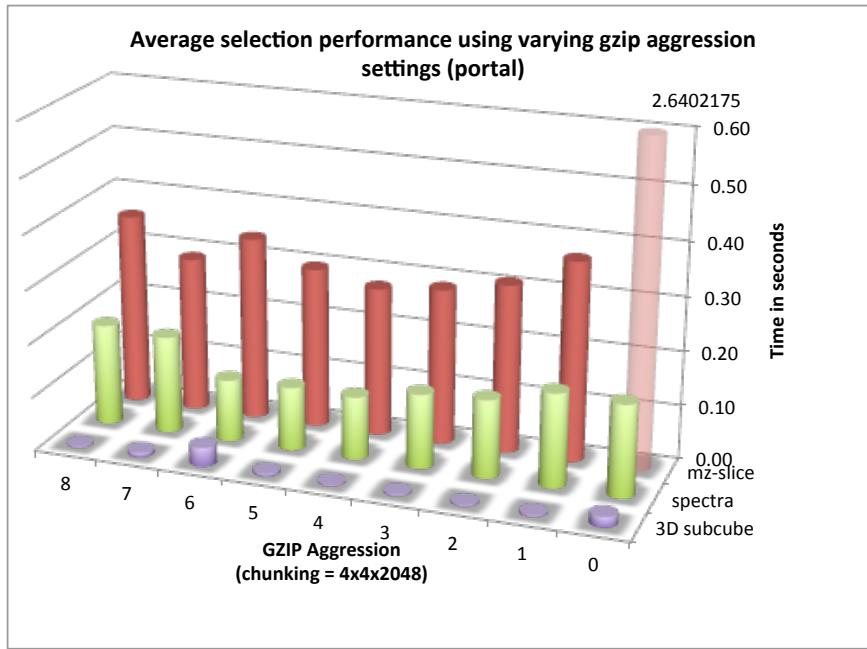


Fig. 9.23: Selection performance results using varying gzip aggression settings (portal)

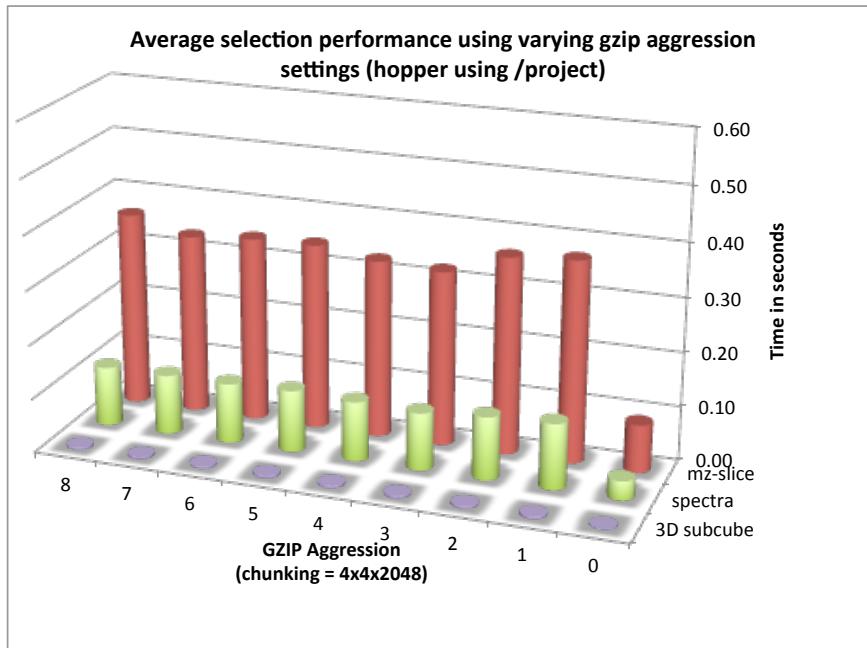


Fig. 9.24: Selection performance results using varying gzip aggression settings (hopper using /project)

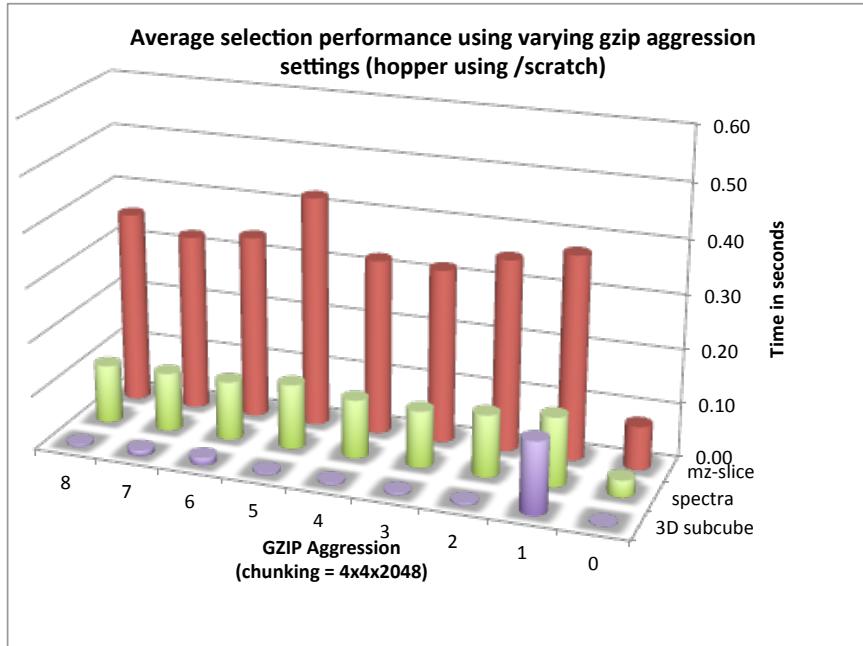


Fig. 9.25: Selection performance results using varying gzip aggression settings (hopper using /scratch)

We parallelize the computation across processes by dividing data along the x axis, i.e., each process computes for its portion of the data:

- `numpy.var(data[xstart : xend, :, zstart : (zstart + 20001)])`

while `xstart` and `xend` are determined based on the process id. The result is then stored in a shared array. The average performance (with error bars indicating the standard deviation) for performing this calculation on hopper using project are shown in Figure [Scaling results for computing the variance for 20000 z-slices \(hopper using /project\)](#). We compute the speed-up by using the time required using 1 process as reference (i.e., the time from the current experiment so that the speed-up using 1 processor is always equal to 1)(see Figure [Speed-up results for computing the variance for 20000 z-slices \(hopper using /project\)](#)). We repeated the same tests also on portal (again using the /project file systems). The results for portal are shown in Figures: i) [Scaling results for computing the variance for 20000 z-slices \(portal\)](#) and ii) [Speed-up results for computing the variance for 20000 z-slices \(portal\)](#).

The main bottleneck in this calculation is again the data selection/load. We observe that we can achieve good speed-up for larger numbers of processes using hopper compared to portal. This behavior is likely due to the better I/O (network) performance of hopper compared to portal. On portal we observe a stable speed-up for up to 5 processes (when using compression) and we achieve a $\approx 3\times$ speed-up. Using hopper we observe a linear speed-up for up to 8 processes. Afterwards, we still observe speed-up, however, at a lower and less stable rate. As before, we observe that using compression yields better performance on portal while reducing the performance when using hopper.

In the context of the OpenMSI web-based data viewer we typically need to extract smaller subsets of the data. We, therefore, next repeated the variance computation for 25 consecutive z slices (similar to the z slice selection use-case used in the previous sections). The timings and speed-up results on portal using default setup —i.e., with $4 \times 4 \times 2048$ chunking and gzip compression, aggression=4— are shown in Figure [Timings and speed-up results for computing the variance for 25 z-slices \(portal\)](#). We observe that even-though the amount of data retrieved is with 0.5MB comparably small —note the data being loaded to fulfill the query is on the order of 39.0625MB—, we can still achieve good speed-ups until 4-7 processes, afterwards the performance degrades again.

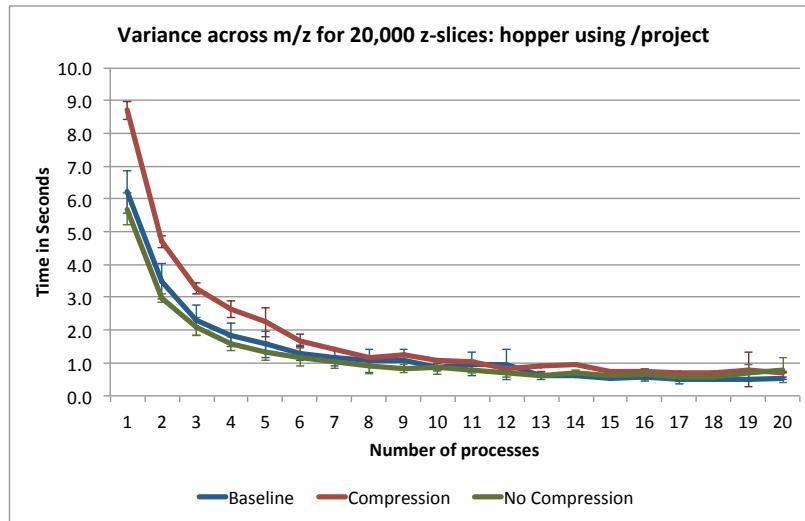


Fig. 9.26: Scaling results for computing the variance for 20000 z-slices (hopper using /project)

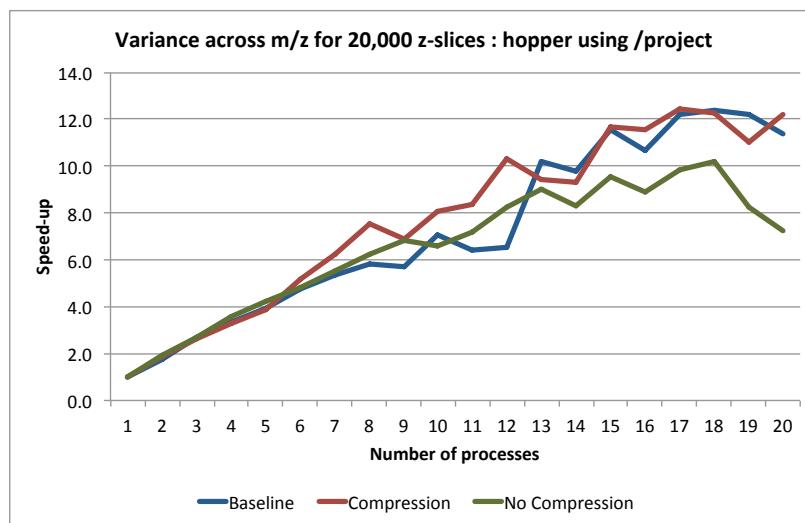


Fig. 9.27: Speed-up results for computing the variance for 20000 z-slices (hopper using /project)

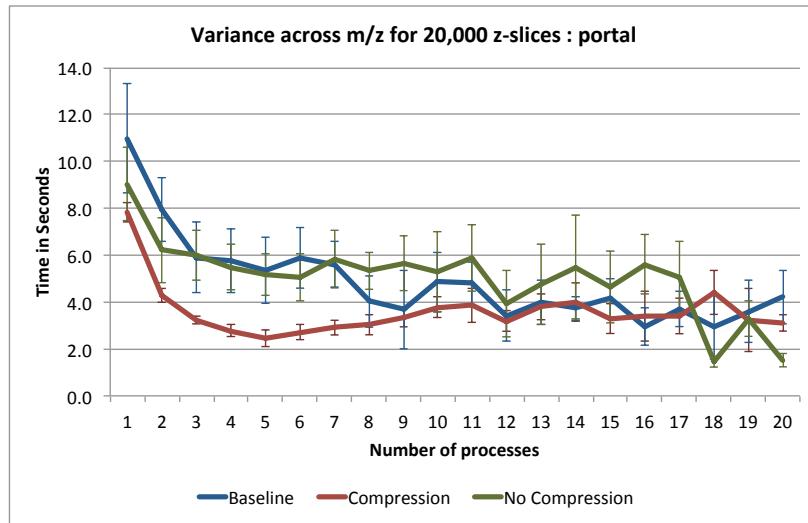


Fig. 9.28: Scaling results for computing the variance for 20000 z-slices (portal)

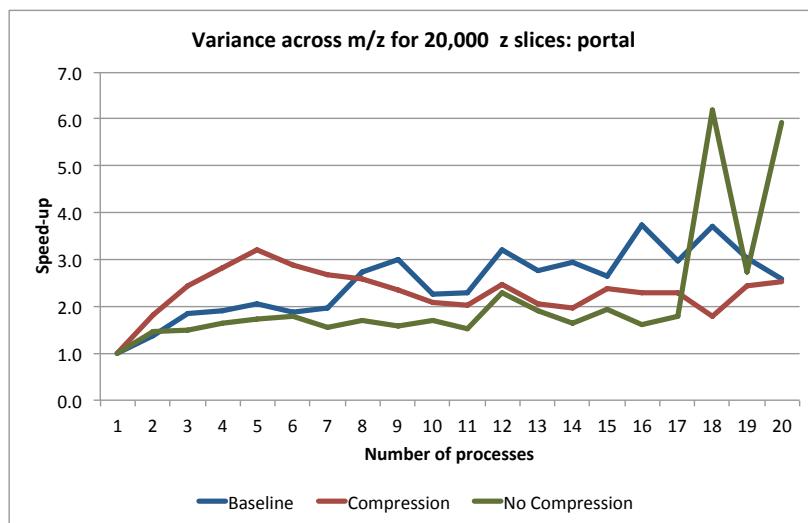


Fig. 9.29: Speed-up results for computing the variance for 20000 z-slices (portal)

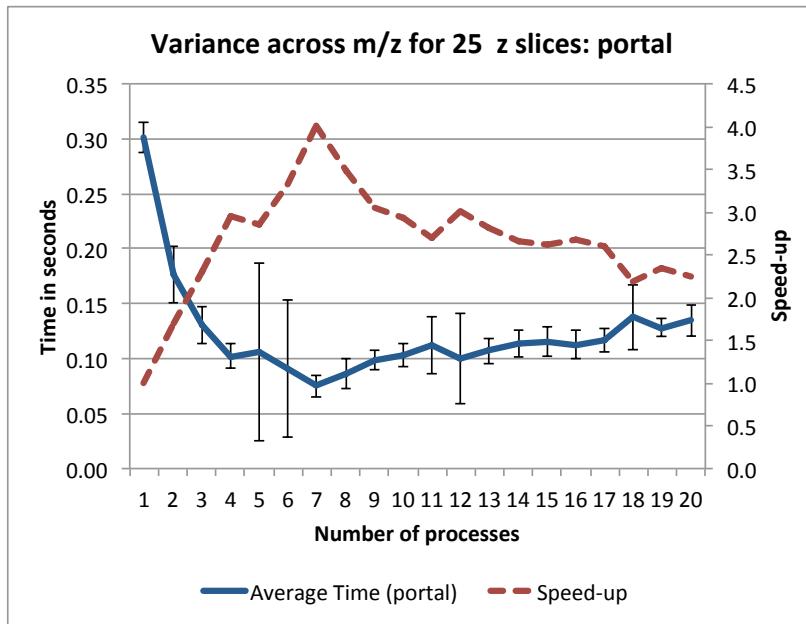


Fig. 9.30: Timings and speed-up results for computing the variance for 25 z-slices (portal)

9.8 Discussion

9.8.1 Data Layout

Use of chunking has many benefits but choosing the correct chunk size can be complicated. In the context of MSI data, the choice of a good data layout is complicated by: i) the large difference between the size of the spatial x/y and the z (mz , mass) dimension and ii) the need for regularly performing orthogonal data selection operations (namely selection of spectra $[x, y, :]$ and full slices in z $[:, :, z]$). Our experiments have shown that a chunking of $4 \times 4 \times 2048$ may work well for most cases, i.e., it provides a good compromise in performance between the different selection operations while maintaining acceptable write performance and limiting the worst-case overhead in file size.

Our experiments have also shown that MSI data lends itself well to compression (we have seen reductions in file size on the order of $3\times$ to $9\times$ on real MSI datasets). We have also seen that the use of data compression (here `gzip`) may also improve the selection performance by reducing the amount of data that needs to be loaded from disk (see results from `portal`). This is particularly true for I/O (and or network) bound systems, such as `portal`. However, we have also seen (on `hopper`) that the use of compression can also decrease the selection performance due to the time required for decompression (see results `hopper`). Having direct access to uncompressed data may, hence, be advantageous for any analyses that require a large number of random accesses to the data from a high-performance compute systems (such as `hopper`) where the time required for decompression is larger than the time saved for data transfer. However, the reduced storage requirements and overall more stable selection performance results suggest that the use of compression may be advantageous.

Based on the results from this study we currently use a data layout of $4 \times 4 \times 2048$ with `gzip` compression and `aggression=4` as default for storing MSI data using the OMSI HDF5 data format.

9.8.2 System Performance

In a serial setting we observe that `hopper`'s `/scratch` filesystem generally provides better selective read performance than the `/project` file system. This is not unexpected and overall the performance of both file systems appears to be sufficient to perform most common MSI analysis tasks. However, based on the test results it appears that

on `portal`: i) the selection performance is highly dependent on system load (which appeared to be high on many occasions) and ii) the selection performance is bound by the performance of the I/O system. Since the performance using `/project` is significantly higher on `hopper` login nodes than on `portal`, it appears that the bandwidth of the network connection of `portal` to the GPFS `/project` file system may be too low to ensure a reliably fast operation of web-applications that require repeated access to large datasets. This, however, is essential for production use of science gateways that aim to make advanced data viewing and analysis capabilities accessible to the application community (such as the OpenMSI science gateway for MSI data). While we were able to achieve usable I/O performance on `portal` through the use of chunking and compression, we have also seen that even from `/project` we can achieve significantly better performance on `hopper` when storing the data in a raw, uncompressed form (i.e., we should be able to get much better selective I/O performance on `portal` using `/project`). While `portal` provides a good platform for development of science gateways and web applications, the question remains whether `portal` is powerful enough—with respect to both compute, I/O and network performance—to provide a reliable, high-performance platform for hosting production science gateways.

9.8.3 Future Work

In future we plan to evaluate the performance of the different data layouts in a: i) local parallel (multi-processing) and ii) distribution parallel (MPI) environment.

While `gzip` is one of the most widely available compression algorithms in HDF5 it is not necessarily one with the best performance. In future we plan to evaluate the use of other compression algorithms—such as, `szip`⁷, `LZF`⁸, HDF5 N-Bit Filter⁹, HDF5 Scale+Offset Filter¹⁰ etc.—to further improve the overall read performance and to reduce the larger overheads for compression we have seen on `hopper`. In addition to compression, HDF5 also provides a shuffle filter¹¹ which can potentially further improve the effectiveness of data compression¹².

⁷ http://www.hdfgroup.org/doc_resource/SZIP/

⁸ <http://h5py.alrven.org/lzf/>

⁹ http://www.hdfgroup.org/HDF5/doc/RM/RM_H5P.html#Property-SetNbit

¹⁰ http://www.hdfgroup.org/HDF5/doc/RM/RM_H5P.html#Property-SetScaleoffset

¹¹ http://www.hdfgroup.org/HDF5/doc/RM/RM_H5Z.html

¹² http://www.hdfgroup.org/HDF5/doc_resource/H5Shuffle_Perf.pdf,

OMSI PACKAGE

10.1 Subpackages

The omsi package defines the main BASTet software stack used, e.g., by the OpenMSI project. It contains a large range of functionality for interacting analyses, OpenMSI HDF5 data files, analysis workflows and other related infrastructure. The following is a rough overview of the various packages and modules

- **Analysis** `omsi.analysis` Package containing the base classes that facilitate the integration of new analysis with the BASTet software stack (e.g., the file format) and collection of specific analysis functionality.

<code>omsi.analysis</code>	Package containing the base classes that facilitate the integration of new analysis
<code>omsi.analysis.compound_stats</code>	Package containing shared third-party code modules included here to reduce the ne
<code>omsi.analysis.findpeaks</code>	Package of peak-finding related analysis modules.
<code>omsi.analysis.msi_filtering</code>	Module with third-party modules, functions, classes used by some of the analysis m
<code>omsi.analysis.multivariate_stats</code>	Multivariate statistics analysis

- **Data Format** `omsi.dataformat` Package for implementation and specification of file formats. In particular this package contains the base API for interacting with OpenMSI HDF5 datasets.

<code>omsi.dataformat</code>	Package for implementation and specification of file formats.
<code>omsi.dataformat.omsi_file</code>	Module for specification of the OpenMSI file API.

- **Workflow** `omsi.workflow` Package with modules for specification and execution of analysis tasks and complex analysis workflows.

<code>omsi.workflow</code>	Package with modules for specification and execution of analysis tasks and complex analysis work
<code>omsi.workflow.dirver</code>	
<code>omsi.workflow.executor</code>	Package with executors of analysis workflows.

- **Data Structures** `omsi.datastructure` Package with a collection of various data structures and related classes used throughout the software stack, e.g., for metadata, analysis parameter data, runtime information data etc.

<code>omsi.datastructures</code>	Package with a collection of various data structures and related classes used throughout th
<code>omsi.datastructures.metadata</code>	Package with metadata datastructures

- **Shared** `omsi.shared` Package used to implement shared functionality and helper functions.

<code>omsi.shared</code>	Package used to implement shared functionality and helper functions.
<code>omsi.shared.thirdparty</code>	

- **Tools** `omsi.tools` Package for collecting tools (e.g., command-line programs) to help with particular tasks. This includes, e.g., tools for data conversion, document generation, etc.

<code>omsi.tools</code>	Package for collecting tools (e.g.,)
<code>omsi.tools.misc</code>	Collection of miscellaneous tools.

- **Templates** `omsi.templates` This package provides a collection of code templates to ease the development of additional components, e.g., analysis modules. As such, this package is NOT intended for direct usage but is rather just a library of code templates.

`omsi.templates` This package provides a collection of code templates to ease the development of additional components, e.g.,

- **Examples** `omsi.examples` Package with a collection of various misc. example scripts.

<code>omsi.examples</code>	Package with a collection of various misc.
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10.1.1 analysis Package

<code>omsi.analysis</code>	Package containing the base classes that facilitate the integration of new analysis with the BASTet software stack (e.g., the file format) and collection of specific analysis functionality.
<code>omsi.analysis.base</code>	Module specifying the base analysis API for integrating new analysis modules.
<code>omsi.analysis.generic</code>	Generic analysis class used to represent analyses of unknown type.
<code>omsi.analysis.analysis_views</code>	Helper module with functions and classes for interfacing with analysis results.
<code>omsi.analysis.compound_stats</code>	Package containing shared third-party code modules including:
<code>omsi.analysis.compound_stats.omsi_score_compounds</code>	omsi_score_compounds
<code>omsi.analysis.findpeaks</code>	Package of peak-finding related analysis modules.
<code>omsi.analysis.msi_filtering</code>	Module with third-party modules, functions, classes used for mass spectrometry filtering.
<code>omsi.analysis.multivariate_stats</code>	Multivariate statistics analysis

analysis Package

Package containing the base classes that facilitate the integration of new analysis with the BASTet software stack (e.g., the file format) and collection of specific analysis functionality.

```
class omsi.analysis.analysis_data(name='undefined', data=None, dtype='float32')
    Bases: dict
```

Define an output dataset for the analysis that should be written to the omsi HDF5 file

The class can be used like a dictionary but restricts the set of keys that can be used to the following required keys which should be provided during initialization.

Required Keyword Arguments:

Parameters

- **name** – The name for the dataset in the HDF5 format
- **data** – The numpy array to be written to HDF5. The data write function `omsi_file_experiment.create_analysis` used for writing of the data to file can in principle also handle other primitive data types by explicitly converting them to numpy. However, in this case the dtype is determined based on the numpy conversion and correct behavior is not guaranteed. I.e., even single scalars should be stored as a 1D numpy array here. Default value is None which is mapped to `np.empty(shape=(0), dtype=dtype)` in `__init__`

- **dtype** – The data type to be used during writing. For standard numpy data types this is just the dtype of the dataset, i.e., [‘data’].dtype. Other allowed datatypes are:
 - For string: omsi_format.str_type (omsi_format is located in omsi.dataformat.omsi_file)
 - To generate data links: ana_hdf5link (analysis_data)

ana_hdf5link = -1

```
class omsi.analysis.analysis_base
Bases: omsi.datastructures.analysis_data.parameter_manager
```

Base class for omsi analysis functionality. The class provides a large set of functionality designed to facilitate storage of analysis data in the omsi HDF5 file format. The class also provides a set of functions to enable easy integration of new analysis with the OpenMSI web-based viewer (see Viewer functions below for details).

Slicing:

This class supports basic slicing to access data stored in the main member variables. By default the data is retrieved from __data_list and the __getitem__(key) function, which implements the [.] operator, returns __data_list[key][‘data’]. The key is a string indicating the name of the parameter to be retrieved. If the key is not found in the __data_list then the function will try to retrieve the data from self.parameters list instead. By adding “parameter/key” or “dependency/key” one may also explicitly retrieve values from the parameters.

Instance Variables:

Variables

- **analysis_identifier** – Define the name for the analysis used as key in search operations
- **__data_list** – List of analysis_data to be written to the HDF5 file. Derived classes need to add all data that should be saved for the analysis in the omsi HDF5 file to this dictionary. See omsi.analysis.analysis_data for details.
- **parameters** – List of parameter_data objects of all analysis parameters (including those that may have dependencies).
- **data_names** – List of strings of all names of analysis output datasets. These are the target keys for __data_list.
- **profile_time_and_usage** – Boolean indicating whether we should profile the execute_analysis(...) function when called as part of the execute(..) function. The default value is false. Use the enable_time_and_usage_profiling(..) function to determine which profiling should be performed. The time_and_usage profile uses python’s cProfile (or Profile) to monitor how often and for how long particular parts of the analysis code executed.
- **profile_memory** – Boolean indicating whether we should monitor memory usage (line-by-line) when executing the execute_analysis(..) function. The default value is false. Use the enable_time_and_usage_profiling(..) function to determine which profiling should be performed.
- **omsi_analysis_storage** – List of omsi_file_analysis object where the analysis is stored. The list may be empty.
- **mpi_comm** – In case we are running with MPI, this is the MPI communicator used for running the analysis. Default is MPI.Comm_world/
- **mpi_root** – In case we are running with MPI, this is the root rank where data is collected to (e.g., runtime data and analysis results)

- **update_analysis** – If the value is True, then we should execute the analysis before using the outputs. If False, then the analysis has been executed with the current parameter settings.
- **driver** – Workflow driver to be used when executing multiple analyses, e.g., via execute_recursive or execute_all. Default value is None in which case a new default driver will be used each time we execute a workflow.

Execution Functions:

- **execute** : Then main function the user needs to call in order to execute the analysis
- “**execute_analysis**: This function needs to be implemented by child classes of *analysis_base* to implement the specifics of executing the analysis.

I/O functions:

These functions can be optionally overwritten to control how the analysis data should be written/read from the omsi HDF5 file. Default implementations are provided here, which should be sufficient for most cases.

- **add_custom_data_to_omsi_file**: The default implementation is empty as the default data write is managed by the *omsi_file_experiment.create_analysis()* function. Overwrite this function, in case that the analysis needs to write data to the HDF5 omsi file beyond what the defualt omsi data API does.
- **read_from_omsi_file**: The default implementation tries to reconstruct the original data as far as possible, however, in particular in case that a custom add_custom_data_to_omsi_file function has been implemented, the default implementation may not be sufficien. The default implementation reconstructs: i) analysis_identifier and reads all custom data into ii)_data_list. Note, an error will be raised in case that the analysis type specified in the HDF5 file does not match the analysis type specified by get_analysis_type(). This function can be optionally overwritten to implement a custom data read.

Viewer functions:

Several convenient functions are used to allow the OpenMSI online viewer to interact with the analysis and to visualize it. The default implementations provided here simply indicate that the analysis does not support the data access operations required by the online viewer. Overwrite these functions in the derived analysis classes in order to interface them with the viewer. All viewer-related functions start with v__

NOTE: the default implementation of the viewer functions defined in *analysis_base* are designed to take care of the common requirement for providing viewer access to data from all dependencies of an analysis. In many cases, the default implementation is often sill called at the end of custom viewer functions.

NOTE: The viewer functions typically support a viewer_option parameter. viewer_option=0 is expected to refer to the analysis itself.

- **v_qslice**: Retrieve/compute data slices as requested via qslice URL requests. The corresponding view of the DJANGO data access server already translates all input parameters and takes care of generating images/plots if needed. This function is only responsible for retrieving the data.
- **v_qspectrum**: Retrieve/compute spectra as requested via qspectrum URL requests. The corresponding view of the DJANGO data access server already translates all input parameters and takes care of generating images/plots if needed. This function is only responsible for retrieving the data.
- **v_qmz**: Define the m/z axes for image slices and spectra as requested by qspectrum URL requests.
- **v_qspectrum_viewer_options**: Define a list of strings, describing the different viewer options available for the analysis for qspectrum requests (i.e., v_qspectrum). This feature allows the analysis developer to define multiple different visualization modes for the analysis. For example, when performing a data reduction (e.g., PCA or NMF) one may want to show the raw spectra or the loadings vector of the projection in the spectrum view (v_qspectrum). By providing different viewer options we allow the user to decide which option they are most interested in.

- `v_qslice_viewer_options`: Define a list of strings, describing the different viewer options available for the analysis for qslice requests (i.e., `v_qslice`). This feature allows the analysis developer to define multiple different visualization modes for the analysis. For example, when performing a data reduction (e.g., PCA or NMF) one may want to show the raw spectra or the loadings vector of the projection in the spectrum view (`v_qspectrum`). By providing different viewer options we allow the user to decide which option they are most interested in.

Initialize the basic data members

`add_custom_data_to_omsi_file(analysis_group)`

This function can be optionally overwritten to implement a custom data write function for the analysis to be used by the `omsi_file` API.

Note, this function should be used only to add additional data to the analysis group. The data that is written by default is still written by the `omsi_file_experiment.create_analysis()` function, i.e., the following data is written by default: i) `analysis_identifier`, ii) `get_analysis_type`, iii) `__data_list`, iv) `parameters`, v) `runinfo`. Since the `omsi_file_experiment.create_analysis()` functions takes care of setting up the basic structure of the analysis storage (included the subgroups for storing parameters and data dependencies) this setup can generally be assumed to exist before this function is called. This function is called automatically at the end `omsi_file_experiment.create_analysis()` (i.e., actually `omsi_file_analysis.__populate_analysis__(..)`) so that this function typically does not need to be called explicitly.

Parameters `analysis_group` – The h5py.Group object where the analysis is stored.

`add_parameter(name, help, dtype=<type 'unicode'>, required=False, default=None, choices=None, data=None, group=None)`

Add a new parameter for the analysis. This function is typically used in the constructor of a derived analysis to specify the parameters of the analysis.

Parameters

- `name` – The name of the parameter
- `help` – Help string describing the parameter
- `type` – Optional type. Default is string.
- `required` – Boolean indicating whether the parameter is required (True) or optional (False). Default False.
- `default` – Optional default value for the parameter. Default None.
- `choices` – Optional list of choices with allowed data values. Default None, indicating no choices set.
- `data` – The data assigned to the parameter. None by default.
- `group` – Optional group string used to organize parameters. Default None, indicating that parameters are automatically organized by driver class (e.g. in required and optional parameters)

Raises `ValueError` is raised if the parameter with the given name already exists.

`analysis_identifier_defined()`

Check whether the analysis identifier is defined by the user, i.e., set to value different than undefined
:return: bool

`check_ready_to_execute()`

Check if all inputs are ready to determine if the analysis is ready to run.

Returns List of `omsi_analysis_parameter` objects that are not ready. If the returned list is empty, then the analysis is ready to run.

clear_analysis()
Clear all analysis data—i.e., parameter, dependency data, output results, runtime data

clear_analysis_data()
Clear the list of analysis data

clear_and_restore(analysis_manager=None, resave=False)
Clear all analysis data and restore the results from file

Parameters

- **analysis_manager** – Instance of omsi_analysis_manager (e.g., an omsi_file_experiment) where the analysis should be saved.
- **resave** – Boolean indicating whether the analysis should be saved again, even if it has been saved before. This parameter only has effect if analysis_manager is given.

Returns self, i.e., the updated analysis object with all data replaced with HDF5 references

clear_parameter_data()
Clear the list of parameter data

clear_run_info_data()
Clear the runtime information data

define_missing_parameters()
Called by the execute function before self.update_analysis_parameters to set any required parameters that have not been defined to their respective default values.

This function may be overwritten in child classes to customize the definition of default parameter values and to apply any modifications (or checks) of parameters before the analysis is executed. Any changes applied here will be recorded in the parameter of the analysis.

enable_memory_profiling(enable=True)
Enable or disable line-by-line profiling of memory usage of execute_analysis.

Parameters **enable_memory** (bool) – Enable (True) or disable (False) line-by-line profiling of memory usage

Raises ImportError is raised if a required package for profiling is not available.

enable_time_and_usage_profiling(enable=True)
Enable or disable profiling of time and usage of code parts of execute_analysis.

Parameters **enable** (bool) – Enable (True) or disable (False) profiling

Raises ImportError is raised if a required package for profiling is not available.

execute(kwargs)**
Use this function to run the analysis.

Parameters **kwargs** – Parameters to be used for the analysis. Parameters may also be set using the __setitem__ mechanism or as batches using the set_parameter_values function.

Returns This function returns the output of the execute analysis function.

Raises AnalysisReadyError in case that the analysis is not ready to be executed. This may be the case, e.g, when a dependent input parameter is not ready to be used.

classmethod execute_all(force_update=False, executor=None)
Execute all analysis instances that are currently defined.

Parameters

- **force_update** – Boolean indicating whether we should force that all analyses are executed again, even if they have already been run with the same settings before. False by default.

- **executor** – Optional workflow executor to be used for the execution of all analyses. The executor will be cleared and then all analyses will be added to executor. Default value is None, in which case the function creates a default executor to be used.

Returns The workflow executor used

`execute_analysis()`

Implement this function to implement the execution of the actual analysis.

This function may not require any input parameters. All input parameters are recorded in the parameters and dependencies lists and should be retrieved from there, e.g, using basic slicing `self[paramName]`

Input parameters may be added for internal use ONLY. E.g, we may add parameters that are used internally to help with parallelization of the `execute_analysis` function. Such parameters are not recorded and must be strictly optional so that `analysis_base.execute(...)` can call the function.

Returns This function may return any developer-defined data. Note, all output that should be recorded must be put into the data list.

`execute_recursive(**kwargs)`

Recursively execute this analysis and all its dependencies if necessary

We use a workflow driver to control the execution. To define the workflow driver we can set the `self.driver` variable. If no workflow driver is given (i.e, `self.driver==None`), then the default driver will be created. To change the default driver, see `omsi.workflow.base.workflow_executor_base.DEFAULT_EXECUTOR_CLASS`

Parameters `kwargs` – Parameters to be used for the analysis. Parameters may also be set using the `__setitem__` mechanism or as batches using the `set_parameter_values` function.

Returns Same as `execute`

`get_all_analysis_data()`

Get the complete list of all analysis datasets to be written to the HDF5 file

`get_all_dependency_data()`

Get the complete list of all direct dependencies to be written to the HDF5 file

NOTE: These are only the direct dependencies as specified by the analysis itself. Use `get_all_dependency_data_recursive(..)` to also get the indirect dependencies of the analysis due to dependencies of the dependencies themselves.

Returns List of parameter_data objects that define dependencies.

`get_all_parameter_data(exclude_dependencies=False)`

Get the complete list of all parameter datasets to be written to the HDF5 file

Parameters `exclude_dependencies` – Boolean indicating whether we should exclude parameters that define dependencies from the list

`get_all_run_info()`

Get the dict with the complete info about the last run of the analysis

`get_analysis_data(index)`

Given the index return the associated dataset to be written to the HDF5 file

:param index : Retrun the index entry of the private member `__data_list`.

`get_analysis_data_by_name(dataname)`

Given the key name of the data return the associated analysis_data object.

Parameters `dataname` – Name of the analysis data requested from the private `__data_list` member.

Returns The analysis_data object or None if not found.

get_analysis_data_names()

Get a list of all analysis dataset names.

get_analysis_identifier()

Return the name of the analysis used as key when searching for a particular analysis

classmethod get_analysis_instances()

Generator function used to iterate through all instances of analysis_base. The function creates references for all weak references stored in `cls._analysis_instances` and returns the references if it exists and cleans up the any invalid references after the iteration is complete. :return: References to analysis_base objects

get_analysis_type()

Return a string indicating the type of analysis performed

static get_default_dtypes()

Get a list of available default dtypes used for analyses. Same as `data_dtypes.get_dtypes()`.

static get_default_parameter_groups()

Get a list of commonly used parameter groups and associated descriptions.

Use of default groups provides consistency and allows other system to design custom behavior around the semantic of parameter groups

Returns Dictionary where the keys are the short names of the groups and the values are dicts with following keys:value pairs: ‘name’ , ‘description’. Use the ‘name’ to define the group to be used.

get_help_string()

Get a string describing the analysis.

Returns Help string describing the analysis and its parameters

get_memory_profile_info()

Based on the memory profile of the `execute_analysis(..)` function get the string describing the line-by-line memory usage.

Returns String describing the memory usage profile. None is returned in case that no memory profiling data is available.

get_num_analysis_data()

Retrun the number of analysis datasets to be wirtten to the HDF5 file

get_num_dependency_data()

Return the number of dependencies to be wirtten to the HDF5 file

get_num_parameter_data()

Return the number of parameter datasets to be wirtten to the HDF5 file

get_omsi_analysis_storage()

Get a list of known locations where this analysis has been saved.

Returns List of `omsi.dataformat.omsi_file.analysis`. `omsi_file_analysis` objects where the analysis is saved.

get_parameter_data(index)

Given the index return the associated dataset to be written to the HDF5 file

:param index : Return the index entry of the private member parameters.

get_parameter_data_by_name (dataname)

Given the key name of the data return the associated parameter_data object.

Parameters **dataname** – Name of the parameter requested from the parameters member.

Returns The parameter_data object or None if not found

get_parameter_names ()

Get a list of all parameter dataset names (including those that may define dependencies).

get_profile_stats_object (consolidate=True, stream=None)

Based on the execution profile of the execute_analysis(..) function get pstats.Stats object to help with the interpretation of the data.

Parameters

- **consolidate** – Boolean flag indicating whether multiple stats (e.g., from multiple cores) should be consolidated into a single stats object. Default is True.
- **stream** – The optional stream parameter to be used fo the pstats.Stats object.

Returns A single pstats.Stats object if consolidate is True. Otherwise the function returns a list of pstats.Stats objects, one per recorded statistic. None is returned in case that the stats objects cannot be created or no profiling data is available.

has_omsi_analysis_storage ()

Check whether a storage location is known where the analysis has been saved.

Returns Boolean indicating whether self.omsi_analysis_storage is not empty

keys ()

Get a list of all valid keys, i.e., a combination of all input parameter and output names.

Returns List of strings with all input parameter and output names.

classmethod locate_analysis (data_object, include_parameters=False)

Given a data_object try to locate the analysis that creates the object as an output of its execution (and optionally analyses that have the object as an input).

Parameters

- **data_object** – The data object of interest.
- **include_parameters** – Boolean indicating whether also input parameters should be considered in the search in addition to the outputs of an analysis

Returns dependency_dict pointing to the relevant object or None in case the object was not found.

read_from_omsi_file (analysis_object, load_data=True, load_parameters=True, load_runtime_data=True, dependencies_omsi_format=True, ignore_type_conflict=False)

This function can be optionally overwritten to implement a custom data read.

The default implementation tries to reconstruct the original data as far as possible, however, in particular in case that a custom add_custom_data_to_omsi_file function has been implemented, the default implementation may not be sufficient. The default implementation reconstructs: i) analysis_identifier and reads all custom data into iii)_data_list. Note, an error will be raised in case that the analysis type specified in the HDF5 file does not match the analysis type specified by get_analysis_type()

Parameters

- **analysis_object** – The omsi_file_analysis object associated with the hdf5 data group with the analysis data_list

- **load_data** – Should the analysis data be loaded from file (default) or just stored as h5py data objects
- **load_parameters** – Should parameters be loaded from file (default) or just stored as h5py data objects.
- **load_runtime_data** – Should runtime data be loaded from file (default) or just stored as h5py data objects
- **dependencies_omsi_format** – Should dependencies be loaded as omsi_file API objects (default) or just as h5py objects.
- **ignore_type_conflict** – Set to True to allow the analysis to be loaded into the current analysis object even if the type indicated in the file does not match the class. Default value is False. This behavior can be useful when different analysis have compatible data structures or when we want to load the data in to a generic analysis container, e.g, analysis_generic.

Returns `bool` Boolean indicating whether the data was read successfully

Raise `TypeError` : A type error will be raised in case that the analysis type specified by the file does not match the analysis type provided by `self.get_analysis_type()`

record_execute_analysis_outputs (`analysis_output`)

Function used internally by execute to record the output of the custom `execute_analysis(...)` function to the `_data_list`.

This function may be overwritten in child classes in order to customize the behavior for recording data outputs. Eg., for some analyses one may only want to record a particular set of outputs, rather than all outputs generated by the analysis.

Parameters `analysis_output` – The output of the `execute_analysis(...)` function to be recorded

results_ready ()

Check whether the results of the analysis are ready to be used :return: Boolean

set_analysis_identifier (`identifier`)

Set the name of the analysis to identifier

Side Effects: This function modifies `self.analysis_identifier`

Parameters `identifier` (`str`) – The new analysis identifier string to be used (should be unique)

set_parameter_values (**`kwargs`)

Set all parameters given as input to the function. The inputs are placed in the `self.parameters` list. If the parameter refers to an existing h5py.Dataset, h5py.Group, managed h5py object, or is an instance of an existing omis_analysis_base object, then a dependency_dict will be created and stored as value instead.

Parameters `kwargs` – Dictionary of keyword arguments. All keys are expected to be strings.

All values are expected to be either i) numpy arrays, ii) int, float, str or unicode variables, iii) h5py.Dataset or h5py.Group, iv) or any the omsi_file API class objects. For iii) and iv) one may provide a tuple consisting of the dataobject t[0] and an additional selection string t[1].

update_analysis_parameters (**`kwargs`)

Record the analysis parameters passed to the `execute()` function.

The default implementation simply calls the `set_parameter_values(...)` function. This function may be overwritten to customize the behavior of how parameters are recorded by the `execute` function.

Parameters `kwargs` – Dictionary of keyword arguments with the parameters passed to the `execute(..)` function

classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- mzSpectra : Array with the static mz values for the spectra.
- labelSpectra : Label for the spectral mz axis
- mzSlice : Array of the static mz values for the slices or None if identical to the mzSpectra.
- labelSlice : Label for the slice mz axis or None if identical to labelSpectra.
- values_x: The values for the x axis of the image (or None)
- label_x: Label for the x axis of the image
- values_y: The values for the y axis of the image (or None)
- label_y: Label for the y axis of the image
- values_z: The values for the z axis of the image (or None)
- label_z: Label for the z axis of the image

classmethod v_qslice (analysis_object, z, viewer_option=0)

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **z** – Selection string indicating which z values should be selected.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like [:,:,zmin:zmax].

Raises NotImplementedError in case that v_qslice is not supported by the analysis.

classmethod v_qslice_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qslice. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually

a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qslice requests (i.e., v_qslic(...)) is not available).

classmethod v_qspectrum(analysis_object, x, y, viewer_option=0)

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **x** – x selection string
- **y** – y selection string
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns

The following two elements are expected to be returned by this function :

1. 1D, 2D or 3D numpy array of the requested spectra. NOTE: The mass (m/z) axis must be the last axis. For index selection x=1,y=1 a 1D array is usually expected. For indexList selections x=[0]&y=[1] usually a 2D array is expected. For range selections x=0:1&y=1:2 we one usually expects a 3D array.
2. None in case that the spectra axis returned by v_qmz are valid for the returned spectrum. Otherwise, return a 1D numpy array with the m/z values for the spectrum (i.e., if custom m/z values are needed for interpretation of the returned spectrum). This may be needed, e.g., in cases where a per-spectrum peak analysis is performed and the peaks for each spectrum appear at different m/z values.

classmethod v_qspectrum_viewer_options(analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qspectrum. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qspectrum requests (i.e., v_qspectrum(...)) is not available).

write_analysis_data(analysis_group=None)

This function is used to write the actual analysis data to file. If not implemented, then the omsi_file_analysis API's default behavior is used instead.

Parameters `analysis_group` – The h5py.Group object where the analysis is stored. May be None on cores that do not perform any writing but which need to participate in communication, e.g., to collect data for writing.

exception `omsi.analysis.AnalysisReadyError` (`value, params=None`)

Bases: `exceptions.Exception`

Custom exception used to indicate that an analysis is not ready to execute.

Initialize the AnalysisReadyError

Parameters

- `value` – Error message string
- `params` – Optional list of dependent parameters that are not ready to be used.

class `omsi.analysis.analysis_generic(name_key='undefined')`

Bases: `omsi.analysis.base.analysis_base`

This analysis class is used if the specific analysis type is unknown, e.g., when loading custom user-defined analysis data that may have not be available in the standard omsi package used.

Initialize the basic data members

Parameters `name_key` – The name for the analysis

`DEFAULT_OUTPUT_PREFIX = 'output_'`

execute (`**kwargs`)

Overwrite the default implementation of execute to update parameter specifications/types when wrapping functions where the types are not known a priori.

Parameters `kwargs` – Custom analysis parameters

Returns The result of execute_analysis()

execute_analysis ()

Nothing to do here.

classmethod `from_function(analysis_function, output_names=None, parameter_specs=None, name_key='undefined')`

Create a generic analysis class for a given analysis function.

This functionality is useful to ease quick scripting on analyses but should not be used in production.

NOTE: `_analysis_function` is a reserved parameter name used to store the analysis function and may not be used as an input parameter for the analysis function.

Parameters

- `analysis_function` – The analysis function to be wrapped for provenance tracking and storage
- `output_names` – Optionally, define a list of the names of the outputs
- `parameter_specs` – Optional list of `omsi.datastructures.analysis_data.parameter_data` with additional information about the parameters of the function.
- `name_key` – The name for the analysis, i.e., the analysis identifier

Returns A new generic analysis class

classmethod `get_analysis_type()`

Return a string indicating the type of analysis performed

get_real_analysis_type()

This class is designed to handle generic (including unkown) types of analysis. In cases, e.g., were this class is used to store analysis data from an HDF5 file we may have an actual analysis type available even if we do not have a special analysis class may not be available in the current installation

```
read_from_omsi_file(analysis_object,          load_data=True,      load_parameters=True,
                     load_runtime_data=True, dependencies_omsi_format=True, ignore_type_conflict=False)
```

See `omsi.analysis.analysis_base.read_from_omsi_file(...)` for details. The function is overwritten here mainly to initialize the `self.real_analysis_type` instance variable but otherwise uses the default behavior.

classmethod v_qmz(analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Implement support for qmz URL requests for the viewer

classmethod v_qslice(analysis_object, z, viewer_option=0)

Implement support for qslice URL requests for the viewer

classmethod v_qslice_viewer_options(analysis_object)

Define which viewer_options are supported for qspectrum URL's

classmethod v_qspectrum(analysis_object, x, y, viewer_option=0)

Implement support for qspectrum URL requests for the viewer

classmethod v_qspectrum_viewer_options(analysis_object)

Define which viewer_options are supported for qspectrum URL's

write_analysis_data(analysis_group=None)

This function is used to write the actual analysis data to file. If not implemented, then the `omsi_file_analysis` API's default behavior is used instead.

Parameters `analysis_group` – The h5py.Group object where the analysis is stored. May be None on cores that do not perform any writing but which need to participate in communication, e.g., to collect data for writing.

class omsi.analysis.omsi_findpeaks_global(name_key='undefined')

Bases: `omsi.analysis.base.analysis_base`

Basic global peak detection analysis. The default implementation computes the peaks on the average spectrum and then computes the peak-cube data, i.e., the values for the detected peaks at each pixel.

TODO: The current version assumes 2D data

Initialize the basic data members

execute_analysis()

Execute the global peak finding for the given msidata and mzdata.

classmethod v_qmz(analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Implement support for qmz URL requests for the viewer

classmethod v_qslice(analysis_object, z, viewer_option=0)

Implement support for qslice URL requests for the viewer

classmethod v_qslice_viewer_options(analysis_object)

Define which viewer_options are supported for qspectrum URL's

classmethod v_qspectrum(analysis_object, x, y, viewer_option=0)

Implement support for qspectrum URL requests for the viewer

classmethod v_qspectrum_viewer_options(analysis_object)

Define which viewer_options are supported for qspectrum URL's

```
class omsi.analysis.omsi_findpeaks_local (name_key='undefined')
Bases: omsi.analysis.base.analysis_base
```

Class defining a basic gloabl peak finding. The default implementation computes the peaks on the average spectrum and then computes the peak-cube data, i.e., the values for the detected peaks at each pixel.

TODO: The current version assumes 2D data

Initialize the basic data members

```
execute_analysis (msidata_subblock=None)
```

Execute the local peak finder for the given msidata.

Parameters **msidata_subblock** – Optional input parameter used for parallel execution of the analysis only. If msidata_subblock is set, then the given subblock will be processed in SERIAL instead of processing self['msidata'] in PARALLEL (if available). This parameter is strictly optional and intended for internal use only.

```
classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)
```

Implement support for qmz URL requests for the viewer

```
classmethod v_qslicce (analysis_object, z, viewer_option=0)
```

Implement support for qslicce URL requests for the viewer

```
classmethod v_qslicce_viewer_options (analysis_object)
```

Define which viewer_options are supported for qspectrum URL's

```
classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)
```

Implement support for qspectrum URL requests for the viewer

```
classmethod v_qspectrum_viewer_options (analysis_object)
```

Define which viewer_options are supported for qspectrum URL's

```
write_analysis_data (analysis_group=None)
```

This function is used to write the actual analysis data to file. If not implemented, then the omsi_file_analysis API's default behavior is used instead.

Parameters **analysis_group** – The h5py.Group object where the analysis is stored.

```
class omsi.analysis.omsi_nmf (name_key='undefined')
Bases: omsi.analysis.base.analysis_base
```

Class defining a basic nmf analysis.

The function has primarily been tested we MSI datasets but should support arbitrary n-D arrays (n>=2). The last dimension of the input array must be the spectrum dimnensions.

Initalize the basic data members

```
execute_analysis()
```

Execute the nmf for the given msidata

```
classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)
```

Implement support for qmz URL requests for the viewer

```
classmethod v_qslicce (analysis_object, z, viewer_option=0)
```

Implement support for qslicce URL requests for the viewer

```
classmethod v_qslicce_viewer_options (analysis_object)
```

Define which viewer_options are supported for qspectrum URL's

```
classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)
```

Implement support for qspectrum URL requests for the viewer

classmethod v_qspectrum_viewer_options (analysis_object)

Define which viewer_options are supported for qspectrum URL's

class omsi.analysis.omsi_cx (name_key='undefined')

Bases: *omsi.analysis.base.analysis_base*

Class used to implement CX factorization on MSI data.

Initialize the basic data members

classmethod comp_lev_exact (A, k, axis)

This function computes the column or row leverage scores of the input matrix.

Parameters

- **A** – n-by-d matrix
- **k** – rank parameter, $k \leq \min(n,d)$
- **axis** – 0: compute row leverage scores; 1: compute column leverage scores.

Returns 1D array of leverage scores. If axis = 0, the length of lev is n. otherwise, the length of lev is d.

dimension_index = {'pixelDim': 1, 'imageDim': 0}

execute_analysis ()

EDIT_ME:

Replace this text with the appropriate documentation for the analysis. Describe what your analysis does and how a user can use it. Note, a user will call the function execute(...) which takes care of storing parameters, collecting execution data etc., so that you only need to implement your analysis, the rest is taken care of by analysis_base. omsi uses Sphynx syntax for the documentation.

Keyword Arguments:

Parameters mydata – ...

classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- **mz_spectra** : Array with the static mz values for the spectra.
- **label_spectra** : Lable for the spectral mz axis
- **mz_slice** : Array of the static mz values for the slices or None if identical to the **mz_spectra**.
- **label_slice** : Lable for the slice mz axis or None if identical to **label_spectra**.

classmethod v_qslice (analysis_object, z, viewer_option=0)

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **z** – Selection string indicating which z values should be selected.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like [::,zmin:zmax].

classmethod v_qslice_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qslice. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qslice requests (i.e., v_qslice(...) is not available).

classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **x** – x selection string
- **y** – y selection string
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns

The following two elements are expected to be returned by this function :

1. 1D, 2D or 3D numpy array of the requested spectra. NOTE: The mass (m/z) axis must be the last axis. For index selection x=1,y=1 a 1D array is usually expected. For indexList selections x=[0]&y=[1] usually a 2D array is expected. For range selections x=0:1&y=1:2 we one usually expects a 3D array.
2. None in case that the spectra axis returned by v_qmz are valid for the returned spectrum. Otherwise, return a 1D numpy array with the m/z values for the spectrum (i.e., if custom m/z values are needed for interpretation of the returned spectrum). This may be needed,

e.g., in cases where a per-spectrum peak analysis is performed and the peaks for each spectrum appear at different m/z values.

classmethod v_qspectrum_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qspectrum. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qspectrum requests (i.e., v_qspectrum(...) is not available).

class omsi.analysis.omsi_kmeans (name_key='undefined')

Bases: *omsi.analysis.base.analysis_base*

Class defining a basic nmf analysis for a 2D MSI data file or slice of the data

Initialize the basic data members

execute_analysis ()

Execute the kmeans clustering for the given msidata

class omsi.analysis.omsi_tic_norm (name_key='undefined')

Bases: *omsi.analysis.base.analysis_base*

TIC Normalization analysis.

Initialize the basic data members

execute_analysis ()

Normalize the data based on the total intensity of a spectrum or the intensities of a select set of ions.

Calculations are performed using a memory map approach to avoid loading all data into memory. TIC normalization can as such be performed even on large files (assuming sufficient disk space).

Keyword Arguments:

Parameters

- **msidata** (*h5py.dataset or numpy array (3D)*) – The input MSI dataset
- **mzdata** – The mz axis do the dataset
- **maxCount** – ...
- **mzTol** – ...
- **infIons** – List of informative ions

record_execute_analysis_outputs (analysis_output)

We are not returning any outputs here, but we are going to record them manually. :param analysis_output:
The output of the execute_analysis(...) function.

classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- mz_spectra : Array with the static mz values for the spectra.
- label_spectra : Lable for the spectral mz axis
- mz_slice : Array of the static mz values for the slices or None if identical to the mz_spectra.
- label_slice : Lable for the slice mz axis or None if identical to label_spectra.

classmethod v_qslicex (analysis_object, z, viewer_option=0)

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **z** – Selection string indicting which z values should be selected.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like [::,zmin:zmax].

classmethod v_qslicex_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qslice. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qslice requests (i.e., v_qslicex(...) is not available).

classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **x** – x selection string
- **y** – y selection string
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns

The following two elements are expected to be returned by this function :

1. 1D, 2D or 3D numpy array of the requested spectra. NOTE: The mass (m/z) axis must be the last axis. For index selection x=1,y=1 a 1D array is usually expected. For indexList selections x=[0]&y=[1] usually a 2D array is expected. For range selections x=0:1&y=1:2 we one usually expects a 3D array/
2. None in case that the spectra axis returned by v_qmz are valid for the returned spectrum. Otherwise, return a 1D numpy array with the m/z values for the spectrum (i.e., if custom m/z values are needed for interpretation of the returned spectrum). This may be needed, e.g., in cases where a per-spectrum peak analysis is performed and the peaks for each spectrum appear at different m/z values.

classmethod v_qspectrum_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qspectrum. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

param analysis_object The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qspectrum requests (i.e., v_qspectrum(...) is not available).

base Module

Module specifying the base analysis API for integrating new analysis with the toolkit and the OpenMSI science gateway.

exception omsi.analysis.base.AnalysisReadyError (value, params=None)

Bases: exceptions.Exception

Custom exception used to indicate that an analysis is not ready to execute.

Initialize the AnalysisReadyError

Parameters

- **value** – Error message string
- **params** – Optional list of dependent parameters that are not ready to be used.

class omsi.analysis.base.analysis_base

Bases: *omsi.datastructures.analysis_data.parameter_manager*

Base class for omsi analysis functionality. The class provides a large set of functionality designed to facilitate storage of analysis data in the omsi HDF5 file format. The class also provides a set of functions to enable easy intergration of new analysis with the OpenMSI web-based viewer (see Viewer functions below for details).

Slicing:

This class supports basic slicing to access data stored in the main member variables. By default the data is retrieved from `__data_list` and the `__getitem__(key)` function, which implements the `[..]` operator, returns `__data_list[key]['data']`. The key is a string indicating the name of the parameter to be retrieved. If the key is not found in the `__data_list` then the function will try to retrieve the data from `self.parameters` list instead. By adding “parameter/key” or “dependency/key” one may also explicitly retrieve values from the parameters.

Instance Variables:

Variables

- **`analysis_identifier`** – Define the name for the analysis used as key in search operations
- **`__data_list`** – List of analysis_data to be written to the HDF5 file. Derived classes need to add all data that should be saved for the analysis in the omsi HDF5 file to this dictionary. See `omsi.analysis.analysis_data` for details.
- **`parameters`** – List of parameter_data objects of all analysis parameters (including those that may have dependencies).
- **`data_names`** – List of strings of all names of analysis output datasets. These are the target keys for `__data_list`.
- **`profile_time_and_usage`** – Boolean indicating whether we should profile the `execute_analysis(...)` function when called as part of the `execute(...)` function. The default value is false. Use the `enable_time_and_usage_profiling(..)` function to determine which profiling should be performed. The `time_and_usage` profile uses pythons cProfile (or Profile) to monitor how often and for how long particular parts of the analysis code executed.
- **`profile_memory`** – Boolean indicating whether we should monitor memory usage (line-by-line) when executing the `execute_analysis(...)` function. The default value is false. Use the `enable_time_and_usage_profiling(..)` function to determine which profiling should be performed.
- **`omsi_analysis_storage`** – List of `omsi_file_analysis` object where the analysis is stored. The list may be empty.
- **`mpi_comm`** – In case we are running with MPI, this is the MPI communicator used for runnign the analysis. Default is `MPI.Comm_world`/
- **`mpi_root`** – In case we are running with MPI, this is the root rank where data is collected to (e.g., runtime data and analysis results)
- **`update_analysis`** – If the value is True, then we should execute the analysis before using the outputs. If False, then the analysis has been executed with the current parameter settings.
- **`driver`** – Workflow driver to be used when executing multiple analyses, e.g., via `execute_recursive` or `execute_all`. Default value is `None` in which case a new default driver will be used each time we execute a workflow.

Execution Functions:

- `execute` : Then main function the user needs to call in order to execute the analysis
- “`execute_analysis`: This function needs to be implemented by child classes of `analysis_base` to implement the specifics of executing the analysis.

I/O functions:

These functions can be optionally overwritten to control how the analysis data should be written/read from the omsi HDF5 file. Default implementations are provided here, which should be sufficient for most cases.

- `add_custom_data_to_omsi_file`: The default implementation is empty as the default data write is managed by the `omsi_file_experiment.create_analysis()` function. Overwrite this function, in case that the analysis needs to write data to the HDF5 omsi file beyond what the defualt omsi data API does.
- `read_from_omsi_file`: The default implementation tries to reconstruct the original data as far as possible, however, in particular in case that a custom `add_custom_data_to_omsi_file` function has been implemented, the default implementation may not be sufficien. The default implementation reconstructs: i) `analysis_identifier` and reads all custom data into ii)`_data_list`. Note, an error will be raised in case that the analysis type specified in the HDF5 file does not match the analysis type specified by `get_analysis_type()`. This function can be optionally overwritten to implement a custom data read.

Viewer functions:

Several convenient functions are used to allow the OpenMSI online viewer to interact with the analysis and to visualize it. The default implementations provided here simply indicate that the analysis does not support the data access operations required by the online viewer. Overwrite these functions in the derived analysis classes in order to interface them with the viewer. All viewer-related functions start with `v_____`.

NOTE: the default implementation of the viewer functions defined in `analysis_base` are designed to take care of the common requirement for providing viewer access to data from all dependencies of an analysis. In many cases, the default implementation is often sill called at the end of custom viewer functions.

NOTE: The viewer functions typically support a `viewer_option` parameter. `viewer_option=0` is expected to refer to the analysis itself.

- `v_qslice`: Retrieve/compute data slices as requested via qslice URL requests. The corresponding view of the DJANGO data access server already translates all input parameters and takes care of generating images/plots if needed. This function is only responsible for retrieving the data.
- `v_qspectrum`: Retrieve/compute spectra as requested via qspectrum URL requests. The corresponding view of the DJANGO data access server already translates all input parameters and takes care of generating images/plots if needed. This function is only responsible for retrieving the data.
- `v_qmz`: Define the m/z axes for image slices and spectra as requested by qspectrum URL requests.
- `v_qspectrum_viewer_options`: Define a list of strings, describing the different viewer options available for the analysis for qspectrum requests (i.e., `v_qspectrum`). This feature allows the analysis developer to define multiple different visualization modes for the analysis. For example, when performing a data reduction (e.g., PCA or NMF) one may want to show the raw spectra or the loadings vector of the projection in the spectrum view (`v_qspectrum`). By providing different viewer options we allow the user to decide which option they are most interested in.
- `v_qslic_viewer_options`: Define a list of strings, describing the different viewer options available for the analysis for qslice requests (i.e., `v_qslic`). This feature allows the analysis developer to define multiple different visualization modes for the analysis. For example, when performing a data reduction (e.g., PCA or NMF) one may want to show the raw spectra or the loadings vector of the projection in the spectrum view (`v_qspectrum`). By providing different viewer options we allow the user to decide which option they are most interested in.

Initialize the basic data members

`add_custom_data_to_omsi_file(analysis_group)`

This function can be optionally overwritten to implement a custom data write function for the analysis to be used by the `omsi_file` API.

Note, this function should be used only to add additional data to the analysis group. The data that is written by default is still written by the `omsi_file_experiment.create_analysis()` function, i.e., the following data is written by default: i) analysis_identifier ,ii) get_analysis_type, iii) __data_list, iv) parameters, v) runinfo . Since the `omsi_file_experiment.create_analysis()` functions takes care of setting up the basic structure of the analysis storage (included the subgroups for storing parameters and data dependencies) this setup can generally be assumed to exist before this function is called. This function is called automatically at the end `omsi_file_experiment.create_analysis()` (i.e., actually `omsi_file_analysis.__populate_analysis__(..)`) so that this function typically does not need to be called explicitly.

Parameters `analysis_group` – The h5py.Group object where the analysis is stored.

add_parameter (`name, help, dtype=<type 'unicode'>, required=False, default=None, choices=None, data=None, group=None`)

Add a new parameter for the analysis. This function is typically used in the constructor of a derived analysis to specify the parameters of the analysis.

Parameters

- `name` – The name of the parameter
- `help` – Help string describing the parameter
- `type` – Optional type. Default is string.
- `required` – Boolean indicating whether the parameter is required (True) or optional (False). Default False.
- `default` – Optional default value for the parameter. Default None.
- `choices` – Optional list of choices with allowed data values. Default None, indicating no choices set.
- `data` – The data assigned to the parameter. None by default.
- `group` – Optional group string used to organize parameters. Default None, indicating that parameters are automatically organized by driver class (e.g. in required and optional parameters)

Raises ValueError is raised if the parameter with the given name already exists.

analysis_identifier_defined()

Check whether the analysis identifier is defined by the user, i.e., set to value different than undefined
:return: bool

check_ready_to_execute()

Check if all inputs are ready to determine if the analysis is ready to run.

Returns List of omsi_analysis_parameter objects that are not ready. If the returned list is empty, then the analysis is ready to run.

clear_analysis()

Clear all analysis data—i.e., parameter, dependency data, output results, runtime data

clear_analysis_data()

Clear the list of analysis data

clear_and_restore (`analysis_manager=None, resave=False`)

Clear all analysis data and restore the results from file

Parameters

- `analysis_manager` – Instance of omsi_analysis_manager (e.g., an omsi_file_experiment) where the analysis should be saved.

- **resave** – Boolean indicating whether the analysis should be saved again, even if it has been saved before. This parameter only has effect if analysis_manager is given.

Returns self, i.e., the updated analysis object with all data replaced with HDF5 references

clear_parameter_data()
Clear the list of parameter data

clear_run_info_data()
Clear the runtime information data

define_missing_parameters()
Called by the execute function before self.update_analysis_parameters to set any required parameters that have not been defined to their respective default values.

This function may be overwritten in child classes to customize the definition of default parameter values and to apply any modifications (or checks) of parameters before the analysis is executed. Any changes applied here will be recorded in the parameter of the analysis.

enable_memory_profiling(enable=True)
Enable or disable line-by-line profiling of memory usage of execute_analysis.

Parameters **enable_memory** (bool) – Enable (True) or disable (False) line-by-line profiling of memory usage

Raises ImportError is raised if a required package for profiling is not available.

enable_time_and_usage_profiling(enable=True)
Enable or disable profiling of time and usage of code parts of execute_analysis.

Parameters **enable** (bool) – Enable (True) or disable (False) profiling

Raises ImportError is raised if a required package for profiling is not available.

execute(kwargs)**
Use this function to run the analysis.

Parameters **kwargs** – Parameters to be used for the analysis. Parameters may also be set using the __setitem__ mechanism or as batches using the set_parameter_values function.

Returns This function returns the output of the execute analysis function.

Raises AnalysisReadyError in case that the analysis is not ready to be executed. This may be the case, e.g, when a dependent input parameter is not ready to be used.

classmethod execute_all(force_update=False, executor=None)
Execute all analysis instances that are currently defined.

Parameters

- **force_update** – Boolean indicating whether we should force that all analyses are executed again, even if they have already been run with the same settings before. False by default.
- **executor** – Optional workflow executor to be used for the execution of all analyses. The executor will be cleared and then all analyses will be added to executor. Default value is None, in which case the function creates a default executor to be used.

Returns The workflow executor used

execute_analysis()
Implement this function to implement the execution of the actual analysis.

This function may not require any input parameters. All input parameters are recorded in the parameters and dependencies lists and should be retrieved from there, e.g, using basic slicing self[paramName]

Input parameters may be added for internal use ONLY. E.g, we may add parameters that are used internally to help with parallelization of the execute_analysis function. Such parameters are not recorded and must be strictly optional so that analysis_base.execute(...) can call the function.

Returns This function may return any developer-defined data. Note, all output that should be recorded must be put into the data list.

execute_recursive(kwargs)**

Recursively execute this analysis and all its dependencies if necessary

We use a workflow driver to control the execution. To define the workflow driver we can set the self.driver variable. If no workflow driver is given (i.e, self.driver==None), then the default driver will be created. To change the default driver, see *omsi.workflow.base.workflow_executor_base.DEFAULT_EXECUTOR_CLASS*

Parameters kwargs – Parameters to be used for the analysis. Parameters may also be set using the __setitem__ mechanism or as batches using the set_parameter_values function.

Returns Same as execute

get_all_analysis_data()

Get the complete list of all analysis datasets to be written to the HDF5 file

get_all_dependency_data()

Get the complete list of all direct dependencies to be written to the HDF5 file

NOTE: These are only the direct dependencies as specified by the analysis itself. Use get_all_dependency_data_recursive(..) to also get the indirect dependencies of the analysis due to dependencies of the dependencies themselves.

Returns List of parameter_data objects that define dependencies.

get_all_parameter_data(exclude_dependencies=False)

Get the complete list of all parameter datasets to be written to the HDF5 file

Parameters exclude_dependencies – Boolean indicating whether we should exclude parameters that define dependencies from the list

get_all_run_info()

Get the dict with the complete info about the last run of the analysis

get_analysis_data(index)

Given the index return the associated dataset to be written to the HDF5 file

:param index : Retrun the index entry of the private member __data_list.

get_analysis_data_by_name(dataname)

Given the key name of the data return the associated analysis_data object.

Parameters dataname – Name of the analysis data requested from the private __data_list member.

Returns The analysis_data object or None if not found.

get_analysis_data_names()

Get a list of all analysis dataset names.

get_analysis_identifier()

Return the name of the analysis used as key when searching for a particular analysis

classmethod get_analysis_instances()

Generator function used to iterate through all instances of analysis_base. The function creates references for all weak references stored in cls._analysis_instances and returns the references if it exists and cleans up the any invalid references after the iteration is complete. :return: References to analysis_base objects

get_analysis_type()

Return a string indicating the type of analysis performed

static get_default_dtypes()

Get a list of available default dtypes used for analyses. Same as *data_dtotypes.get_dtotypes()*.

static get_default_parameter_groups()

Get a list of commonly used parameter groups and associated descriptions.

Use of default groups provides consistency and allows other system to design custom behavior around the semantic of parameter groups

Returns Dictionary where the keys are the short names of the groups and the values are dicts with following keys:value pairs: ‘name’ , ‘description’. Use the ‘name’ to define the group to be used.

get_help_string()

Get a string describing the analysis.

Returns Help string describing the analysis and its parameters

get_memory_profile_info()

Based on the memory profile of the execute_analysis(..) function get the string describing the line-by-line memory usage.

Returns String describing the memory usage profile. None is returned in case that no memory profiling data is available.

get_num_analysis_data()

Retrun the number of analysis datasets to be wirten to the HDF5 file

get_num_dependency_data()

Return the number of dependencies to be wirten to the HDF5 file

get_num_parameter_data()

Return the number of parameter datasets to be wirten to the HDF5 file

get_omsi_analysis_storage()

Get a list of known locations where this analysis has been saved.

Returns List of *omsi.dataformat.omsi_file.analysis. omsi_file_analysis* objects where the analysis is saved.

get_parameter_data(index)

Given the index return the associated dataset to be written to the HDF5 file

:param index : Return the index entry of the private member parameters.

get_parameter_data_by_name(dataname)

Given the key name of the data return the associated parameter_data object.

Parameters **dataname** – Name of the parameter requested from the parameters member.

Returns The parameter_data object or None if not found

get_parameter_names()

Get a list of all parameter dataset names (including those that may define dependencies).

get_profile_stats_object(consolidate=True, stream=None)

Based on the execution profile of the execute_analysis(..) function get pstats.Stats object to help with the interpretation of the data.

Parameters

- **consolidate** – Boolean flag indicating whether multiple stats (e.g., from multiple cores) should be consolidated into a single stats object. Default is True.
- **stream** – The optional stream parameter to be used for the pstats.Stats object.

Returns A single pstats.Stats object if consolidate is True. Otherwise the function returns a list of pstats.Stats objects, one per recorded statistic. None is returned in case that the stats objects cannot be created or no profiling data is available.

`has_omsi_analysis_storage()`

Check whether a storage location is known where the analysis has been saved.

Returns Boolean indicating whether self.omsi_analysis_storage is not empty

`keys()`

Get a list of all valid keys, i.e., a combination of all input parameter and output names.

Returns List of strings with all input parameter and output names.

`classmethod locate_analysis(data_object, include_parameters=False)`

Given a data_object try to locate the analysis that creates the object as an output of its execution (and optionally analyses that have the object as an input).

Parameters

- **data_object** – The data object of interest.
- **include_parameters** – Boolean indicating whether also input parameters should be considered in the search in addition to the outputs of an analysis

Returns dependency_dict pointing to the relevant object or None in case the object was not found.

`read_from_omsi_file(analysis_object, load_data=True, load_parameters=True, load_runtime_data=True, dependencies_omsi_format=True, ignore_type_conflict=False)`

This function can be optionally overwritten to implement a custom data read.

The default implementation tries to reconstruct the original data as far as possible, however, in particular in case that a custom add_custom_data_to_omsi_file function has been implemented, the default implementation may not be sufficient. The default implementation reconstructs: i) analysis_identifier and reads all custom data into iii)_data_list. Note, an error will be raised in case that the analysis type specified in the HDF5 file does not match the analysis type specified by get_analysis_type()

Parameters

- **analysis_object** – The omsi_file_analysis object associated with the hdf5 data group with the analysis data_list
- **load_data** – Should the analysis data be loaded from file (default) or just stored as h5py data objects
- **load_parameters** – Should parameters be loaded from file (default) or just stored as h5py data objects.
- **load_runtime_data** – Should runtime data be loaded from file (default) or just stored as h5py data objects
- **dependencies_omsi_format** – Should dependencies be loaded as omsi_file API objects (default) or just as h5py objects.
- **ignore_type_conflict** – Set to True to allow the analysis to be loaded into the current analysis object even if the type indicated in the file does not match the class. Default value is False. This behavior can be useful when different analysis have compatible

data structures or when we want to load the data in to a generic analysis container, e.g., analysis_generic.

Returns bool Boolean indicating whether the data was read successfully

Raise TypeError : A type error will be raised in case that the analysis type specified by the file does not match the analysis type provided by self.get_analysis_type()

record_execute_analysis_outputs (analysis_output)

Function used internally by execute to record the output of the custom execute_analysis(...) function to the __data_list.

This function may be overwritten in child classes in order to customize the behavior for recording data outputs. Eg., for some analyses one may only want to record a particular set of outputs, rather than all outputs generated by the analysis.

Parameters analysis_output – The output of the execute_analysis(...) function to be recorded

results_ready ()

Check whether the results of the analysis are ready to be used :return: Boolean

set_analysis_identifier (identifier)

Set the name of the analysis to identifier

Side Effects: This function modifies self.analysis_identifier

Parameters identifier (str) – The new analysis identifier string to be used (should be unique)

set_parameter_values (kwargs)**

Set all parameters given as input to the function. The inputs are placed in the self.parameters list. If the parameter refers to an existing h5py.Dataset, h5py.Group, managed h5py object, or is an instance of an existing omsi_analysis_base object, then a dependency_dict will be created and stored as value instead.

Parameters kwargs – Dictionary of keyword arguments. All keys are expected to be strings.

All values are expected to be either i) numpy arrays, ii) int, float, str or unicode variables, iii) h5py.Dataset or h5py.Group, iv) or any the omsi_file API class objects. For iii) and iv) one may provide a tuple consisting of the dataobject t[0] and an additional selection string t[1].

update_analysis_parameters (kwargs)**

Record the analysis parameters passed to the execute() function.

The default implementation simply calls the set_parameter_values(...) function. This function may be overwritten to customize the behavior of how parameters are recorded by the execute function.

Parameters kwargs – Dictionary of keyword arguments with the parameters passed to the execute(..) function

classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- mzSpectra : Array with the static mz values for the spectra.
- labelSpectra : Label for the spectral mz axis
- mzSlice : Array of the static mz values for the slices or None if identical to the mzSpectra.
- labelSlice : Label for the slice mz axis or None if identical to labelSpectra.
- values_x: The values for the x axis of the image (or None)
- label_x: Label for the x axis of the image
- values_y: The values for the y axis of the image (or None)
- label_y: Label for the y axis of the image
- values_z: The values for the z axis of the image (or None)
- label_z: Label for the z axis of the image

classmethod v_qslice (analysis_object, z, viewer_option=0)

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **z** – Selection string indicating which z values should be selected.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like [::,zmin:zmax].

Raises NotImplementedError in case that v_qslice is not supported by the analysis.

classmethod v_qslice_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qslice. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qslice requests (i.e., v_qslice(...) is not available).

classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **x** – x selection string
- **y** – y selection string
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns

The following two elements are expected to be returned by this function :

1. 1D, 2D or 3D numpy array of the requested spectra. NOTE: The mass (m/z) axis must be the last axis. For index selection x=1,y=1 a 1D array is usually expected. For indexList selections x=[0]&y=[1] usually a 2D array is expected. For range selections x=0:1&y=1:2 we one usually expects a 3D array.
2. None in case that the spectra axis returned by v_qmz are valid for the returned spectrum. Otherwise, return a 1D numpy array with the m/z values for the spectrum (i.e., if custom m/z values are needed for interpretation of the returned spectrum). This may be needed, e.g., in cases where a per-spectrum peak analysis is performed and the peaks for each spectrum appear at different m/z values.

classmethod v_qspectrum_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qspectrum. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qspectrum requests (i.e., v_qspectrum(...) is not available).

write_analysis_data (analysis_group=None)

This function is used to write the actual analysis data to file. If not implemented, then the omsi_file_analysis API's default behavior is used instead.

Parameters **analysis_group** – The h5py.Group object where the analysis is stored. May be None on cores that do not perform any writing but which need to participate in communication, e.g., to collect data for writing.

generic Module

Generic analysis class used to represent analyses of unknown type, e.g., when loading a custom user-defined analysis from file for which the indicate class may not be available with the local installation. In this case we want to at least be able to load and investigate the data.

class omsi.analysis.generic.**analysis_generic** (*name_key='undefined'*)
Bases: *omsi.analysis.base.analysis_base*

This analysis class is used if the specific analysis type is unknown, e.g., when loading custom user-defined analysis data that may have not be available in the standard omsi package used.

Initialize the basic data members

Parameters `name_key` – The name for the analysis
`DEFAULT_OUTPUT_PREFIX = 'output_'`
execute (`**kwargs`)
Overwrite the default implementation of execute to update parameter specifications/types when wrapping functions where the types are not known a priori.
Parameters `kwargs` – Custom analysis parameters
Returns The result of execute_analysis()

execute_analysis ()
Nothing to do here.
classmethod from_function (`analysis_function, output_names=None, parameter_specs=None, name_key='undefined'`)
Create a generic analysis class for a given analysis function.

This functionality is useful to ease quick scripting on analyses but should not be used in production.

NOTE: `__analysis_function` is a reserved parameter name used to store the analysis function and may not be used as an input parameter for the analysis function.

Parameters

- **analysis_function** – The analysis function to be wrapped for provenance tracking and storage
- **output_names** – Optionally, define a list of the names of the outputs
- **parameter_specs** – Optional list of `omsi.datastructures.analysis_data.parameter_data` with additional information about the parameters of the function.
- **name_key** – The name for the analysis, i.e., the analysis identifier

Returns A new generic analysis class

classmethod get_analysis_type ()
Return a string indicating the type of analysis performed

get_real_analysis_type ()
This class is designed to handle generic (including unkown) types of analysis. In cases, e.g., were this class is used to store analysis data from an HDF5 file we may have an actual analysis type available even if we do not have a special analysis class may not be available in the current installation

read_from_omsi_file (`analysis_object, load_data=True, load_parameters=True, load_runtime_data=True, dependencies_omsi_format=True, ignore_type_conflict=False`)
See `omsi.analysis.analysis_base.read_from_omsi_file(...)` for details. The function is overwritten here mainly to initialize the `self.real_analysis_type` instance variable but otherwise uses the default behavior.

classmethod v_qmz (`analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0`)
Implement support for qmz URL requests for the viewer

classmethod v_qslice (`analysis_object, z, viewer_option=0`)
Implement support for qslice URL requests for the viewer

classmethod v_qslice_viewer_options (`analysis_object`)
Define which viewer_options are supported for qspectrum URL's

classmethod v_qspectrum (`analysis_object, x, y, viewer_option=0`)
Implement support for qspectrum URL requests for the viewer

classmethod v_qspectrum_viewer_options (analysis_object)

Define which viewer_options are supported for qspectrum URL's

write_analysis_data (analysis_group=None)

This function is used to write the actual analysis data to file. If not implemented, then the omsi_file_analysis API's default behavior is used instead.

Parameters analysis_group – The h5py.Group object where the analysis is stored. May be None on cores that do not perform any writing but which need to participate in communication, e.g., to collect data for writing.

omsi.analysis.generic.**bastet_analysis** (*output_names=None*, *parameter_specs=None*,
name_key='undefined')

Decorator used to wrap a function and replace it with an analysis_generic object that behaves like a function but adds the ability for saving the analysis to file and tracking provenance

This is essentially the same as analysis_generic.from_function(....).

Parameters

- **func** – The function to be wrapped
- **output_names** – Optional list of strings with the names of the outputs
- **parameter_specs** – Optional list of omsi.datastructures.analysis_data.parameter_data with additional information about the parameters of the function.
- **name_key** – Optional name for the analysis, i.e., the analysis identifier

Returns analysis_generic instance for the wrapped function

analysis_views Module

Helper module with functions and classes for interfacing with different analysis algorithms. Many of these functions are used to ease interaction with the analysis module in a generic fashion, without having to explicitly know about all the different available modules, e.g., we can just look up modules by name and interact with them directly.

class omsi.analysis.analysis_views.analysis_views

Bases: object

Helper class for interfacing different analysis algorithms with the web-based viewer

Nothing to do here.

classmethod analysis_name_to_class (class_name)

Convert the given string indicating the class to a python class.

Parameters class_name – Name of the analysis class. This may be a fully qualified name, e.g., *omsi.analysis.multivariate_stat.omsi_nmf* or a name relative to the omsi.analysis module, e.g., *multivariate_stat.omsi_nmf*.

Raises Attribute error in case that the class cannot be restored.

classmethod available_analysis ()

Get all available analysis, i.e., all analysis that are subclasses of analysis_base.

Returns Dictionary where the dict-keys are the full qualified name of the module and the values are the analysis class corresponding to that module.

classmethod available_analysis_descriptions ()

Get all available analysis, i.e., all analysis that are subclasses of analysis_base. For each analysis compile the list of input parameters, outputs, the corresponding class etc.

Returns Dictionary where the dict-keys are the full qualified name of the module and the values are dicts with class, list of analysis paremeter names, list of analysis outputs.

classmethod `get_axes` (*analysis_object*, *qslice_viewer_option=0*, *qspectrum_viewer_option=0*)

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- *mz_spectra* : Array with the static mz values for the spectra.
- *label_spectra* : Lable for the spectral mz axis
- *mz_slice* : Array of the static mz values for the slices or None if identical to the *mz_spectra*.
- *label_slice* : Lable for the slice mz axis or None if identical to *label_spectra*.
- *values_x*: The values for the x axis of the image (or None)
- *label_x*: Label for the x axis of the image
- *values_y*: The values for the y axis of the image (or None)
- *label_y*: Label for the y axis of the image
- *values_z*: The values for the z axis of the image (or None)
- *label_z*: Label for the z axis of the image

classmethod `get_qslice_viewer_options` (*analysis_object*)

Get a list of strings describing the different default viewer options for qslice.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed.

Returns Array of strings indicating the different available viewer options. The array may be empty if now viewer_options are available, i.e., `get_slice` and `get_spectrum` are undefined for the given analysis.

classmethod `get_qspectrum_viewer_options` (*analysis_object*)

Get a list of strings describing the different default viewer options for qspectrum.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed.

Returns Array of strings indicating the different available viewer options. The array may be empty if now viewer_options are available, i.e., `get_slice` and `get_spectrum` are undefined for the given analysis.

classmethod `get_slice` (*analysis_object*, *z*, *operations=None*, *viewer_option=0*)

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **z** – Selection string indicating which z values should be selected.
- **operations** – JSON string with list of dictionaries or a python list of dictionaries. Each dict specifies a single data transformation or data reduction that are applied in order. See omsi.shared.omsi_data_selection.transform_and_reduce_data(...) for details.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like [::,zmin:zmax].

classmethod `get_spectra(analysis_object, x, y, operations=None, viewer_option=0)`

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **x** – x selection string
- **y** – y selection string
- **operations** – JSON string with list of dictionaries or a python list of dictionaries. Each dict specifies a single data transformation or data reduction that are applied in order. See omsi.shared.omsi_data_selection.transform_and_reduce_data(...) for details.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns 2D or 3D numpy array of the requested spectra. The mass (m/z) axis must be the last axis.

classmethod `supports_slice(analysis_object)`

Get whether a default slice selection behavior is defined for the analysis.

Parameters `analysis_object` – The omsi_file_analysis object for which slicing should be performed

Returns Boolean indicating whether get_slice(...) is defined for the analysis object.

classmethod `supports_spectra(analysis_object)`

Get whether a default spectra selection behavior is defined for the analysis.

Parameters `analysis_object` – The omsi_file_analysis object for which slicing should be performed.

Returns Boolean indicating whether get_spectra(...) is defined for the analysis object.

Subpackages

findpeaks Package

findpeaks Package Package of peak-finding related analysis modules.

class omsi.analysis.findpeaks.**omsi_findpeaks_global** (*name_key*=’undefined’)
Bases: *omsi.analysis.base.analysis_base*

Basic global peak detection analysis. The default implementation computes the peaks on the average spectrum and then computes the peak-cube data, i.e., the values for the detected peaks at each pixel.

TODO: The current version assumes 2D data

Initialize the basic data members

execute_analysis()

Execute the global peak finding for the given msidata and mzdata.

classmethod v_qmz (*analysis_object*, *qslice_viewer_option*=0, *qspectrum_viewer_option*=0)
Implement support for qmz URL requests for the viewer

classmethod v_qslice (*analysis_object*, *z*, *viewer_option*=0)
Implement support for qslice URL requests for the viewer

classmethod v_qslicevieweroptions (*analysis_object*)
Define which viewer_options are supported for qspectrum URL’s

classmethod v_qspectrum (*analysis_object*, *x*, *y*, *viewer_option*=0)
Implement support for qspectrum URL requests for the viewer

classmethod v_qspectrumevieweroptions (*analysis_object*)
Define which viewer_options are supported for qspectrum URL’s

class omsi.analysis.findpeaks.**omsi_findpeaks_local** (*name_key*=’undefined’)
Bases: *omsi.analysis.base.analysis_base*

Class defining a basic gloabl peak finding. The default implementation computes the peaks on the average spectrum and then computes the peak-cube data, i.e., the values for the detected peaks at each pixel.

TODO: The current version assumes 2D data

Initialize the basic data members

execute_analysis (*msidata_subblock*=None)
Execute the local peak finder for the given msidata.

Parameters msidata_subblock – Optional input parameter used for parallel execution of the analysis only. If msidata_subblock is set, then the given subblock will be processed in SERIAL instead of processing self[‘msidata’] in PARALLEL (if available). This parameter is strictly optional and intended for internal use only.

classmethod v_qmz (*analysis_object*, *qslice_viewer_option*=0, *qspectrum_viewer_option*=0)
Implement support for qmz URL requests for the viewer

classmethod v_qslice (*analysis_object*, *z*, *viewer_option*=0)
Implement support for qslice URL requests for the viewer

classmethod v_qslicevieweroptions (*analysis_object*)
Define which viewer_options are supported for qspectrum URL’s

classmethod v_qspectrum (*analysis_object*, *x*, *y*, *viewer_option*=0)
Implement support for qspectrum URL requests for the viewer

classmethod v_qspectrumevieweroptions (*analysis_object*)
Define which viewer_options are supported for qspectrum URL’s

write_analysis_data(analysis_group=None)

This function is used to write the actual analysis data to file. If not implemented, then the omsi_file_analysis API's default behavior is used instead.

Parameters **analysis_group** – The h5py.Group object where the analysis is stored.

omsi_findpeaks_global Module Global peak finder computing peaks and associated ion-images for the full MSI data.

class omsi.analysis.findpeaks.omsi_findpeaks_global.**omsi_findpeaks_global**(name_key='undefined')
Bases: *omsi.analysis.base.analysis_base*

Basic global peak detection analysis. The default implementation computes the peaks on the average spectrum and then computes the peak-cube data, i.e., the values for the detected peaks at each pixel.

TODO: The current version assumes 2D data

Initialize the basic data members

execute_analysis()

Execute the global peak finding for the given msidata and mzdata.

classmethod **v_qmz**(analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Implement support for qmz URL requests for the viewer

classmethod **v_qslice**(analysis_object, z, viewer_option=0)

Implement support for qslice URL requests for the viewer

classmethod **v_qslice_viewer_options**(analysis_object)

Define which viewer_options are supported for qspectrum URL's

classmethod **v_qspectrum**(analysis_object, x, y, viewer_option=0)

Implement support for qspectrum URL requests for the viewer

classmethod **v_qspectrum_viewer_options**(analysis_object)

Define which viewer_options are supported for qspectrum URL's

omsi_findpeaks_local Module Local peak finding analysis module.

class omsi.analysis.findpeaks.omsi_findpeaks_local.**omsi_findpeaks_local**(name_key='undefined')
Bases: *omsi.analysis.base.analysis_base*

Class defining a basic gloabl peak finding. The default implementation computes the peaks on the average spectrum and then computes the peak-cube data, i.e., the values for the detected peaks at each pixel.

TODO: The current version assumes 2D data

Initialize the basic data members

execute_analysis(msidata_subblock=None)

Execute the local peak finder for the given msidata.

Parameters **msidata_subblock** – Optional input parameter used for parallel execution of the analysis only. If msidata_subblock is set, then the given subblock will be processed in SERIAL instead of processing self['msidata'] in PARALLEL (if available). This parameter is strictly optional and intended for internal use only.

classmethod **v_qmz**(analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Implement support for qmz URL requests for the viewer

classmethod **v_qslice**(analysis_object, z, viewer_option=0)

Implement support for qslice URL requests for the viewer

```
classmethod v_qslice_viewer_options (analysis_object)
    Define which viewer_options are supported for qspectrum URL's

classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)
    Implement support for qspectrum URL requests for the viewer

classmethod v_qspectrum_viewer_options (analysis_object)
    Define which viewer_options are supported for qspectrum URL's

write_analysis_data (analysis_group=None)
    This function is used to write the actual analysis data to file. If not implemented, then the
    omsi_file_analysis API's default behavior is used instead.

    Parameters analysis_group – The h5py.Group object where the analysis is stored.
```

findpeaks.third_party Package

findpeaks.third_party Package Package containing shared third-party code modules included here to reduce the need for external dependencies when only small parts of external code are used.

findpeaks Module

```
class omsi.analysis.findpeaks.third_party.findpeaks(x, y, sizes-
                                                    mooth, slwindow,
                                                    peakheight)
```

Name = ‘findpeaks’

display()

peakdet()

Converted from MATLAB script at <http://billauer.co.il/peakdet.html>

Currently returns two lists of tuples, but maybe arrays would be better

```
function [maxtab, mintab]=peakdet(v, delta, x) %PEAKDET Detect peaks in a vector % [MAXTAB,
MINTAB] = PEAKDET(V, DELTA) finds the local % maxima and minima ("peaks") in the vector V.
% MAXTAB and MINTAB consists of two columns. Column 1 % contains indices in V, and column 2 the
found values. % % With [MAXTAB, MINTAB] = PEAKDET(V, DELTA, X) the indices % in MAXTAB
and MINTAB are replaced with the corresponding % X-values. % % A point is considered a maximum
peak if it has the maximal % value, and was preceded (to the left) by a value lower by % DELTA.
```

% Eli Billauer, 3.4.05 (Explicitly not copyrighted). % This function is released to the public domain; Any
use is allowed.

sliding_window_minimum()

A iterator which takes the size of the window, k , and an iterable, li . Then returns an iterator such that the
ith element yielded is equal to $\min(list(li)[\max(i - k + 1, 0):i+1])$.

Each yield takes amortized $O(1)$ time, and overall the generator takes $O(k)$ space.

smoothListGaussian()

findpeaks.experimental Package

findpeaks.experimental Package Module with experimental analysis code, i.e., code that is not (yet) used
in production but is under development. Often this is code that is used in a specific research.

omsi_peakcube Module

```
omsi.analysis.findpeaks.experimental.omsi_peakcube.main(argv=None)
class omsi.analysis.findpeaks.experimental.omsi_peakcube.omsi_peakcube(name_key='undefined')
    Bases: omsi.analysis.base.analysis_base
        Initialize the basic data members

    execute_analysis()

    getGlobalMz(peaksBins, peaksMZdata, HCpeaksLabels, HCLabelsList)
    getPeakCube(peaksIntensities, peaksArrayIndex, HCpeaksLabels, HCLabelsList)
    record_execute_analysis_outputs(analysis_output)
        We are recording our outputs manually as part of the execute function

    classmethod v_qmz(analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)
        Implement support for qmz URL requests for the viewer

    classmethod v_qslice(analysis_object, z, viewer_option=0)
        Implement support for qslice URL requests for the viewer

    classmethod v_qslice_viewer_options(analysis_object)
        Define which viewer_options are supported for qspectrum URL's

    classmethod v_qspectrum(analysis_object, x, y, viewer_option=0)
        Implement support for qspectrum URL requests for the viewer

    classmethod v_qspectrum_viewer_options(analysis_object)
        Define which viewer_options are supported for qspectrum URL's
```

```
omsi.analysis.findpeaks.experimental.omsi_peakcube.stop()
```

pfrun Module

```
omsi.analysis.findpeaks.experimental.pfrun.generateScript(scriptfile, PF-
                                                       content=None,
                                                       repo=None)
omsi.analysis.findpeaks.experimental.pfrun.main(argv)
omsi.analysis.findpeaks.experimental.pfrun.printHelp(thisfilename)
omsi.analysis.findpeaks.experimental.pfrun.queuePCjob(pcstring, therepo=None)
omsi.analysis.findpeaks.experimental.pfrun.run_lpf(omsInFile, expIndex, dataIndex,
                                                 ph, slw, smw)
omsi.analysis.findpeaks.experimental.pfrun.run_npg(omsInFile, expIndex, dataIndex,
                                                 LPFIndex, mzth, tcut)
omsi.analysis.findpeaks.experimental.pfrun.run_peakcube(omsInFile, expIndex,
                                                 dataIndex, LPFIndex,
                                                 NPGIndex)
omsi.analysis.findpeaks.experimental.pfrun.stop()
```

omsi_lpf Module

```
omsi.analysis.findpeaks.experimental.omsi_lpf.cl_peakfind(self, msidt, smoothsize,
                                                               slwindow, peakheight)
omsi.analysis.findpeaks.experimental.omsi_lpf.execute_analysis(self)
omsi.analysis.findpeaks.experimental.omsi_lpf.main(argv=None)
    Then main function
```

```
class omsi.analysis.findpeaks.experimental.omsi_lpf.omsi_lpf(name_key='undefined')
Bases: omsi.analysis.base.analysis_base
```

```
omsi.analysis.findpeaks.experimental.omsi_lpf.v_qmz
classmethod(function) -> method
```

Convert a function to be a class method.

A class method receives the class as implicit first argument, just like an instance method receives the instance. To declare a class method, use this idiom:

```
class C: def f(cls, arg1, arg2, ...): ... f = classmethod(f)
```

It can be called either on the class (e.g. C.f()) or on an instance (e.g. C().f()). The instance is ignored except for its class. If a class method is called for a derived class, the derived class object is passed as the implied first argument.

Class methods are different than C++ or Java static methods. If you want those, see the staticmethod builtin.

```
omsi.analysis.findpeaks.experimental.omsi_lpf.v_qslice
classmethod(function) -> method
```

Convert a function to be a class method.

A class method receives the class as implicit first argument, just like an instance method receives the instance. To declare a class method, use this idiom:

```
class C: def f(cls, arg1, arg2, ...): ... f = classmethod(f)
```

It can be called either on the class (e.g. C.f()) or on an instance (e.g. C().f()). The instance is ignored except for its class. If a class method is called for a derived class, the derived class object is passed as the implied first argument.

Class methods are different than C++ or Java static methods. If you want those, see the staticmethod builtin.

```
omsi.analysis.findpeaks.experimental.omsi_lpf.v_qslice_viewer_options
classmethod(function) -> method
```

Convert a function to be a class method.

A class method receives the class as implicit first argument, just like an instance method receives the instance. To declare a class method, use this idiom:

```
class C: def f(cls, arg1, arg2, ...): ... f = classmethod(f)
```

It can be called either on the class (e.g. C.f()) or on an instance (e.g. C().f()). The instance is ignored except for its class. If a class method is called for a derived class, the derived class object is passed as the implied first argument.

Class methods are different than C++ or Java static methods. If you want those, see the staticmethod builtin.

```
omsi.analysis.findpeaks.experimental.omsi_lpf.v_qspectrum
classmethod(function) -> method
```

Convert a function to be a class method.

A class method receives the class as implicit first argument, just like an instance method receives the instance. To declare a class method, use this idiom:

```
class C: def f(cls, arg1, arg2, ...): ... f = classmethod(f)
```

It can be called either on the class (e.g. C.f()) or on an instance (e.g. C().f()). The instance is ignored except for its class. If a class method is called for a derived class, the derived class object is passed as the implied first argument.

Class methods are different than C++ or Java static methods. If you want those, see the staticmethod builtin.

```
omsi.analysis.findpeaks.experimental.omsi_lpf.v_qspectrum_viewer_options  
classmethod(function) -> method
```

Convert a function to be a class method.

A class method receives the class as implicit first argument, just like an instance method receives the instance. To declare a class method, use this idiom:

```
class C: def f(cls, arg1, arg2, ...): ... f = classmethod(f)
```

It can be called either on the class (e.g. C.f()) or on an instance (e.g. C().f()). The instance is ignored except for its class. If a class method is called for a derived class, the derived class object is passed as the implied first argument.

Class methods are different than C++ or Java static methods. If you want those, see the staticmethod builtin.

omsi_npg Module

```
class omsi.analysis.findpeaks.experimental.omsi_npg.Node (label)  
omsi.analysis.findpeaks.experimental.omsi_npg.main (argv=None)
```

```
class omsi.analysis.findpeaks.experimental.omsi_npg.omsi_npg (name_key='undefined')  
Bases: omsi.analysis.base.analysis_base
```

Initialize the basic data members

```
Find (x)
```

```
MakeSet (x)
```

```
Union (x, y)
```

```
execute_analysis ()
```

```
getClustersInfo (GpeaksLabels, GLabelsList)
```

```
getCoordIdxB (xCoord, yCoord)
```

```
getCoordInfoB (xCoord, yCoord, peaksLabels)
```

```
getCoordPeaksB (xCoord, yCoord)
```

```
getNearestPeakIndex (myPeaksArray, myPeak)
```

```
getPixelMap (Nx, Ny)
```

```
classmethod getnpgimage (PeaksLabels, LabelsList, peaksArrayIndex, peaksIntensities, z)
```

```
classmethod getnpgspec (PeaksLabels, LabelsList, peaksArrayIndex, peaksIntensities, xCoord, yCoord)
```

```
myHC (labelsMMz, TreeCut)
```

```
record_execute_analysis_outputs (analysis_output)
```

We are recording our outputs manually as part of the execute function

```
splitLabelsList (LabelData, Thres, SplitMax)
```

```
classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)
```

Implement support for qmz URL requests for the viewer

```
classmethod v_qslic (analysis_object, z, viewer_option=0)
```

Implement support for qslic URL requests for the viewer

```
classmethod v_qslic_viewer_options (analysis_object)
```

Define which viewer_options are supported for qspectrum URL's

```
classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)
    Implement support for qspectrum URL requests for the viewer
classmethod v_qspectrum_viewer_options (analysis_object)
    Define which viewer_options are supported for qspectrum URL's
omsi.analysis.findpeaks.experimental.omsi_npg.stop()
```

mypeakfinder Module

```
omsi.analysis.findpeaks.experimental.mypeakfinder.generateScript (scriptfile,
    PFcon-
    tent=None,
    repo=None)
omsi.analysis.findpeaks.experimental.mypeakfinder.getJobOutput (jobname,
    runtype)
omsi.analysis.findpeaks.experimental.mypeakfinder.getPFCmd (pfstring,      lpfstring,
    npgstring,   LPFIndex,
    NPGIndex,    Skip-
    NPG,        SkipPeakCube,
    IndexFile=None)
omsi.analysis.findpeaks.experimental.mypeakfinder.main (argv)
omsi.analysis.findpeaks.experimental.mypeakfinder.monitorJob (jobid,      jobname,
    runtype='pf')
omsi.analysis.findpeaks.experimental.mypeakfinder.printHelp (thisfilename)
omsi.analysis.findpeaks.experimental.mypeakfinder.stop()
```

multivariate_stats Package

multivariate_stats Package Multivariate statistics analysis

class omsi.analysis.multivariate_stats.omsi_nmf (name_key='undefined')

Bases: *omsi.analysis.base.analysis_base*

Class defining a basic nmf analysis.

The function has primarily been tested we MSI datasets but should support arbitrary n-D arrays (n>=2). The last dimension of the input array must be the spectrum dimnensions.

Initialize the basic data members

execute_analysis ()

Execute the nmf for the given msidata

classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Implement support for qmz URL requests for the viewer

classmethod v_qslice (analysis_object, z, viewer_option=0)

Implement support for qslice URL requests for the viewer

classmethod v_qslice_viewer_options (analysis_object)

Define which viewer_options are supported for qspectrum URL's

classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)

Implement support for qspectrum URL requests for the viewer

classmethod v_qspectrum_viewer_options (analysis_object)

Define which viewer_options are supported for qspectrum URL's

```
class omsi.analysis.multivariate_stats.omsi_cx(name_key='undefined')
Bases: omsi.analysis.base.analysis_base
```

Class used to implement CX factorization on MSI data.

Initialize the basic data members

```
classmethod comp_lev_exact(A, k, axis)
```

This function computes the column or row leverage scores of the input matrix.

Parameters

- **A** – n-by-d matrix
- **k** – rank parameter, $k \leq \min(n,d)$
- **axis** – 0: compute row leverage scores; 1: compute column leverage scores.

Returns 1D array of leverage scores. If axis = 0, the length of lev is n. otherwise, the length of lev is d.

```
dimension_index = {'pixelDim': 1, 'imageDim': 0}
```

```
execute_analysis()
```

EDIT_ME:

Replace this text with the appropriate documentation for the analysis. Describe what your analysis does and how a user can use it. Note, a user will call the function execute(...) which takes care of storing parameters, collecting execution data etc., so that you only need to implement your analysis, the rest is taken care of by analysis_base. omsi uses Sphynx syntax for the documentation.

Keyword Arguments:

Parameters **mydata** – ...

```
classmethod v_qmz(analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)
```

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- **mz_spectra** : Array with the static mz values for the spectra.
- **label_spectra** : Lable for the spectral mz axis
- **mz_slice** : Array of the static mz values for the slices or None if identical to the **mz_spectra**.
- **label_slice** : Lable for the slice mz axis or None if identical to **label_spectra**.

```
classmethod v_qslice(analysis_object, z, viewer_option=0)
```

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **z** – Selection string indicating which z values should be selected.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like [::,zmin:zmax].

classmethod v_qslice_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qslice. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qslice requests (i.e., v_qslice(...) is not available).

classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **x** – x selection string
- **y** – y selection string
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns

The following two elements are expected to be returned by this function :

1. 1D, 2D or 3D numpy array of the requested spectra. NOTE: The mass (m/z) axis must be the last axis. For index selection x=1,y=1 a 1D array is usually expected. For indexList selections x=[0]&y=[1] usually a 2D array is expected. For range selections x=0:1&y=1:2 we one usually expects a 3D array.
2. None in case that the spectra axis returned by v_qmz are valid for the returned spectrum. Otherwise, return a 1D numpy array with the m/z values for the spectrum (i.e., if custom m/z values are needed for interpretation of the returned spectrum). This may be needed, e.g., in cases where a per-spectrum peak analysis is performed and the peaks for each spectrum appear at different m/z values.

classmethod v_qspectrum_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qspectrum. The

default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters analysis_object – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qspectrum requests (i.e., v_qspectrum(...) is not available).

class omsi.analysis.multivariate_stats.**omsi_kmeans** (*name_key*=’undefined’)

Bases: *omsi.analysis.base.analysis_base*

Class defining a basic nmf analysis for a 2D MSI data file or slice of the data

Initialize the basic data members

execute_analysis()

Execute the kmeans clustering for the given msidata

omsi_nmf Module Module for performing non-negative matrix factorization (NMF) for MSI data.

class omsi.analysis.multivariate_stats.omsi_nmf. **omsi_nmf** (*name_key*=’undefined’)

Bases: *omsi.analysis.base.analysis_base*

Class defining a basic nmf analysis.

The function has primarily been tested on MSI datasets but should support arbitrary n-D arrays (n>=2). The last dimension of the input array must be the spectrum dimensions.

Initialize the basic data members

execute_analysis()

Execute the nmf for the given msidata

classmethod **v_qmz** (*analysis_object*, *qslice_viewer_option*=0, *qspectrum_viewer_option*=0)

Implement support for qmz URL requests for the viewer

classmethod **v_qslice** (*analysis_object*, *z*, *viewer_option*=0)

Implement support for qslice URL requests for the viewer

classmethod **v_qslice_viewer_options** (*analysis_object*)

Define which viewer_options are supported for qspectrum URL’s

classmethod **v_qspectrum** (*analysis_object*, *x*, *y*, *viewer_option*=0)

Implement support for qspectrum URL requests for the viewer

classmethod **v_qspectrum_viewer_options** (*analysis_object*)

Define which viewer_options are supported for qspectrum URL’s

multivariate_stats.third_party Package

multivariate_stats.third_party Package Package containing shared third-party code modules included here to reduce the need for external dependencies when only small parts of external code are used.

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`omsi.analysis.multivariate_stats.third_party.nmf.nlssubprob(V, W, Hinit, tol, maxiter)`

H, grad: output solution and gradient iter: #iterations used V, W: constant matrices Hinit: initial solution tol: stopping tolerance maxiter: limit of iterations

`omsi.analysis.multivariate_stats.third_party.nmf(V, Winit, Hinit, tol, timelimit, maxiter)`

(W,H) = nmf(V,Winit,Hinit,tol,timelimit,maxiter) W,H: output solution Winit,Hinit: initial solution tol: tolerance for a relative stopping condition timelimit, maxiter: limit of time and iterations

multivariate_stats.experimental Package

multivariate_stats.experimental Package Module with experimental analysis code, i.e., code that is not (yet) used in production but is under development. Often this is code that is used in a specific research.

msi_filtering Package

msi_filtering Package Module with third-party modules, functions, classes used by some of the analysis modules in the containing package.

`class omsi.analysis.msi_filtering.omsi_tic_norm(name_key='undefined')`
Bases: `omsi.analysis.base.analysis_base`

TIC Normalization analysis.

Initialize the basic data members

`execute_analysis()`

Normalize the data based on the total intensity of a spectrum or the intensities of a select set of ions.

Calculations are performed using a memory map approach to avoid loading all data into memory. TIC normalization can as such be performed even on large files (assuming sufficient disk space).

Keyword Arguments:

Parameters

- **msidata** (*h5py.dataset or numpy array (3D)*) – The input MSI dataset
- **mzdata** – The mz axis do the dataset
- **maxCount** – ...
- **mzTol** – ...
- **infIons** – List of informative ions

record_execute_analysis_outputs (*analysis_output*)

We are not returning any outputs here, but we are going to record them manually. :param analysis_output:
The output of the execute_analysis(...) function.

classmethod v_qmz (*analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0*)

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- **mz_spectra** : Array with the static mz values for the spectra.
- **label_spectra** : Lable for the spectral mz axis
- **mz_slice** : Array of the static mz values for the slices or None if identical to the **mz_spectra**.
- **label_slice** : Lable for the slice mz axis or None if identical to **label_spectra**.

classmethod v_qslice (*analysis_object, z, viewer_option=0*)

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **z** – Selection string indicating which z values should be selected.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like [::,zmin:zmax].

classmethod v_qslice_viewer_options (*analysis_object*)

Get a list of strings describing the different default viewer options for the analysis for qslice. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters `analysis_object` – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qslice requests (i.e., `v_qslice(...)` is not available).

classmethod `v_qspectrum(analysis_object, x, y, viewer_option=0)`

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- `analysis_object` – The omsi_file_analysis object for which slicing should be performed
- `x` – x selection string
- `y` – y selection string
- `viewer_option` – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns

The following two elements are expected to be returned by this function :

1. 1D, 2D or 3D numpy array of the requested spectra. NOTE: The mass (m/z) axis must be the last axis. For index selection `x=1,y=1` a 1D array is usually expected. For indexList selections `x=[0]&y=[1]` usually a 2D array is expected. For range selections `x=0:1&y=1:2` we one usually expects a 3D array/
2. None in case that the spectra axis returned by `v_qmz` are valid for the returned spectrum. Otherwise, return a 1D numpy array with the m/z values for the spectrum (i.e., if custom m/z values are needed for interpretation of the returned spectrum). This may be needed, e.g., in cases where a per-spectrum peak analysis is performed and the peaks for each spectrum appear at different m/z values.

classmethod `v_qspectrum_viewer_options(analysis_object)`

Get a list of strings describing the different default viewer options for the analysis for qspectrum. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

param `analysis_object` The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qspectrum requests (i.e., `v_qspectrum(...)` is not available).

omsi_tic_norm Module Module with the TIC normalization analysis.

class omsi.analysis.msi_filtering.omsi_tic_norm.**omsi_tic_norm**(*name_key='undefined'*)
Bases: *omsi.analysis.base.analysis_base*

TIC Normalization analysis.

Initialize the basic data members

execute_analysis()

Normalize the data based on the total intensity of a spectrum or the intensities of a select set of ions.

Calculations are performed using a memory map approach to avoid loading all data into memory. TIC normalization can as such be performed even on large files (assuming sufficient disk space).

Keyword Arguments:

Parameters

- **msidata** (*h5py.dataset or numpy array (3D)*) – The input MSI dataset
- **mzdata** – The mz axis do the dataset
- **maxCount** – ...
- **mzTol** – ...
- **infIons** – List of informative ions

record_execute_analysis_outputs(analysis_output)

We are not returning any outputs here, but we are going to record them manually. :param analysis_output:
The output of the execute_analysis(...) function.

classmethod v_qmz(analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- **mz_spectra** : Array with the static mz values for the spectra.
- **label_spectra** : Lable for the spectral mz axis
- **mz_slice** : Array of the static mz values for the slices or None if identical to the **mz_spectra**.
- **label_slice** : Lable for the slice mz axis or None if identical to **label_spectra**.

classmethod v_qslice(analysis_object, z, viewer_option=0)

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **z** – Selection string indicating which z values should be selected.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like [::,zmin:zmax].

classmethod v_qslice_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qslice. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qslice requests (i.e., v_qslice(...) is not available).

classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **x** – x selection string
- **y** – y selection string
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns

The following two elements are expected to be returned by this function :

1. 1D, 2D or 3D numpy array of the requested spectra. NOTE: The mass (m/z) axis must be the last axis. For index selection x=1,y=1 a 1D array is usually expected. For indexList selections x=[0]&y=[1] usually a 2D array is expected. For range selections x=0:1&y=1:2 we one usually expects a 3D array/
2. None in case that the spectra axis returned by v_qmz are valid for the returned spectrum. Otherwise, return a 1D numpy array with the m/z values for the spectrum (i.e., if custom m/z values are needed for interpretation of the returned spectrum). This may be needed, e.g., in cases where a per-spectrum peak analysis is performed and the peaks for each spectrum appear at different m/z values.

classmethod v_qspectrum_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qspectrum. The

default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

param analysis_object The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qspectrum requests (i.e., v_qspectrum(...) is not available).

msi_filtering.third_party Package

msi_filtering.third_party Package Package containing shared third-party code modules included here to reduce the need for external dependencies when only small parts of external code are used.

msi_filtering.experimental Package

msi_filtering.experimental Package Module with experimental analysis code, i.e., code that is not (yet) used in production but is under development. Often this is code that is used in a specific research.

omsi_filter_by_mask Module Module for performing masking for MSI data.

class omsi.analysis.msi_filtering.experimental.omsi_filter_by_mask (*name_ke*
Bases: *omsi.analysis.base.analysis_base*

Class defining a basic mask creation a 2D MSI data file or slice of the data

Initialize the basic data members

execute_analysis()

classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- **mz_spectra** : Array with the static mz values for the spectra.
- **label_spectra** : Label for the spectral mz axis
- **mz_slice** : Array of the static mz values for the slices or None if identical to the **mz_spectra**.

- `label_slice` : Label for the slice mz axis or None if identical to `label_spectra`.

classmethod `v_qslice` (*analysis_object*, *z*, *viewer_option*=0)

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **`analysis_object`** – The `omsi_file_analysis` object for which slicing should be performed
- **`z`** – Selection string indicating which z values should be selected.
- **`viewer_option`** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like `[::,zmin:zmax]`.

classmethod `v_qslice_viewer_options` (*analysis_object*)

Get a list of strings describing the different default viewer options for the analysis for `qslice`. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the `qspectrum` should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters `analysis_object` – The `omsi_file_analysis` object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support `qslice` requests (i.e., `v_qslice(...)` is not available).

classmethod `v_qspectrum` (*analysis_object*, *x*, *y*, *viewer_option*=0)

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- **`analysis_object`** – The `omsi_file_analysis` object for which slicing should be performed
- **`x`** – x selection string
- **`y`** – y selection string
- **`viewer_option`** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns

The following two elements are expected to be returned by this function :

1. 1D, 2D or 3D numpy array of the requested spectra. NOTE: The mass (m/z) axis must be the last axis. For index selection `x=1,y=1` a 1D array is usually expected. For `indexList` selections `x=[0]&y=[1]` usually a 2D array is expected. For range selections `x=0:1&y=1:2` we one usually expects a 3D array.
2. None in case that the spectra axis returned by `v_qmz` are valid for the returned spectrum. Otherwise, return a 1D numpy array with the m/z values for the spectrum (i.e., if custom

m/z values are needed for interpretation of the returned spectrum). This may be needed, e.g., in cases where a per-spectrum peak analysis is performed and the peaks for each spectrum appear at different m/z values.

classmethod v_qspectrum_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qspectrum. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

param analysis_object The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qspectrum requests (i.e., v_qspectrum(...) is not available).

omsi_mask_by_cluster Module Module for performing making a mask from cluster matrix for MSI data.

class omsi.analysis.msi_filtering.experimental.omsi_mask_by_cluster.**omsi_mask_by_cluster**(name
Bases: *omsi.analysis.base.analysis_base*

Class defining a basic mask creation a 2D MSI data file or slice of the data

Initialize the basic data members

execute_analysis()**classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)**

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- mz_spectra : Array with the static mz values for the spectra.
- label_spectra : Label for the spectral mz axis
- mz_slice : Array of the static mz values for the slices or None if identical to the mz_spectra.
- label_slice : Label for the slice mz axis or None if identical to label_spectra.

classmethod v_qslice (analysis_object, z, viewer_option=0)

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **z** – Selection string indicating which z values should be selected.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like [::,zmin:zmax].

classmethod v_qslice_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qslice. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qslice requests (i.e., v_qslice(...) is not available).

classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **x** – x selection string
- **y** – y selection string
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns

The following two elements are expected to be returned by this function :

1. 1D, 2D or 3D numpy array of the requested spectra. NOTE: The mass (m/z) axis must be the last axis. For index selection x=1,y=1 a 1D array is usually expected. For indexList selections x=[0]&y=[1] usually a 2D array is expected. For range selections x=0:1&y=1:2 we one usually expects a 3D array.
2. None in case that the spectra axis returned by v_qmz are valid for the returned spectrum. Otherwise, return a 1D numpy array with the m/z values for the spectrum (i.e., if custom m/z values are needed for interpretation of the returned spectrum). This may be needed, e.g., in cases where a per-spectrum peak analysis is performed and the peaks for each spectrum appear at different m/z values.

classmethod v_qspectrum_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qspectrum. The

default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

param analysis_object The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qspectrum requests (i.e., v_qspectrum(...) is not available).

compound_stats Package

compound_stats Package Package containing shared third-party code modules included here to reduce the need for external dependencies when only small parts of external code are used.

omsi_score_midas Module MIDAS spectrum analysis

class omsi.analysis.compound_stats.omsi_score_midas.**omsi_score_midas** (*name_key='undefined'*)
Bases: *omsi.analysis.base.analysis_base*

Class for executing midas on an MSI or local peak finding dataset.

Initialize the basic data members

execute_analysis (*spectrum_indexes=None*, *compound_list=None*)

Execute the local peak finder for the given msidata.

Parameters

- **spectrum_indexes** – List with a list of integer indices of the subset of spectra that should be processed by this MPI task. If spectrum_indexes is set, then the given subblock will be processed in SERIAL instead of processing self['fpl_data'] in PARALLEL (if available). This parameter is strictly optional and intended for internal use only to facilitate the efficient parallel implementation.
- **compound_list** – List of the compounds from the database file. This parameter is used to avoid having to read the compound database on every compute task that calls this function when running in parallel. This parameter is strictly optional and intended for internal use only to facilitate the efficient parallel implementation.

Returns

A tuple with an array of hit_tables with the scores for each pixel and a 2D array of pixel indices describing for each spectrum the (x,y) pixel location in the image. The hit_table is an array of (#spectra x #compounds). The hit_table is a structured numpy array with the following columns:

- ‘score’, float, MIDAS score of row
- ‘id’, str, database ID e.g. ‘MetaCyC_7884’
- ‘name’, str, database name, e.g. ‘glycine’
- ‘mass’, float, mass in Da of IDed compound
- ‘n_peaks’, int, number of peaks in data

- ‘n_match’, int, number of peaks in data matched

omsi_score_pactolus Module MIDAS spectrum analysis

```
class omsi.analysis.compound_stats.omsi_score_pactolus.omsi_score_pactolus(name_key='undefined')
Bases: omsi.analysis.base.analysis_base
```

Class for executing Pactolus on a local peak finding dataset.

Initialize the basic data members

```
execute_analysis(spectrum_indexes=None, file_lookup_table=None)
```

Execute the local peak finder for the given msidata.

Parameters

- **spectrum_indexes** – List with a list of integer indicies of the subset of spectra that should be processed by this MPI task. If spectrum_indexes is set, then the given subblock will be processed in SERIAL instead of processing self['fpl_data'] in PARALLEL (if available). This parameter is strictly optional and intended for internal use only to facilitate the efficient parallel implementation.
- **file_lookup_table** – The Pactolus lookup table with the list of tree files and their mass.

Returns

A series of numpy arrays with the score data for each pixel and a 2D array of pixel indices describing for each spectrum the (x,y) pixel location in the image.

```
[‘pixel_index’, ‘score’, ‘id’, ‘name’, ‘mass’, ‘n_peaks’, ‘n_match’]
```

- ‘pixel_index’, int, 2D array of pixel indices describing for each spectrum the (x,y) pixel location in the image
- ‘score’, float, MIDAS score of row
- ‘id’, str, database ID e.g. ‘MetaCyC_7884’
- ‘name’, str, database name, e.g. ‘glycine’
- ‘mass’, float, mass in Da of IDed compound
- ‘n_peaks’, int, number of peaks in data
- ‘n_match’, int, number of peaks in data matched

compound_stats.third_party Package

compound_stats.third_party Package Package containing shared third-party code modules included here to reduce the need for external dependencies when only small parts of external code are used.

compound_stats.experimental Package

compound_stats.experimental Package Module with experimental analysis code, i.e., code that is not (yet) used in production but is under development. Often this is code that is used in a specific research.

10.1.2 dataformat Package

Main module for specification of data formats. This module also contains the *omsi_file* module which specifies the OpenMSI HDF5 data format. In addition it defines the base class for third-party file readers (i.e., *file_reader_base*) and implements various basic file readers for third-party formats, e.g., *img_file* and *mzml_file* for IMG and MZML data files respectively (among others).

<i>omsi.dataformat.omsi_file</i>	Module for specification of the OpenMSI file API.
<i>omsi.dataformat.omsi_file.analysis</i>	Module for managing custom analysis data in OMSI HDF5 files.
<i>omsi.dataformat.omsi_file.common</i>	Module for common data format classes and functionality.
<i>omsi.dataformat.omsi_file.dependencies</i>	Base module for managing of dependencies between data in OpenMSI files.
<i>omsi.dataformat.omsi_file.experiment</i>	OMSI file module for management of experiment data.
<i>omsi.dataformat.omsi_file.format</i>	This module defines the basic format for storing mass spectrometry data.
<i>omsi.dataformat.omsi_file.instrument</i>	Module for managing instrument related data in OMSI files.
<i>omsi.dataformat.omsi_file.main_file</i>	Module for managing OpenMSI HDF5 data files.
<i>omsi.dataformat.omsi_file.metadata_collection</i>	Module for management of general metadata storage entities.
<i>omsi.dataformat.omsi_file.methods</i>	Module for management of method specific data in OMSI data files.
<i>omsi.dataformat.omsi_file.msidata</i>	Module for managing MSI data in OMSI data files.
<i>omsi.dataformat.file_reader_base</i>	Module for base classes for implementation and integration of file readers.
<i>omsi.dataformat.bruckerflex_file</i>	This module provides functionality for reading bruker flex mass spectra.
<i>omsi.dataformat.img_file</i>	This module provides functionality for reading img mass spectra.
<i>omsi.dataformat.imzml_file</i>	This module provides functionality for reading imzML mass spectra.
<i>omsi.dataformat.mzml_file</i>	This module provides functionality for reading mzml mass spectra.

OMSI Dataformat Package

Main module for specification of the OpenMSI HDF5-based data format. The module contains various sub-modules, with the main goal to organize different categories of data.

Naming conventions for objects inside the HDF5 file are defined in the *omsi_file.format* module. These are used by the manager API classes to then implement the specific format.

The basic idea behind the design of the OpenMSI file format is the concept of managed objects. Managed objects are objects in an HDF5 file (usually HDF5 Groups –similar to directories just within a file) that have a corresponding interface class in the API. These classes in the API always start with the prefix *omsi_file_* and inherit from *omsi_file.common.omsi_file_common*.

To make it easy to nest different objects, we also have the concept of manager helper classes, which encapsulate common functionality for creation and interaction with the objects when they are contained in another object. Manager helper classes follow the following naming convention *omsi_<objectname>_manager*, where *objectname* is name of the object to be managed. E.g., *omsi_instrument_manager* is used to help place instrument groups inside another managed object. This is done by inheriting from the given manager helper class.

This means, multiple inheritance is used in order to nest other managed modules with other interfaces. This allows us to easily encapsulate common interaction features in centralized locations and construct more complex containers simply via inheritance.

The user of multiple inheritance and *super* can be tricky in python. To simplify the use and ensure stability we use the following conventions:

- All *omsi_file_** manager classes must except the h5py.Group object they manage as input and call *super(..).__init__(managed_group)* with the managed group as parameter in their *__init__*.
- All *omsi_<objectname>_manager* manager helper classes must except the h5py.Group that contains the object(s) that should be managed using the helper class as input and call *super(..).__init__(managed_group)* with the managed group as parameter in their *__init__*.

- All *omsi_file_** manager classes must inherit from *omsi_file.common.omsi_file_common*
- All *omsi_<objectname>_manager* helper classes must inherit from *object* (i.e., we use new-style classes).

omsi_file Package

Module for specification of the OpenMSI file API.

format Module

This module defines the basic format for storing mass spectrometry imaging data, metadata, and analysis in HDF5 in compliance with OpenMSI file format.

```
class omsi.dataformat.omsi_file.format.omsi_format_analysis
    Bases: omsi.dataformat.omsi_file.format.omsi_format_common
```

Specification for storing analysis related data.

Variables

- *analysis_groupname* – *analysis_* : Group with additional analysis results
- *analysis_identifier* – *analysis_identifier* : Identifier for the analysis to enable look-up by analysis id
- *analysis_type* – *analysis_type* : Dataset used to store the analysis type descriptor string
- *analysis_parameter_group* – Group for storing analysis parameters. Dependent parameters are stored separately using a *omsi_format_dependencies* group.
- *analysis_runinfo_group* – Group for storing run information, e.g., where was the analysis run, how long did it take etc.

```
analysis_groupname = 'analysis_'
analysis_identifier = 'analysis_identifier'
analysis_parameter_group = 'parameter'
analysis_parameter_help_attr = 'help'
analysis_runinfo_group = 'runinfo'
analysis_type = 'analysis_type'
current_version = '0.2'
```

```
class omsi.dataformat.omsi_file.format.omsi_format_common
    Bases: object
```

Specification of common attributes, and names for the file format.

Variables

- *str_type* – *str_type* = *h5py.new_vlen(str)* : Datatype used for storing strings in hdf5
- *type_attribute* – Name of the optional type attribute indicating which *omsi_file_** class should be used to interact with a given group.

```
current_version = '0.1'
str_type = dtype('O')
```

```
str_type_unicode = True
timestamp_attribute = 'timestamp'
type_attribute = 'omsi_type'
version_attribute = 'version'

class omsi.dataformat.omsi_file.format.omsi_format_data
    Bases: omsi.dataformat.omsi_file.format.omsi_format_common

Specification for storing raw data information.
```

Variables

- **data_groupname** – The base name for the hdf5 group containing the imaging data
- **dataset_name** – The base name for storing raw data. In the case of MSI data, this is the 3D data cube stored as 3D (full_cube), 2D (partial_cube) or 1D (partial_spectra) dataset, depending on the format_type.
- **data_dependency_group** – Optional group for storing data dependencies

```
current_version = '0.1'
data_groupname = 'data_'
dataset_name = 'data_'

class omsi.dataformat.omsi_file.format.omsi_format_dependencies
    Bases: omsi.dataformat.omsi_file.format.omsi_format_common
```

Specification for the management of a collection of dependencies.

Variables **dependencies_groupname** – dependency : Name of the group the dependencies are stored in.

```
current_version = '0.1'
dependencies_groupname = 'dependency'
```

```
class omsi.dataformat.omsi_file.format.omsi_format_dependencydata
    Bases: omsi.dataformat.omsi_file.format.omsi_format_common
```

Specification for the storage of a single dependency.

This type of group does not have specific name to allow the user to specify a specific link_name to ease retrieval of the data.

Variables

- **dependency_parameter** – parameter_name : Name of string dataset used to store the name of the dependent parameter
- **dependency_selection** – selection : Name of the string dataset used to store a selection string if needed.
- **dependency_mainname** – main_name : Name of the string dataset used to store the description of the link to the object that this depends on.
- **dependency_datasetname** – ‘data_name’ : Name fo the string dataset used to store the name of dataset within the mainname highlevel object.

```
current_version = '0.3'
dependency_datasetname = 'data_name'
dependency_mainname = 'main_name'
```

```
dependency_parameter = 'parameter_name'
dependency_parameter_help_attr = 'help'
dependency_selection = 'selection'
dependency_typename = 'dependency_type'

class omsi.dataformat.omsi_file.format.omsi_format_experiment
Bases: omsi.dataformat.omsi_file.format.omsi_format_common

Specification of file format specific name conventions

Variables

- exp_groupname – entry_ : The base name for a group containing data about an experiment
- exp_identifier_name – experiment_identifier : The identifier dataset for an experiment


current_version = '0.1'
exp_groupname = 'entry_'
exp_identifier_name = 'experiment_identifier'

class omsi.dataformat.omsi_file.format.omsi_format_file
Bases: omsi.dataformat.omsi_file.format.omsi_format_common

Specification of main-file related specific name conventions

current_version = '0.1'

class omsi.dataformat.omsi_file.format.omsi_format_instrument
Bases: omsi.dataformat.omsi_file.format.omsi_format_metadata_collection

Specification for storing instrument related information

Variables

- instrument_groupname – instrument : Group with information about the intrument used
- instrument_mz_name – mz : Name of the dataset for the intrument's mz data values
- instrument_name – name : The dataset with the name of the instrument


current_version = '0.2'
instrument_groupname = 'instrument'
instrument_mz_name = 'mz'
instrument_name = 'name'

class omsi.dataformat.omsi_file.format.omsi_format_metadata_collection
Bases: omsi.dataformat.omsi_file.format.omsi_format_common

Specification of the basic format for a general-purpose metadata storage

Variables

- metadata_collection_groupname_default – Default name for the group where the collection of metadata is stored.
- description_value_attribute – The attribute to be associated with each metadata value describing the content in a human-readable form

```

- **unit_value_attribute** – The attribute to be associated with each metadata value describing the unit

- **ontology_value_attribute** – Optional ontology associated with a metadata value

```
current_version = '0.1'

description_value_attribute = 'description'

metadata_collection_groupname_default = 'metadata'

ontology_value_attribute = 'ontology'

unit_value_attribute = 'unit'
```

class omsi.dataformat.omsi_file.format.omsi_format_methods

Bases: *omsi.dataformat.omsi_file.format.omsi_format_metadata_collection*

Specification of the basic format for storing method-related information

Variables

- **methods_groupname** – *methods* : The group storing all the information about the method

- **methods_old_groupname** – *method* : The group object was refactored to methods. To ensure that old files can still be read, this variable was added and is checked as well if needed.

- **methods_name** – *name* : The dataset with the name of the method

```
current_version = '0.3'
```

```
methods_groupname = 'methods'
```

```
methods_name = 'name'
```

```
methods_old_groupname = 'sample'
```

class omsi.dataformat.omsi_file.format.omsi_format_msidata

Bases: *omsi.dataformat.omsi_file.format.omsi_format_data*

Specification of the basic format for storing an MSI dataset consisting of a complete 3D cube (or a 3D cube completed with 0s for missing data)

Variables

- **format_types** – Data layout types supported for storing MSI data.

- **mzdata_name** – Global mz axis for the MSI data cube.

- **format** – Dataset in HDF5 with the format_type descriptor.

```
current_version = '0.1'
```

```
format_name = 'format'
```

```
format_types = {'full_cube': 1, 'partial_cube': 2, 'partial_spectra': 3}
```

```
mzdata_name = 'mz'
```

class omsi.dataformat.omsi_file.format.omsi_format_msidata_partial_cube

Bases: *omsi.dataformat.omsi_file.format.omsi_format_msidata*

Specification of the basic format for storing an MSI datasets that define a partial cube with full spectra

Variables

- **xy_index_name** – 2D dataset indicating for each spectrum its start location in the main dataset
- **inv_xy_index_name** – 2D dataset with n rows and 2 columns indicating for each spectrum i the (x,y) pixel index the spectrum belongs to. This index is stored for convenience purposes but is not actually needed for data access.
- **shape_name** – Simple [3] indicating the true image size in x,y,mz

```
inv_xy_index_name = 'inv_xy_index'
shape_name = 'shape'
xy_index_name = 'xyindex'

class omsi.dataformat.omsi_file.format.omsi_format_msidata_partial_spectra
    Bases: omsi.dataformat.omsi_file.format.omsi_format_msidata_partial_cube

Specification of the basic format for storing an MSI dataset of a full or partial cube with partial spectra
```

Variables

- **mz_index_name** – 1D dataset of the same size as the spectrum data, indicating the indices into the global m/z list
- **xy_index_end_name** – 2D dataset indicating for each spectrum its end location (index not included) in the main dataset

```
mz_index_name = 'mz_index'
xy_index_end_name = 'xyindexend'
```

common Module

Module for common data format classes and functionality.

```
class omsi.dataformat.omsi_file.common.omsi_file_common (managed_group)
    Bases: object
```

Base class for definition of file format modules for the OpenMSI data format.

Use of super()

This class inherits only from object and calls super in the `__init__` without parameters. In the standard design pattern of the *omsi.dataformat.omsi_file module*, it is, therefore, the last class we inherit from in the case of multiple inheritance.

Multiple inheritance is used in *omsi.dataformat.omsi_file module* when a class contains other managed objects and uses the manager classes, e.g, *omsi_instrument_manger* etc. to get all the features needed to manage those objects.

All child classes of *omsi_file_common* also call `super(..).__init__(manager_group)` but using a single input parameter indicating the manager `h5py.Group` object that contains the given object.

Variables

- **managed_group** – The `h5py.Group` object managed by the class
- **name** – The path to the object in the hdf5 file. Same as `managed_group.name`
- **file** – The `h5py.File` object the `managed_group` is associated with. Same as `managed_group.file`

static `create_path_string` (*filename, objectname*)

Given the name of the file and the object path within the file, create a string describing the external reference to the data

Parameters

- **filename** – The full or relative path to the file
- **objectname** – The object path in the HDF5 file

Returns String describing the path to the object

classmethod `get_h5py_object` (*omsi_object, resolve_dependencies=False*)

This static method is a convenience function used to retrieve the corresponding h5py interface object for any omsi file API object.

Parameters

- **omsi_object** – omsi file API input object for which the corresponding h5py.Group, h5py.File, or h5py.Dataset object should be retrieved. The omsi_object input may itself also be a h5py.Group, h5py.File, or h5py.Dataset, in which case omsi_object itself is returned by the function.
- **resolve_dependencies** – Set to True if omsi_file_dependencydata objects should be resolved to retrieve the dependent object the dependency is pointing to. Dependencies are resolved recursively, i.e., if a dependency points to another dependency then that one will be resolved as well. Default value is False, i.e., the omis_file_dependency object itself is returned.

Returns h5py.Group, h5py.File, or h5py.Dataset corresponding to the given omsi_object.

Raises ValueError A ValueError is raised in case that an unsupported omsi_object object is given, i.e., the input object is not a omsi_file API object nor a h5py Group, File, or Dataset object.

get_managed_group()

Return the h5py object with the analysis data.

The returned object can be used to read data directly from the HDF5 file. Write operations to the analysis group can be performed only if the associated omsi_file was opened with write permissions.

Returns h5py object for the analysis group.

classmethod `get_num_items` (*file_group, basename=''*)

Get the number of object with the given basename at the given path

Parameters

- **file_group** – The h5py object to be examined
- **basename** – The name that should be searched for.

Returns Number of objects with the given basename at the given path

classmethod `get_omsi_object` (*h5py_object, resolve_dependencies=False*)

This static method is convenience function used to retrieve the corresponding interface class for a given h5py group object.

Parameters

- **h5py_object** – h5py object for which the corresponding omsi_file API object should be generated. This may also be a string describing the requested object based on a combination of the path to the file and a path of the object <filename.h5>:<object_path>

- **resolve_dependencies** – Set to True if omsi_file_dependencydata objects should be resolved to retrieve the dependent object the dependency is pointing to. Dependencies are resolved recursively, i.e., if a dependency points to another dependency then that one will be resolved as well. Default value is False, i.e., the omis_file_dependency object itself is returned.

Returns

None in case no corresponding object was found. Otherwise an instance of:

- omsi_file : If the given object is a h5py.File object
- omsi_file_experiment : If the given object is an experiment group
- omsi_file_methods : If the given object is a method group
- omsi_file_instrument : If the given object is an instrument group
- omsi_file_analysis : If the given object is an analysis group
- omsi_file_msidata : If the given object is a MSI data group
- omsi_file_dependencydata : If the given object is a dependency group
- The input h5py_object: If the given object is a h5py.Dataset or h5py.Group
- None: In case that an unknown type is given.

get_timestamp()

Get the timestamp when the analysis group was created in the HDF5 file.

Returns Python timestamp string generated using time.ctime(). None may be returned in case that the timestamp does not exists or cannot be retrieved from the file for some reason.

get_version()

Get the omsi version for the representation of this object in the HDF5 file

classmethod is_managed(in_object)

Check whether the given object is managed by any omsi API class.

Parameters **in_object** (Any omsi_file API object or h5py.Dataset or h5py.Group or h5py.File object.) – The object to be checked

items()

Get the list of items associated with the h5py.Group object managed by this object

static parse_path_string(path)

Given a string of the form <filename.h5>:<object_path> retrieve the name of the file and the object path.

Parameters **path** – The string defining the file and object path.

Returns Tuple with the filename and the object path. Both may be None depending on whether an object_path is given and whether the path string is valid.

Raises ValueError in case that an invalid string is given

static same_file(filename1, filename2)

Check whether two files are the same.

This function uses the os.path.samefile(...) method to compare files and falls back to comparing the absolute paths of files if samefile should fail or cannot be imported.

Parameters

- **filename1** – The name of the first file
- **filename2** – The name of the second file

Returns

```
class omsi.dataformat.omsi_file.common.omsi_file_object_manager(*args, **kwargs)
Bases: object
```

Base class used to define manager helper classes used to manage contained managed objects. Managed objects are HDF5.Groups (or Datasets) with a corresponding manager API class and may be nested within other Managed objects.

What is a manager helper class?

Manager classes are used in the design of *omsi.dataformat.omsi_file* to encapsulate functionality needed for management of other manager objects. The expected use of this class, hence, is through multiple inheritance where the main base class is *omsi.dataformat.omsi_file.common.omsi_file_common*. This is important due to the use of super to accomodate multiple inheritance to allow object to manage an arbitrary number of other object and inherit from other object as well.

Use of super()

This class inherits only from object but calls super in the `__init__(manager_group)` with the `manager_group` as only input parameter, in the expectation that this class is used using multiple inheritance with *omsi_file_common* as main base class .

Multiple inheritance is used in *omsi.dataformat.omsi_file module* when a class contains other managed objects and uses the manager classes (such as this one) to get all the features needed to manage those objects.

All child classes of *omsi_file_common* call `super(..).__init__(manager_group)` and all manager helper classes (such as this one) use a single input parameter indicating the manager h5py.Group object that contains the given object.

main_file Module

Module for managing OpenMSI HDF5 data files.

```
class omsi.dataformat.omsi_file.main_file.omsi_file(filename, mode='a', **kwargs)
Bases:           omsi.dataformat.omsi_file.experiment.omsi_experiment_manager,
                omsi.dataformat.omsi_file.common.omsi_file_common
```

API for creating and managing a single OpenMSI data file.

Use of super()

This class inherits from *omsi.dataformat.omsi_file.common.omsi_file_common* . Consistent with the design pattern for multiple inheritance of the *omsi.dataformat.omsi_file* module, the `__init__` function calls `super(..).__init__(manager_group)` with a single parameter indicating the parent group.

Inherited Instance Variables

Variables

- **managed_group** – The group that is managed by this object
- **name** – Name of the managed group

Open the given file or create it if does not exist.

The creation of the object may fail if the file does not exist, and the selected mode is ‘r’ or ‘r+’.

Keyword arguments:

Parameters

- **filename** – string indicating the name+path of the OpenMSI data file. Alternatively this may also be an h5py.File instance (or an h5py.Group, h5py.Dataset instance from which we can get the file)
- **mode** – read/write mode. One of :
 - r = readonly, file must exist.
 - r+ = read/write, file must exist.
 - w = Create file, truncate if exists.
 - w- = create file, fail if exists.
 - a = read/write if exists, create otherwise (default)
- ****kargs** – Other keyword arguments to be used for opening the file using h5py. See the h5py.File documentation for details. For example to use parallel HDF5, the following additional parameters can be given driver='mpio', comm:MPI.COMM_WORLD.

close_file()

Close the msi data file

flush()

Flush all I/O

get_filename()

Get the name of the omsi file

Returns String indicating the filename (possibly including the full path, depending on how the object has been initialized)

get_h5py_file()

Get the h5py object for the omsi file

Returns h5py reference to the HDF5 file

classmethod is_valid_dataset(name)

Perform basic checks for the given filename, whether it is a valid OMSI file.

Parameters **name** – Name of the file to be checked.

Returns Boolean indicating whether the file is valid

write_xdmf_header(xdmf_filename)

Write XDMF header file for the current HDF5 datafile

Parameters **xmrf_filename** – The name of the xdmf XML header file to be created for the HDF5 file.

experiment Module

OMSI file module for management of experiment data.

class *omsi.dataformat.omsi_file.experiment.omsi_experiment_manager*(*experiment_parent*)
Bases: *omsi.dataformat.omsi_file.common.omsi_file_object_manager*

Experiment manager helper class used to define common functionality needed for experiment-related data. Usually, a class that defines a format that contains an omsi_file_experiment object will inherit from this class (in addition to omsi_file_common) to acquire the common features.

For more details see: *omsi.dataformat.omsi_file.omsi_common.omsi_file_object_manager*

Variables `experiment_parent` – The h5py.Group parent object containing the instrument object to be managed.

create_experiment (`exp_identifier=None, flush_io=True`)

Create a new group in the file for a new experiment and return the omsi_file_experiment object for the new experiment.

Parameters

- `exp_identifier` (*string or None (default)*) – The string used to identify the analysis
- `flush_io` – Call flush on the HDF5 file to ensure all HDF5 bufferes are flushed so that all data has been written to file.

Returns omsi_file_experiment object for the newly created group for the experiment

get_experiment (`exp_index`)

Get the omsi_format_experiment object for the experiment with the given index

Parameters `exp_index` (*uint*) – The index of the requested experiment

Returns h5py reference to the experiment with the given index. Returns None in case the experiment does not exist.

get_experiment_by_identifier (`exp_identifier_string`)

Get the omsi_format_experiment object for the experiment with the given identifier.

Parameters `exp_identifier_string` (*string*) – The string used to identify the analysis

Returns Returns h5py object of the experiment group or None in case the experiment is not found.

static get_experiment_path (`exp_index=None`)

Based on the index of the experiment return the full path to the hdf5 group containing the data for an experiment.

Parameters `exp_index` – The index of the experiment.

Returns String indicating the path to the experiment.

get_num_experiments()

Get the number of experiments in this file.

Returns Integer indicating the number of experiments.

class omsi.dataformat.omsi_file.experiment.**omsi_file_experiment** (`exp_group`)
Bases: *omsi.dataformat.omsi_file.methods.omsi_methods_manager, omsi.dataformat.omsi_file.instrument.omsi_instrument_manager, omsi.dataformat.omsi_file.analysis.omsi_analysis_manager, omsi.dataformat.omsi_file.msidata.omsi_msidata_manager, omsi.dataformat.omsi_file.common.omsi_file_common*

Class for managing experiment specific data

Use of super():

This class inherits from *omsi.dataformat.omsi_file.common.omsi_file_common*. Consistent with the design pattern for multiple inheritance of the *omsi.dataformat.omsi_file* module, the `__init__` function calls `super(...).__init__(manager_group)` with a single parameter indicating the parent group.

Inherited instance variable:

Variables

- `managed_group` – The group that is managed by this object

- **methods_parent** – The parent group containing the methods object (same as managed_group)
- **instrument_parent** – The parent group containing the instrument object (same as managed_group)
- **name** – Name of the managed group

Initialize the experiment object given the h5py object of the experiment group

Parameters `exp_group` – The h5py object with the experiment group of the omsi hdf5 file.

get_experiment_identifier()

Get the HDF5 dataset with the identifier description for the experiment.

Returns h5py object of the experiment identifier or None in case not present

get_experiment_index()

Determine the index of the experiment based on the name of the group :return: Integer index of the experiment

get_instrument_info(check_parent=False)

Inherited from omsi_instrument_manager parent class. Overwritten here to change the default parameter setting for check_parent. See *omsi.dataformat.omsi_file.instrument.omsi_instrument_manager* for details.

get_method_info(check_parent=False)

Inherited from omsi_method_manager parent class. Overwritten here to change the default parameter setting for check_parent. See *omsi.dataformat.omsi_file.methods.omsi_method_manager* for details

set_experiment_identifier(identifier)

Overwrite the current identifier string for the experiment with the given string

Parameters `identifier` – The new experiment identifier string.

metadata_collection Module

Module for management of general metadata storage entities. These are often specialized —e.g., omsi_file_instrument, omsi_file_sample—to store specific metadata and add more functionality.

class `omsi.dataformat.omsi_file.metadata_collection.omsi_file_metadata_collection(metadata_group)`
Bases: *omsi.dataformat.omsi_file.common.omsi_file_common*

Class for managing method specific data.

Use of super():

This class inherits from *omsi.dataformat.omsi_file.common.omsi_file_common*. Consistent with the design pattern for multiple inheritance of the *omsi.dataformat.omsi_file* module, the `__init__` function calls `super(...).__init__(manager_group)` with a single parameter indicating the parent group.

Inherited Instance Variables

Variables

- **managed_group** – The group that is managed by this object
- **name** – Name of the managed group

Initialize the metadata collection object given the h5py object of the metadata collection

Parameters `metadata_group` – The h5py object with the metadata collection group of the omsi hdf5 file.

add_metadata (metadata)

Add a new metadata entry

Parameters **metadata** – Instance of *omsi.shared.metadata_data.metadata_value* or describing *omsi.shared.metadata_data.metadata_dict* with the metadata to be added.

get_metadata (key=None)

Get dict with the full description of the metadata for the given key or all metadata if no key is given.

Returns *omsi.shared.metadata_data.metadata_value* object if a key is given or a *omsi.shared.metadata_data.metadata_dict* with all metadata if no key is specified.

Raises KeyError is raised in case that the specified key does not exist

keys ()

Get a list of all metadata keys

Returns List of string with the metadata keys

values ()

Convenience function returning a list of all metadata objects. This is equivalent get_metadata(key=None).values(), however, for consistency with other dict-like interfaces this function returns a list of *omsi.shared.metadata_data.metadata_value* objects rather than the *omsi.shared.metadata_data.metadata_dict*

Returns List of *omsi.shared.metadata_data.metadata_value* with all metadata

class *omsi.dataformat.omsi_file.metadata_collection.omsi_metadata_collection_manager* (*metadata_p*
Bases: *omsi.dataformat.omsi_file.common.omsi_file_object_manager*

This is a file format manager helper class used to define common functionality needed for management of metadata-related data. Usually, a class that defines a format that contains an *omsi_file_metadata* object will inherit from this class (in addition to *omsi_file_common*) to acquire the common features.

For more details see: *omsi.dataformat.omsi_file.omsi_common.omsi_file_object_manager*

Variables **metadata_parent** – The parent h5py.Group object containing the method object to be managed

create_metadata_collection (group_name=None, metadata=None, flush_io=True)

Add a new group for managing metadata

Parameters

- **group_name** (str, None) – Optional name of the new metadata group. If None is given then the *omsi_format_metadata_collection.metadata_collection_groupname_default* will be used
- **metadata** (None, *omsi.shared.metadata_data.metadata_value*, *omsi.shared.metadata_data.metadata_dict*) – Additional metadata to be added to the collection after creation
- **flush_io** – Call flush on the HDF5 file to ensure all HDF5 buffers are flushed so that all data has been written to file

Returns *omsi_file_metadata_collection* object

get_default_metadata_collection (omsi_object=None)

Get the default metadata collection object if it exists

Parameters **omsi_object** – The omsi file API object or h5py.Group object that we should check. If set to None (default) then the self.metadata_parent will be used

Returns None, *omsi_file_metadata_collection*

get_metadata_collections(*omsi_object=None, name=None*)

Get all metadata_collections defined for given OpenMSI file API object or h5py.Group.

Parameters

- **omsi_object** – The omsi file API object or h5py.Group object that we should check. If set to None (default) then the self.metadata_parent will be used
- **name** – If name is specified, then only retrieve collections with the given name

Returns List of omsi_file_metadata_collection objects for the requested group. The function returns None in case that the h5py.Group for the omsi_object could not be determined.

has_default_metadata_collection(*omsi_object*)

Check whether the omsi API object (or h5py.Group) contains any a metadata collection with the default name.

Returns bool**has_metadata_collections**(*omsi_object=None*)

Check whether the given omsi API object (or h5py.Group) contains any metadata collections

Parameters **omsi_object** – The omsi file API object or h5py.Group object that we should check. If set to None (default) then the self.metadata_parent will be used

Returns Boolean indicating whether metadata collections were found

instrument Module

Module for managing instrument related data in OMSI files.

class omsi.dataformat.omsi_file.instrument.*omsi_file_instrument*(*instrument_group*)

Bases: *omsi.dataformat.omsi_file.metadata_collection.omsi_file_metadata_collection*

Class for managing instrument specific data

Use of super():

This class inherits from *omsi.dataformat.omsi_file.common.omsi_file_common*. Consistent with the design pattern for multiple inheritance of the *omsi.dataformat.omsi_file* module, the *__init__* function calls *super(...).__init__(manager_group)* with a single parameter indicating the parent group.

Inherited Instance Variables**Variables**

- **managed_group** – The group that is managed by this object
- **name** – Name of the managed group

Initialize the instrument object given the h5py object of the instrument group

Parameters **instrument_group** – The h5py object with the instrument group of the omsi hdf5 file.

get_instrument_mz()

Get the HDF5 dataset with the mz data for the instrument.

To get the numpy array of the full mz data use: *get_instrument_mz()[:]*

Returns Returns the h5py object with the instrument mz data. Returns None in case no mz data was found for the instrument.

get_instrument_name()

Get the HDF5 dataset with the name of the instrument.

To get the string of the instrument name use: `get_instrument_name()[]`

Returns h5py object to the dataset with the instrument name. Returns None in case no method name is found.

has_instrument_name()

Check whether a name has been saved for the instrument

Returns bool

set_instrument_name(name)

Overwrite the current identifier string for the experiment with the given string.

Parameters `name (string.)` – The new instrument name.

class `omsi.dataformat.omsi_file.instrument.omsi_instrument_manager(instrument_parent)`

Bases: `omsi.dataformat.omsi_file.metadata_collection.omsi_metadata_collection_manager`

Instrument manager helper class used to define common functionality needed for instrument-related data. Usually, a class that defines a format that contains an `omsi_file_methods` object will inherit from this class (in addition to `omsi_file_common`) to acquire the common features.

For more details see: `omsi.dataformat.omsi_file.omsi_common.omsi_file_object_manager`

Variables `instrument_parent` – The h5py.Group parent object containing the instrument object to be managed.

create_instrument_info(instrument_name=None, mzdata=None, flush_io=True)

Add information about the instrument used for creating the images for this experiment.

Parameters

- `instrument_name (string, None)` – The name of the instrument
- `mzdata (numpy array or None)` – Numpy array of the mz data values of the instrument
- `flush_io` – Call flush on the HDF5 file to ensure all HDF5 bufferes are flushed so that all data has been written to file

Returns The function returns the h5py HDF5 handler to the instrument info group created for the experiment.

get_instrument_info(check_parent=True)

Get the HDF5 group opbject with the instrument information.

Parameters `check_parent` – If no method group is available for this dataset should we check whether the parent object (i.e., the experiment group containing the dataset) has information about the method. (default=True)

Returns `omsi_file_instrument` object for the requested instrument info. The function returns None in case no instrument information was found for the experiment

has_instrument_info(check_parent=False)

Check whether custom instrument information is available for this dataset.

Parameters `check_parent` – If no instrument group is available for this dataset should we check whether the parent object (i.e., the experiment group containing the dataset) has information about the instrument. (default=False)

Returns Boolean indicating whether instrument info is available.

methods Module

Module for management of method specific data in OMSI data files

class omsi.dataformat.omsi_file.methods.**omsi_file_methods** (*method_group*)

Bases: *omsi.dataformat.omsi_file.metadata_collection.omsi_file_metadata_collection*

Class for managing method specific data.

Use of super():

This class inherits from *omsi.dataformat.omsi_file.common.omsi_file_common*. Consistent with the design pattern for multiple inheritance of the *omsi.dataformat.omsi_file* module, the `__init__` function calls `super(...).__init__(manager_group)` with a single parameter indicating the parent group.

Inherited Instance Variables

Variables

- **managed_group** – The group that is managed by this object
- **name** – Name of the managed group

Initialize the method object given the h5py object of the method group

Parameters **method_group** – The h5py object with the method group of the omsi hdf5 file.

get_method_name()

Get the HDF5 dataset with the name of the method.

To retrieve the name string use `get_method_name()[]`

Returns h5py object where the method name is stored. Returns None in case no method name is found.

has_method_name()

Check whether an object has a method name

Returns bool

set_method_name(*name_string*)

Overwrite the name string for the method with the given name string

Parameters **name_string** (*string*) – The new method name.

class omsi.dataformat.omsi_file.methods.**omsi_methods_manager** (*methods_parent=None*)

Bases: *omsi.dataformat.omsi_file.metadata_collection.omsi_metadata_collection_manager*

This is a file format manager helper class used to define common functionality needed for methods-related data. Usually, a class that defines a format that contains an *omsi_file_methods* object will inherit from this class (in addition to *omsi_file_common*) to acquire the common features.

For more details see: *omsi.dataforamt.omsi_file.omsi_common.omsi_file_object_manager*

Variables **method_parent** – The parent h5py.Group object containing the method object to be managed

create_method_info(*method_name=None, metadata=None, flush_io=True*)

Add information about the method imaged to the experiment. Note, if a methods group already exists, then that group will be used. If *method_name* is not None, then the existing name will be overwritten by the new value.

Parameters

- **method_name** (*str; None*) – Optional name of the method

- **metadata** (*metadata_value*, *metadata_dict*) – Additional metadata to be stored with the methods
- **flush_io** – Call flush on the HDF5 file to ensure all HDF5 buffers are flushed so that all data has been written to file

Returns h5py object of the newly created method group.

get_method_info (*check_parent=True*)

Get the omsi_file_methods object with the method information.

Parameters **check_parent** – If no method group is available for this dataset should we check whether the parent object (i.e., the experiment group containing the dataset) has information about the method. (default=True)

Returns omsi_file_methods object for the requested method info. The function returns None in case no method information was found for the experiment

has_method_info (*check_parent=False*)

Check whether custom method information is available for this dataset.

Parameters **check_parent** – If no method group is available for this dataset should we check whether the parent object (i.e., the experiment group containing the dataset) has information about the method. (default=False)

Returns Boolean indicating whether method info is available.

msidata Module

Module for managing MSI data in OMSI data files

```
class omsi.dataformat.omsi_file.msidata.omsi_file_msidata(data_group,
                                                          fill_space=True,
                                                          fill_spectra=True,
                                                          preload_mz=False,
                                                          preload_xy_index=False)
Bases:      omsi.dataformat.omsi_file.dependencies.omsi_dependencies_manager,
            omsi.dataformat.omsi_file.methods.omsi_methods_manager,
            omsi.dataformat.omsi_file.instrument.omsi_instrument_manager,
            omsi.dataformat.omsi_file.metadata_collection.omsi_metadata_collection_manager,
            omsi.dataformat.omsi_file.common.omsi_file_common
```

Interface for interacting with mass spectrometry imaging datasets stored in omis HDF5 files. The interface allows users to interact with the data as if it were a 3D cube even if data is missing. Full spectra may be missing in cases where only a region of interest in space has been imaged. Spectra may further be pre-processed so that each spectrum has only information about its peaks so that each spectrum has its own mz-axis.

To load data use standard array syntax, e.g., [1,1,:] can be used to retrieve the spectra at location (1,1).

Use of super():

This class inherits from *omsi.dataformat.omsi_file.common.omsi_file_common*. Consistent with the design pattern for multiple inheritance of the *omsi.dataformat.omsi_file* module, the *__init__* function calls *super(...).__init__(manager_group)* with a single parameter indicating the parent group.

Current limitations:

- The estimates in def __best_dataset__(self,keys) are fairly crude at this point
- The __getitem__ function for the partial_spectra case is not implemented yet.

- The `__setitem__` function for the partial spectra case is not implemented yet (Note, it should also support dynamic expansion of the cube by adding previously missing spectra).
- For the partial cube case, assignment using `__setitem__` function is only supported to valid spectra, i.e., spectra that were specified as occupied during the intital creation process.

Public object variables:**Variables**

- **shape** – Define the full 3D shape of the dataset (i.e., even if the data is stored in sparse manner)
- **dtype** – The numpy datatyp of the main MSI data. This is the same as `dataset.dtype`
- **name** – The name of the corresponding group in the HDF5 file. Used to generate hard-links to the group.
- **format_type** – Define according to which standard the data is stored in the file
- **datasets** – List of h5py objects containing possibly multiple different version of the same MSI data (spectra). There may be multiple versions stored with different layouts in order to optimize the selection process.
- **mz** – dataset with the global mz axis information. If `prelaod_mz` is set in the constructor, then this is a numpy dataset with the preloaded data. Otherwise, this is the h5py dataset pointing to the data on disk.
- **xy_index** – None if `format_type` is ‘full_cube’. Otherwise, this is the 2D array indicating for each x/y location the index of the spectrum in `dataset`. If `prelaod_xy_index` is set in the constructor, then this is a numpy dataset with the preloaded data. Otherwise, this is the h5py dataset pointing to the data on disk. Negative (-1) entries indicate that no spectrum has been record for the given pixel.
- **inv_xy_index** – 2D dataset with n rows and 2 columns indicating for each spectrum in the (x,y) pixel index the spectrum belongs to. This index is stored for convenience purposes but is not actually needed for data access.
- **mz_index** – None if `format_type` is not ‘partial_spectra’. Otherwise this is a dataset of the same size as the spectra data stored in `dataset`. Each entry indicates an index into the `mz` dataset to determine the `mz_data` value for a spectrum. This means `mz[mx_index]` gives the true mz value.
- **xy_index_end** – None if `format_type` is not ‘partial_spectra’. Otherwise this is a 2D array indicating for each x/y location the index where the given spectrum ends in the dataset. If `prelaod_xy_index` is set in the constructor, then this is a numpy dataset with the preloaded data. Otherwise, this is the h5py dataset pointing to the data on disk. Negative (-1) entries indicate that no spectrum has been record for the given pixel.

Private object variables:**Variables**

- **_data_group** – Store the pointer to the HDF5 group with all the data
- **_fill_xy** – Define whether the data should be reconstructed as a full image cube Set using the `set_fill_space` function(..)
- **_fill_mz** – Define whether spectra should be remapped onto a global m/z axis. Set using the `set_fill_spectra` function(..)

Initialize the `oms1_msidata` object.

The fill options are provided to enable a more convenient access to the data independent of how the data is stored in the file. If the fill options are enabled, then the user can interact with the data as if it were a 3D cube while missing data is filled in by the given fill value.

The preload options provided here refer to generally smaller parts of the data for which it may be more efficient to load the data and keep it around rather than doing repeated reads. If the object is used only for a single read and destroyed afterwards, then disabling the preload options may give a slight advantage but in most cases enabling the preload should be Ok (default).

Parameters

- **data_group** – The h5py object for the group with the omsi_msidata.
- **fill_space** – Define whether the data should be padded in space (filled with 0's) when accessing the data using [...] operator so that the data behaves like a 3D cube.
- **fill_spectra** – Define whether the spectra should be completed by adding 0's so that all spectra retrieved via the [...] operator so that always spectra of the full length are returned. This option is provided to ease extension of the class to cases where only partial spectra are stored in the file but is not used at this point.
- **preload_mz** – Should the data for the mz axis be kept in memory or loaded on the fly when needed.
- **preload_xy_index** – Should the xy index (if available) be preloaded into memory or should the required data be loaded on the fly when needed.

`copy_dataset (source, destination, print_status=False)`

Helper function used to copy a source msi dataset one chunk at a time to the destination dataset. The data copy is done one destination chunk at a time to achieve chunk-aligned write.

Parameters

- **source** – The source h5py dataset
- **destination** – The h5py destination h5py dataset.
- **print_status** – Should the function print the status of the conversion process to the command line?

`create_optimized_chunking (chunks=None, compression=None, compression_opts=None, copy_data=True, print_status=False, flush_io=True)`

Helper function to allow one to create optimized copies of the dataset with different internal data layouts to speed up selections. The function expects that the original data has already been written to the data group. The function takes

Parameters

- **chunks** – Specify whether chunking should be used (True, False), or specify the chunk sizes to be used explicitly.
- **compression** – h5py compression option. Compression strategy. Legal values are ‘gzip’, ‘szip’, ‘lzf’. Can also use an integer in range(10) indicating gzip.
- **compression_opts** – h5py compression settings. This is an integer for gzip, 2-tuple for szip, etc.. For gzip (H5 deflate filter) this is the aggression parameter. The aggression parameter is a number between zero and nine (inclusive) to indicate the tradeoff between speed and compression ratio (zero is fastest, nine is best ratio).
- **copy_data** – Should the MSI data be copied by this function to the new dataset or not. If False, then it is up to the user of the function to copy the appropriate data into the returned h5py dataset (not recommended but may be useful for performance optimization).

- **print_status** – Should the function print the status of the conversion process to the command line?
- **flush_io** – Call flush on the HDF5 file to ensure all HDF5 bufferes are flushed so that all data has been written to file

Returns h5py dataset with the new copy of the data

get_h5py_datasets(index=0)

Get the h5py dataset object for the given dataset.

Parameters **index** – The index of the dataset.

Returns h5py object for the requested dataset.

Raises and Index error is generated in case an invalid index is given.

get_h5py_mzdata()

Get the h5py object for the mz datasets.

Returns h5py object of the requested mz dataset.

set_fill_space(fill_space)

Define whether spatial selection should be filled with 0's to retrieve full image slices

Parameters **fill_space** – Boolean indicating whether images should be filled with 0's

set_fill_spectra(fill_spectra)

Define whether spectra should be filled with 0's to map them to the global mz axis when retrieved.

Parameters **fill_spectra** – Define whether m/z values should be filled with 0's.

class omsi.dataformat.omsi_file.msidata.**omsi_msidata_manager**(*msidata_parent*)

Bases: *omsi.dataformat.omsi_file.common.omsi_file_object_manager*

MSI-data manager helper class used to define common functionality needed for msidata-related data. Usually, a class that defines a format that contains an omsi_file_msidata object will inherit from this class (in addition to omsi_file_common) to acquire the common features.

For more details see: *omsi.dataformat.omsi_file.omsi_common.omsi_file_object_manager*

Variables **msidata_parent** – The h5py.Group parent object containing the instrument object to be managed.

Initialize the manger object.

Parameters **msidata_parent** – The h5py.Group parent object for the msi data.

create_msidata_full_cube(data_shape, data_type='f', mzdata_type='f', chunks=None, compression=None, compression_opts=None, flush_io=True)

Create a new mass spectrometry imaging dataset for the given experiment written as a full 3D cube.

Parameters

- **data_shape** – Shape of the dataset. Eg. shape=(10,10,10) creates a 3D dataset with 10 entries per dimension
- **data_type** – numpy style datatype to be used for the dataset.
- **mzdata_type** – numpy style datatype to be used for the mz data array.
- **chunks** – Specify whether chunkning should be used (True,False), or specify the chunk sizes to be used in x,y, and m/z explicitly.
- **compression** – h5py compression option. Compression strategy. Legal values are ‘gzip’, ‘szip’, ‘lzf’. Can also use an integer in range(10) indicating gzip.

- **compression_opts** – h5py compression settings. This is an integer for gzip, 2-tuple for szip, etc.. For gzip (H5 deflate filter) this is the aggression parameter. The aggression parameter is a number between zero and nine (inclusive) to indicate the tradeoff between speed and compression ratio (zero is fastest, nine is best ratio).
- **flush_io** – Call flush on the HDF5 file to ensure all HDF5 bufferes are flushed so that all data has been written to file

Returns

The following two empty (but approbriately sized) h5py datasets are returned in order to be filled with data:

- **data_dataset** : Primary h5py dataset for the MSI data with shape **data_shape** and dtype **data_type**.
- **mz_dataset** : h5py dataset for the mz axis data with shape [data_shape[2]] and dtype **mzdata_type**.

Returns **data_group** : The h5py object with the group in the HDF5 file where the data should be stored.

```
create_msidata_partial_cube(data_shape, mask, data_type='f', mzdata_type='f',
                             chunks=None, compression=None, compression_opts=None,
                             flush_io=True)
```

Create a new mass spectrometry imaging dataset for the given experiment written as a partial 3D cube of complete spectra.

Parameters

- **data_shape** – Shape of the dataset. Eg. shape=(10,10,10) creates a 3D dataset with 10 entries per dimension
- **mask** – 2D boolean NumPy array used as mask to indicate which (x,y) locations have spectra associated with them.
- **data_type** – numpy style datatype to be used for the dataset.
- **mzdata_type** – numpy style datatype to be used for the mz data array.
- **chunks** – Specify whether chunkning should be used (True,False), or specify the chunk sizes to be used in x,y, and m/z explicitly.
- **compression** – h5py compression option. Compression strategy. Legal values are ‘gzip’, ‘szip’, ‘lzf’. Can also use an integer in range(10) indicating gzip.
- **compression_opts** – h5py compression settings. This is an integer for gzip, 2-tuple for szip, etc.. For gzip (H5 deflate filter) this is the aggression parameter. The aggression parameter is a number between zero and nine (inclusive) to indicate the tradeoff between speed and compression ratio (zero is fastest, nine is best ratio).
- **flush_io** – Call flush on the HDF5 file to ensure all HDF5 bufferes are flushed so that all data has been written to file

Returns

The following two empty (but approbriately sized) h5py datasets are returned in order to be filled with data:

- **data_dataset** : Primary h5py dataset for the MSI data with shape **data_shape** and dtype **data_type**.

- `mz_dataset` : h5py dataset for the mz axis data with shape [data_shape[2]] and dtype `mzdata_type`.

Returns

The following already complete dataset

- `xy_index_dataset` : This dataset indicates for each xy location to which index in `data_dataset` the location corresponds to. This dataset is needed to identify where spectra need to be written to.

Returns `data_group` : The h5py object with the group in the HDF5 file where the data should be stored.

```
create_msidata_partial_spectra(spectra_length, len_global_mz, data_type='f', mz-
                                data_type='f', chunks=None, compression=None, com-
                                pression_opts=None, flush_io=True)
```

Create a new mass spectrometry imaging dataset for the given experiment written as a partial 3D cube of partial spectra.

Parameters

- `spectra_length` – 2D boolean NumPy array used indicating for each (x,y) locations the length of the corresponding partial spectrum.
- `len_global_mz` – The total number of m/z values in the global m/z axis for the full 3D cube
- `data_type` – The dtype for the MSI dataset
- `mzdata_type` – The dtype for the mz dataset
- `mzdata_type` – numpy style datatype to be used for the mz data array.
- `chunks` – Specify whether chunkning should be used (True,False), or specify the chunk sizes to be used in x,y, and m/z explicitly.
- `compression` – h5py compression option. Compression strategy. Legal values are ‘gzip’, ‘szip’, ‘lzf’. Can also use an integer in range(10) indicating gzip.
- `compression_opts` – h5py compression settings. This is an integer for gzip, 2-tuple for szip, etc.. For gzip (H5 deflate filter) this is the aggression parameter. The aggression parameter is a number between zero and nine (inclusive) to indicate the tradeoff between speed and compression ratio (zero is fastest, nine is best ratio).
- `flush_io` – Call flush on the HDF5 file to ensure all HDF5 bufferes are flushed so that all data has been written to file

Returns

The following two empty (but approbriately sized) h5py datasets are returned in order to be filled with data:

- `data_dataset` : The primary h5py dataset for the MSI data with shape `data_shape` and dtype `data_type`.
- `mz_index_dataset` : h5py dataset with the `mz_index` values
- `mz_dataset` : h5py dataset for the mz axis data with shape [data_shape[2]] and dtype `mzdata_type`.

Returns

The following already complete dataset

- **xy_index_dataset** [This dataset indicates for each xy location at which index in data_dataset] the corresponding spectrum starts. This dataset is needed to identify where spectra need to be written to.

- **xy_index_end_dataset** [This dataset indicates for each xy location at which index in data_dataset] the corresponding spectrum ends (excluding the given value). This dataset is needed to identify where spectra need to be written to.

Returns data_group : The h5py object with the group in the HDF5 file where the data should be stored.

get_msidata(data_index, fill_space=True, fill_spectra=True, preload_mz=True, preload_xy_index=True)

Get the dataset with the given index for the given experiment.

For more detailed information about the use of the fill_space and fill_spectra and preload_mz and preload_xy_index options, see the init function of omsi.dataformat.omsi_file_msidata.

Parameters

- **data_index** (*unsigned int*) – Index of the dataset.
- **fill_space** – Define whether the data should be padded in space (filled with 0's) when accessing the data using [...] operator so that the data behaves like a 3D cube.
- **fill_spectra** – Define whether the spectra should completed by adding 0's so that all spectra retrived via the [...] opeator so that always spectra of the full length are returned.
- **preload_mz** – Should the data for the mz axis be kept in memory or loaded on the fly when needed.
- **preload_xy_index** – Should the xy index (if available) be preloaderd into memory or should the required data be loaded on the fly when needed.

Returns omsi_file_msidata object for the given data_index or None in case the data with given index does not exist or the access failed for any other reason.

get_msidata_by_name(data_name)

Get the h5py data object for the the msidata with the given name.

Parameters data_name (*string*) – The name of the dataset

Returns h5py object of the dataset or None in case the dataset is not found.

get_num_msidata()

Get the number of raw mass spectrometry images stored for a given experiment

Returns Integer indicating the number of msi datasets available for the experiment.

analysis Module

Module for managing custom analysis data in OMSI HDF5 files.

class omsi.dataformat.omsi_file.analysis.**omsi_analysis_manager**(analysis_parent)

Bases: *omsi.dataformat.omsi_file.common.omsi_file_object_manager*

Analysis manager helper class used to define common functionality needed for analysis-related data. Usually, a class that defines a format that contains an omsi_file_analysis object will inherit from this class (in addition to omsi_file_common) to acquire the common features.

For more details see: *omsi.dataforamt.omsi_file.omsi_common.omsi_file_object_manager*

Variables `analysis_parent` – The h5py.Group parent object containing the instrument object to be managed.

create_analysis (`analysis`, `flush_io=True`, `force_save=False`, `save_unsaved_dependencies=True`,
`mpi_root=0`, `mpi_comm=None`)

Add a new group for storing derived analysis results for the current experiment

Create the analysis group using `omsi_file_analysis.__create__` which in turn uses `omsi_file_analysis.__populate_analysis__(...)` to populate the group with the appropriate data.

NOTE: Dependencies are generally resolved to point to file objects. However, if `save_unsaved_dependencies` is set to False and a given in-memory dependency has not been saved yet, then the value associated with that dependency will be saved instead as part of the parameters and, hence, only the value of the dependency is persevered in that case and not the full dependency chain.

NOTE: Dependencies if they only exists in memory are typically saved recursively unless `save_unsaved_dependencies` is set to False. I.e., calling `create_analysis` may result in the creating of multiple other dependent analyses if they have not been saved before.

Parameters

- **analysis** (`omsi.analysis.analysis_base:`) – Instance of `omsi.analysis.analysis_base` defining the analysis
- **flush_io** (`bool`) – Call flush on the HDF5 file to ensure all HDF5 bufferes are flushed so that all data has been written to file
- **force_save** (`bool`) – Should we save the analysis even if it has been saved in the same location before? If `force_save` is False (default) and the `self.omsi_analysis_storage` parameter of the analysis object contains a matching storage location—i.e., same file and experiment—, then the analysis will not be saved again, but the object will only be retrieved from file. If `force_save` is True, then the analysis will be saved either way and the `self.omsi_analysis_storage` parameter will be extended.
- **save_unsaved_dependencies** (`bool`) – If there are unsaved (in-memory) dependencies, then should those be saved to file as well? Default value is True, i.e., by default all in-memory dependencies that have not been saved yet, i.e., for which the `self.omsi_analysis_storage` of the corresponding **omsi_analysis** base object is empty, are saved as well. If in-memory dependencies have been saved before, then a link to those dependencies will be established, rather than re-saving the dependency.
- **mpi_root** – The root MPI process that should perform the writing. This is to allow all analyses to call the function and have communication in the `analysis.write_analysis_data` function be handled.
- **mpi_comm** – The MPI communicator to be used. None if default should be used (ie., `MPI.COMM_WORLD`)

Returns The `omsi_file_analysis` object for the newly created analysis group and the integer index of the analysis. NOTE: if `force_save` is False (default), then the group returned may not be new but may be simply the first entry in the list of existing storage locations for the given analysis. NOTE: If we are in MPI parallel and we are on a core that does not write any data, then None is returned instead.

static create_analysis_static (`analysis_parent`, `analysis`, `flush_io=True`, `force_save=False`,
`save_unsaved_dependencies=True`, `mpi_root=0`,
`mpi_comm=None`)

Same as `create_analysis(...)` but instead of relying on object-level, this function allows additional parameters (specifically the `analysis_parent`) to be provided as input, rather than being determined based on `self`

Parameters

- **analysis_parent** – The h5py.Group object or omsi.dataformat.omsi_file.common.omsi_file_common object where the analysis should be created
- **kwargs** – Additional keyword arguments for create_analysis(...). See create_analysis(...) for details.

Returns The output of create_analysis

get_analysis(analysis_index)

Get the omsi_format_analysis analysis object for the experiment with the given index.

Parameters **analysis_index** (*Unsigned integer*) – The index of the analysis

Returns omsi_file_analysis object for the requested analysis. The function returns None in case the analysis object was not found.

get_analysis_by_identifier(analysis_identifier_string)

Get the omsi_format_analysis analysis object for the the analysis with the given identifier.

Parameters **analysis_identifier_string** (*string*) – The string used as identifier for the analysis.

Returns h5py obejct of the analysis or None in case the analysis is not found.

get_analysis_identifiers()

Get a list of all identifiers for all analysis stored for the experiment

Returns List of strings of analysis identifiers.

get_num_analysis()

Get the number of raw mass spectrometry images stored for a given experiment

Returns Integer indicating the number of analyses available for the experiment.

class omsi.dataformat.omsi_file.analysis.omsi_file_analysis(analysis_group)

Bases: *omsi.dataformat.omsi_file.dependencies.omsi_dependencies_manager*,
omsi.dataformat.omsi_file.common.omsi_file_common

Class for managing analysis specific data in omsi hdf5 files

Initialize the analysis object given the h5py object of the analysis group.

Parameters **analysis_group** – The h5py object with the analysis group of the omsi hdf5 file.

get_all_analysis_data(load_data=False)

Get all analysis data associated with the analysis.

Parameters **load_data** – load_data: Should the data be loaded or just the h5py objects be stored in the dictionary.

Returns List of analysis_data objects with the names and h5py or numpy objects. Access using [index][‘name’] and [index][‘data’].

get_all_parameter_data(load_data=False, exclude_dependencies=False)

Get all parameter data associated with the analysis.

Parameters **load_data** – Should the data be loaded or just the h5py objects be stored in the dictionary.

Returns List of parameter_data objects with names and h5py or numpy object. Access using [index][‘name’] and [index][‘data’].

get_all_runinfo_data(*load_data=False*)

Get a dict of all runtime information stored in the file

Returns omsi.shared.run_info_data.run_info_dict type python dict with the runtime information restored.

get_analysis_data_names()

This function returns all dataset names (and groups) that are custom to the analysis, i.e., that are not part of the omsi file standard.

Returns List of analysis-specific dataset names.

get_analysis_data_shapes_and_types()

This function returns two dictionaries with all dataset names (and groups) that are custom to the analysis, i.e., that are not part of the omsi file standard, and identifies the shape of the analysis data objects.

Returns Dictionary indicating for each analysis-specific dataset its name (key) and shape (value).
And a second dictionary indicating the name (key) and dtype of the dataset.

get_analysis_identifier()

Get the identifier name of the analysis.

Use get_analysis_identifier() [...] to retrieve the identifier string.

Returns h5py object for the dataset with the identifier string. Returns None, in case no identifier exists. This should not be the case for a valid OpenMSI file.

get_analysis_index()

Based on the name of the group, get the index of the analysis.

Returns Integer index of the analysis in the file.

get_analysis_type()

Get the type for the analysis.

Use get_analysis_type() [...] to retrieve the type string.

Returns h5py object with the dataset of the analysis string. Returns, None in case no analysis type exists. This should not be the case in a valid omsi file.

recreate_analysis(**kwargs)

Load an analysis from file and re-execute it. This is equivalent to omsi_analysis.base.restore_analysis().execute()

Parameters **kwargs** – Additional keyword arguments to be passed to the execute function of the analysis

Returns Instance of the specific analysis object (e.g., omsi_nmf) that inherits from omsi.analysis.analysis_base with the input parameters and dependencies restored from file. The output, however, is the result from re-executing the analysis. None is returned in case the analysis object cannot be created.

restore_analysis(*load_data=True*, *load_parameters=True*, *load_runtime_data=True*, *dependencies_omsi_format=True*)

Load an analysis from file and create an instance of the appropriate analysis object defined by the analysis type (i.e., a derived class of *omsi.analysis.analysis_base*)

Parameters

- **load_data** – Should the analysis data be loaded from file (default) or just stored as h5py data objects
- **load_parameters** – Should parameters be loaded from file (default) or just stored as h5py data objects.

- **load_runtime_data** – Should runtime data be loaded from file (default) or just stored as h5py data objects.
- **dependencies_omsi_format** – Should dependencies be loaded as omsi_file API objects (default) or just as h5py objects.

Returns Instance of the specific analysis object (e.g, omsi_nmf) that inherits from omsi.analysis.analysis_base with the input parameters, output result, and dependencies restored. We can call execute(..) on the returned object to rerun an analysis. May return analysis_generic in case that the specific analysis is not known.

dependencies Module

Base module for managing of dependencies between data in OpenMSI HDF5 files

class omsi.dataformat.omsi_file.dependencies.**omsi_dependencies_manager**(*dependencies_parent*)
Bases: *omsi.dataformat.omsi_file.common.omsi_file_object_manager*

Dependencies manager helper class used to define common functionality needed for managing dependencies. Usually, a class that defines a format that contains an omsi_file_dependencies object will inherit from this class (in addition to omsi_file_common) to acquire the common features.

For more details see: *omsi.dataformat.omsi_file.omsi_common.omsi_file_object_manager*

Variables

- **dependencies_parent** – h5py.Group object containing the dependencies object(s) to be managed
- **dependencies** – omsi_file_dependencies object managed by this object or None

Parameters **dependencies_parent** – Parent group containing the dependencies object to be managed

add_dependency(*dependency*, *flush_io=True*)

Create a new dependency for this dataset

Parameters

- **dependency** – omsi.shared.dependency_dict object describing the data dependency
- **flush_io** – Call flush on the HDF5 file to ensure all HDF5 bufferes are flushed so that all data has been written to file

Returns omsi_file_dependencydata object with the dependency data or None in case that an error occurred and the dependency has not been generated.

create_dependencies(*dependencies_data_list=None*)

Create a managed group for storing data dependencies if none exists and store the given set of dependencies in it. If a self.dependencies object already exists, then the given dependencies will be added.

This is effectively a shortcut to omsi_file_dependencies.__create__(...) with specific settings for the current dependencies object managed by self.

Parameters **dependencies_data_list** – List of dependency_dict objects to be stored as dependencies. Default is None which is mapped to an empty list []

Returns omsi_file_dependencies object created by the function.

get_all_dependency_data(*omsi_dependency_format=True*)

Get all direct dependencies associated with the data object.

This is convenience function providing access to self.dependencies.get_all_dependency_data(...) which is a function of omsi_file_dependencies class.

Parameters omsi_dependency_format – Should the dependencies be retrieved as omsi_analysis_dependency object (True) or as an omsi_file_dependencydata object (False).

Returns List dependency_dict objects containing either omsi file API objects or h5py objects for the dependencies. Access using [index]['name'] and [index]['data'].

```
get_all_dependency_data_graph(include_omsi_dependency=False,           in-
                               include_omsi_file_dependencydata=False,      re-
                               recursive=True,          level=0,         name_key='name',
                               prev_nodes=None,        prev_links=None,    par-
                               parent_index=None,      metadata_generator=None,   meta-
                               data_generator_kwarg=None)
```

Get all direct and indirect dependencies associated with the analysis in form of a graph describing all nodes and links in the provenance hierarchy.

This is convenience function providing access to self.dependencies.get_all_dependency_data_graph(...) which is a function of omsi_file_dependencies class.

Parameters

- **include_omsi_dependency** – Should the dependency_dict object be included in the entries in the nodes dict?
- **include_omsi_file_dependencydata** – Should the omsi_file_dependencydata object be included in the entries in the nodes dict?
- **recursive** – Should we trace dependencies recursively to construct the full graph, or only the direct dependencies. Default true (ie., trace recursively)
- **name_key** – Which key should be used in the dicts to indicate the name of the object? Default value is ‘name’
- **level** – Integer used to indicated the recursion level. Default value is 0.
- **prev_nodes** – List of nodes that have been previously generated. Note, this list will be modified by the call. Note, each node is represented by a dict which is expected to have at least the following keys defined, path, name_key, level (name_key refers to the key defined by the input parameter name_key).
- **prev_links** – Previously established links in the list of nodes. Note, this list will be modified by the call.
- **parent_index** – Index of the parent node in the list of prev_nodes for this call.
- **metadata_generator** – Optional parameter. Pass in a function that generates additional metadata about a given omsi API object. Note, the key’s level and path and name (i.e., name_key) are already set by this function. The metadata_generator may overwrite these key’s, however, the path has to be unique as it is used to identify duplicate nodes. Overwriting the path with a non-unique value, hence, will lead to errors (missing entries) when generating the graph. Note, the metadata_generator function needs to support the following keyword arguments:
 - inDict : The dictionary to which the metadata should be added to.
 - obj : The omsi file API object for which metadata should be generated
 - name : A qualifying name for the object
 - name_key : The key to be used for storing the name

- **metadata_generator_kwargs** – Dictionary of additional keyword arguments that should be passed to the metadata_generator function.

Returns

Dictionary containing two lists. 1) nodes [List of dictionaries, describing the elements] in the dependency graph. 2) links : List of tuples with the links in the graph. Each tuple consists of two integer indices for the nodes list. For each node the following entries are given:

- **dependency_dict**: Optional key used to store the corresponding dependency_dict object.
Used only if include_omsi_dependency is True.
- **omsi_file_dependencydata**: Optional key used to store the corresponding omsi_file_dependencydata object. Used only if include_omsi_file_dependencydata is True.
- name : Name of the dependency. The actual key is specified by name_key
- level : The recursion level at which the object occurs.
- ... : Any other key/value pairs from the dependency_dict dict.

get_all_dependency_data_recursive (*omsi_dependency_format=True*,
omsi_main_parent=None, *dependency_list=None*)

Get all direct and indirect dependencies associated with the data object.

This is convenience function providing access to self.dependencies.get_all_dependency_data_recursive(...) which is a function of omsi_file_dependencies class.

NOTE: omsi_main_parent and omsi_main_parent are used primarily to ensure that the case of circular dependencies are supported properly. Circular dependencies may occur in the case of semantic dependencies (rather than pure use dependencies), e.g., two datasets that are related modalities may reference each other, e.g., MS1 pointing to related MS2 data and the MS2 datasets referencing the corresponding MS1 datasets.

Parameters

- **omsi_dependency_format** – Should the dependencies be retrieved as dependency_dict object (True) or as an omsi_file_dependencydata object (False)
- **omsi_main_parent** – The main parent for which the dependencies are calculated. This is needed to avoid recursion back into the main parent for which we are computing dependencies and avoiding that it is added itself as a dependency for itself. If set to None, then we will use our own self.dependencies_parent object
- **dependency_list** – List of previously visited/created dependencies. This is needed only to avoid deep recursion and duplication due to circular dependencies

Returns List analysis_data objects containing either omsi file API interface objects or h5py objects for the dependcies. Access using [index]['name'] and [index]['data'].

has_dependencies()

Check whether any dependencies exists for this datasets

class omsi.dataformat.omsi_file.dependencies.**omsi_file_dependencies** (*dependencies_group*)
Bases: *omsi.dataformat.omsi_file.common.omsi_file_common*

Class for managing collections of dependencies.

** Use of super()**

This class inherits from `omsi.dataformat.omsi_file.common.omsi_file_common`. Consistent with the design pattern for multiple inheritance of the `omsi.dataformat.omsi_file` module, the `__init__` function calls `super(...).__init__(manager_group)` with a single parameter indicating the parent group.

```
static _omsi_file_dependencies__create_dependency_graph_node(level,      name,
                                                               path,       depen-
                                                               dency_object,
                                                               omsi_object, in-
                                                               clude_omsi_dependency=False,
                                                               in-
                                                               clude_omsi_file_dependencydata=False,
                                                               name_key='name',
                                                               meta-
                                                               data_generator=None,
                                                               meta-
                                                               data_generator_kwarg=None)
```

Internal helper function used to create a new node in the graph

Parameters

- **level** – The recursion level at which the node exists
- **name** – The name of the node
- **path** – The path of the node
- **dependency_object** – The omsi_file_dependencydata object. May be None in case a node to a specific object is set
- **omsi_object** – The OpenMSI file API object. This is required and may NOT be None.
- **include_omsi_dependency** – Should the dependency_dict object be included in the entries in the nodes dict?
- **include_omsi_file_dependencydata** – Should the omsi_file_dependencydata object be included in the entries in the nodes dict?
- **name_key** – Which key should be used in the dicts to indicate the name of the object? Default value is ‘name’
- **metadata_generator** – Optional parameter. Pass in a function that generates additional metadata about a given omsi API object. Note, the key’s level and path and name (i.e., name_key) are already set by this function. The metadata_generator may overwrite these key’s, however, the path has to be unique as it is used to identify duplicate nodes. Overwriting the path with a non-unique value, hence, will lead to errors (missing entries) when generating the graph. Note, the metadata_generator function needs to support the following keyword arguments:
 - `in_dict` : The dictionary to which the metadata should be added to.
 - `obj` : The omsi file API object for which metadata should be generated
 - `name` : A qualifying name for the object
 - `name_key` : The key to be used for storing the name
- **metadata_generator_kwarg** – Dictionary of additional keyword arguments that should be passed to the metadata_generator function.

Returns Dict describing the new node, containing the ‘name’, ‘level’, and ‘path’ and optionally ‘dependency_dict’ and/or ‘omsi_file_dependencydata’ and any additional data generated by the metadata_generator function

add_dependency(dependency_data)

Add a new dependency to the collection.

Parameters **dependency_data** (*omsi.shared.omsi_dependency_data*) – The analysis dependency specification.

Returns the newly created omsi_file_dependencydata object

Raises KeyError in case that a dependency with the same name already exists

get_all_dependency_data(*omsi_dependency_format=True*)

Get all direct dependencies associated with the analysis.

Parameters **omsi_dependency_format** – Should the dependencies be retrieved as omsi_analysis_dependency object (True) or as an omsi_file_dependencydata object (False).

Returns List dependency_dict objects containing either omsi file API objects or h5py objects for the dependencies. Access using [index]['name'] and [index]['data'].

get_all_dependency_data_graph(*include_omsi_dependency=False*,
include_omsi_file_dependencydata=False,
cursive=True,
level=0,
name_key='name',
prev_nodes=None,
prev_links=None,
parent_index=None,
metadata_generator=None,
meta-data_generator_kwarg=None)

Get all direct and indirect dependencies associated with the analysis in form of a graph describing all nodes and links in the provenance hierarchy.

Parameters

- **include_omsi_dependency** – Should the dependency_dict object be included in the entries in the nodes dict?
- **include_omsi_file_dependencydata** – Should the omsi_file_dependencydata object be included in the entries in the nodes dict?
- **recursive** – Should we trace dependencies recursively to construct the full graph, or only the direct dependencies. Default true (ie., trace recursively)
- **name_key** – Which key should be used in the dicts to indicate the name of the object? Default value is ‘name’
- **level** – Integer used to indicated the recursion level. Default value is 0.
- **prev_nodes** – List of nodes that have been previously generated. Note, this list will be modified by the call. Note, each node is represented by a dict which is expected to have at least the following keys defined, path, name_key, level (name_key refers to the key defined by the input parameter name_key).
- **prev_links** – Previously established links in the list of nodes. Note, this list will be modified by the call.
- **parent_index** – Index of the parent node in the list of prev_nodes for this call. May be None in case the parent we are calling this function for is not yet in the list. If None, then we will add our own parent that contains the dependencies to the list.
- **metadata_generator** – Optional parameter. Pass in a function that generates additional metadata about a given omsi API object. Note, the key’s level and path and name (i.e., name_key) are already set by this function. The metadata_generator may overwrite these key’s, however, the path has to be unique as it is used to identify duplicate nodes. Overwriting the path with a non-unique value, hence, will lead to errors (missing entries) when generating the graph. Note, the metadata_generator function needs to support the following keyword arguments:

- `in_dict` : The dictionary to which the metadata should be added to.
- `obj` : The omsi file API object for which metadata should be generated
- `name` : A qualifying name for the object
- `name_key` : The key to be used for storing the name
- `metadata_generator_kwargs` – Dictionary of additional keyword arguments that should be passed to the `metadata_generator` function.

Returns

Dictionary containing two lists. 1) `nodes` [List of dictionaries, describing the elements] in the dependency graph. 2) `links` : List of tuples with the links in the graph. Each tuple consists of two integer indices for the nodes list. For each node the following entries are given:

- **dependency_dict**: **Optional key used to store the corresponding dependency_dict object.**
Used only if `include_omsi_dependency` is True.
- **omsi_file_dependencydata**: **Optional key used to store the corresponding omsi_file_dependencydata object.** Used only if `include_omsi_file_dependencydata` is True.
- `name` : Name of the dependency. The actual key is specified by `name_key`
- `level` : The recursion level at which the object occurs.
- `path` : The full path to the object
- `filename` : The full path to the file
- ... : Any other key/value pairs from the `dependency_dict` dict.

get_all_dependency_data_recursive (`omsi_dependency_format=True`,
`omsi_main_parent=None`, `dependency_list=None`)

Get all direct and indirect dependencies associated with the analysis.

NOTE: `omsi_main_parent` and `omsi_main_parent` are used primarily to ensure that the case of circular dependencies are supported properly. Circular dependencies may occur in the case of semantic dependencies (rather than pure use dependencies), e.g., two datasets that are related modalities may reference each other, e.g., MS1 pointing to related MS2 data and the MS2 datasets referencing the corresponding MS1 datasets.

Parameters

- **omsi_dependency_format** – Should the dependencies be retrieved as dependency_dict object (True) or as an omsi_file_dependencydata object (False)
- **omsi_main_parent** – The main parent for which the dependencies are calculated. This is needed to avoid recursion back into the main parent for which we are computing dependencies and avoiding that it is added itself as a dependency for itself. If set to None, then we will use the omsi_object associated with the parent group of the dependency group.
- **dependency_list** – List of previously visited/created dependencies. This is needed only to avoid deep recursion and duplication due to circular dependencies

Returns List `analysis_data` objects containing either omsi file API interface objects or h5py objects for the dependencies. Access using `[index]['name']` and `[index]['data']`.

get_dependency_omsiobject (`name, recursive=True`)

Get the omsi file API object corresponding to the object the dependency is pointing to.

Parameters

- **name** – Name of the dependency object to be loaded .
- **recursive** – Should the dependency be resolved recursively, i.e., if the dependency points to another dependencies. Default=True.

Returns An omsi file API object (e.g., omsi_file_analysis or omsi_file_msidata) if the link points to a group or the h5py.Dataset the link is pointing to.

`get_omsi_file_dependencydata(name)`

Retrieve the omsi_file_dependencydata object for the dependency with the given name.

class omsi.dataformat.omsi_file.dependencies.**omsi_file_dependencydata**(dependency_group)
Bases: [omsi.dataformat.omsi_file.common.omsi_file_common](#)

Class for managing data groups used for storing data dependencies

Create a new omsi_file_dependencydata object for the given h5py.Group

Parameters **dependency_group** (*h5py.Group with a corresponding omsi type*) – h5py.Group object with the dependency data

`get_dataset_name()`

Get the string indicating the name of dataset. This may be empty as it is only used if the dependency points to an object within a managed omsi API object.

Returns String indicating the name of the optional dataset.

`get_dependency_objecttype(recursive=True)`

Indicated the type of the object the dependency is pointing to.

Parameters **recursive** – Should dependencies be resolved recursively, i.e., if the dependency points to another dependencies. Default=True.

Returns String indicating the class of the omsi file API class that is suited to manage the dependency link or the name of the corresponding h5py class.

`get_dependency_omsiobject(recursive=True, external_mode=None)`

Get the omsi file API object corresponding to the object the dependency is pointing to.

Parameters

- **recursive** – Should dependencies be resolved recursively, i.e., if the dependency points to another dependencies. Default=True.
- **external_mode** – The file open mode (e.g., ‘r’, ‘a’) to be used when we encounter external dependencies, i.e., dependencies that are stored in external files. By default this is set to None, indicating that the same mode should be used in which this (i.e., the current file describing the dependency) was opened. Allowed modes are ‘r’, ‘r+’, and ‘a’. The modes ‘w’, ‘w+’, ‘x’ are prohibited to ensure that we do not break external files.

Returns An omsi file API object (e.g., omsi_file_analysis or omsi_file_msidata) if the link points to a group or the h5py.Dataset the link is pointing to.

`get_dependency_type()`

Get the string describing the type of the dependency

NOTE: If the type is missing in the file but we have a parameter name specified, then the default type ‘parameter’ will be returned other None is returned.

Returns String indicating the type of the dependency or None if the type is not known.

```
get_link_name()
    Get the name of the dependency link

    Returns String indicating the name of the dependency link.

get_mainname()
    Get the main name string describing the name of the object (and possibly path of the file if external)

    Returns String indicating the main name of the object that we link to

get_omsi_dependency()
    Get the dependency information as an omsi.shared.dependency_dict object (as defined in the
    omsi.shared.dependency_dict module)

    Returns dependency_dict object with all the dependency data.

get_parameter_help()
    Get the help string for the parameter name if available.

get_parameter_name()
    Get the string indicating the name of the dependend parameter of the analysis.

    Returns String of the parameter name that has the dependency.

get_selection_string()
    String indicating the applied selection. This is an empty string in case no selection was applied.

    Returns Selection string. See the omsi.shared.omsi_data_selection for helper functions to deal
    with selection strings.
```

file_reader_base Module

Module for base classes for implementation and integration of third-party file readers.

ToDo:

- get_number_of_regions(...) should be updated to return a list of regions, one per dataset
- Need to add base class for multi dataset formats
- Need to add base class for multi dataset+region formats
- Need to implement new file format for combined raw data file (ie., multiple raw files in one folder).

```
class omsi.dataformat.file_reader_base.file_reader_base(basename,                                re-
                                                               requires_slicing=True)
Bases: object
```

Base-class used to define the basic interface that file-readers for a new format need to implement.

__init__ interface:

To avoid the need for custom code subclasses should be able to be constructed by providing just the basename parameter and optional requires_slicing parameter. If additional inputs are needed, then file conversion and management scripts may need to be modified to account for the custom requirements. **Required Attributes:**

Variables

- **data_type** – String indicating the data type to be used (e.g., uint16)
- **shape** – Tuple indicating the shape of the data
- **mz** – Numpy array with the m/z axis data. In the case of multi-data this is a list of numpy arrays, one per dataset.

- **basename** – The basename provided for opening the file.

Required Interface Functions:

- `close_file` : Close any opened files
- `is_valid_dataset` : Check whether a given dir/file is valid under the current format
- `spectrum_iter` : Generator function that iterates over all the spectra in the current data cube and yield the numpy array with the intensity and integer x, y position of the spectrum

Optional Interface Functions:

- `__getitem__` [Implement array slicing for files. Required if the `requires_slicing` parameter] should be supported.
- `supports_regions` : Specify whether the format supports multiple regions (default=False)
- `supports_multidata`: Specify whether the format supports multiple datasets (default=False)
- `supports_multiexperiment`: Specify whether the format supports multiple experiments (default=False)

Construct the base class and define required attributes.

Parameters

- **basename** – The name of the file or directory with the file to be opened by the reader
- **requires_slicing** – Boolean indicating whether the user requires array slicing via the `__getitem__` function to work or not. This is an optimization, because many MSI data formats do not easily support arbitrary slicing of data but rather only iteration over spectra.

static available_formats()

Get dictionary of all available file formats that implement the `file_format_base` API.

Returns Dictionary where the keys are the names of the formats and the values are the corresponding file reader classes.

close_file()

Close the file.

classmethod format_name()

Define the name of the format.

Returns String indicating the name of the format.

get_dataset_metadata()

Get dict of additional metadata associated with the current dataset

NOTE: In the case that multiple regions and/or datasets are supported, this function should return the metadata of the currently selected dataset only. If no particular dataset is selected, then all should be returned.

Returns Instance of `omsi.shared.metadata_data.metadata_dict`

get_number_of_datasets()

File readers with multi dataset support must overwrite this function to retrieve the true number of raw datasets in the file. Default implementation returns 1.

get_number_of_regions()

File readers with multi region support must overwrite this function to retrieve the true number of regions in the file. Default implementation returns 1.

classmethod `is_valid_dataset` (*name*)

Classmethod used to check whether a given directory (or file) defines as valid data file of the file format specified by the current child class

Parameters `name` (*String*) – Name of the dir or file.

Returns Boolean indicating whether the given file or folder is a valid file.

classmethod `size` (*name*)

Classmethod used to check the estimated size for the given file/folder.

Parameters `name` (*String*) – Name of the dir or file.

Returns Integer indicating the size in byte or None if unknown.

classmethod `spectrum_iter` ()

Enable iteration of the spectra of the current data cube.

Iterate over all the spectra in the current data cube and yield the numpy array with the intensity and integer x, y position of the spectrum.

NOTE: As this is a generator one needs to use yield.

Returns

The function yields for each spectrum the following information:

- tuple of (x,y) or (x,y,z) position of the spectrum
- Numpy array with the spectrum

classmethod `supports_multidata` ()

Define whether the file format support multiple independent datasets.

classmethod `supports_multiexperiment` ()

Define whether the file format supports multiple independent experiments, each of which may contain multiple datasets.

classmethod `supports_regions` ()

Define whether the file format support multiple regions.

class `omsi.dataformat.file_reader_base.file_reader_base_multidata` (*basename*, *requires_slicing*)
Bases: `omsi.dataformat.file_reader_base.file_reader_base`

Base-class used to define the basic interface for file-readers used to implement new file formats with support for multiple dataset (e.g, MSI dataset with multiple spectrum types). This class extends `file_reader_base`, and accordingly all required attributes and functions of `file_reader_base` must be implemented by subclasses.

In addition to the `file_reader_base` functions we need to implement the `get_number_of_datasets(...)` and `get_dataset_dependencies(...)` functions.

Variables `select_dataset` – Unsigned integer indicating the currently selected dataset

Construct the base class and define required attributes.

get_dataset_dependencies ()

Get the dependencies between the current dataset and any of the other datasets stored in the current file. If `self.select_dataset` is not set, then the function is expected to return a list of lists with all dependencies for all datasets.

Returns

List of dependencies (or list of lists of dependencies if `self.select_dataset` is None) where each dependency is a dict of the following form:

- ‘omsi_object’: None, # The omsi file API object where the data is stored. Often None.
- ‘link_name’: ms2_link_name, # Name for the dependency link to be used
- ‘basename’: basename, # Basename of the file
- ‘region’: None, # Index of the region in the dataset or None
- ‘dataset’: ind2, # Index of the dataset within the file or None
- ‘help’:scan_types[ms1scan], # Help describing the dependency
- dependency_type’: ... } # Type of dependency see dependency_dict.dependency_type for available types

get_number_of_datasets()

Get the number of available datasets.

set_dataset_selection(dataset_index)

Define the current dataset to be read.

classmethod supports_multidata()

Define whether the file format supports multiple data blocks.

```
class omsi.dataformat.file_reader_base.file_reader_base_with_regions(basename,  
                                         re-  
                                         quires_slicing)
```

Bases: *omsi.dataformat.file_reader_base.file_reader_base*

Base-class used to define the basic interface for file-readers used to implement new file formats with support for multiple imaging regions per file. This class extends file_reader_base, and accordingly all required attributes and functions of file_reader_base must be implemented by subclasses.

Additional required attributes:

- select_region : Integer indicating which region should be selected. If set to None, indicates that the data should be treated as a whole. If set to a region index, then the data should be treated by the reader as if it only pertains to that region, ie., the shape of the data should be set accordingly and __getitem__ should behave as such as well.
- region_dicts : List of dictionaries, where each dictionary describes a given region (e.g., the origin and extend for rectangular regions).

Construct the base class and define required attributes.

get_dataset_dependencies()

Get the dependencies between the current region and any of the other region datasets stored in the current file. If self.select_region is not set, then the function is expected to return a list of lists with all dependencies for all datasets.

Returns

List of dependencies (or list of lists of dependencies if self.select_dataset is None) where each dependency is a dict of the following form:

- ‘omsi_object’: None, # The omsi file API object where the data is stored. Often None.
- ‘link_name’: ms2_link_name, # Name for the dependency link to be used
- ‘basename’: basename, # Basename of the file
- ‘region’: None, # Index of the region in the dataset or None
- ‘dataset’: ind2, # Index of the dataset within the file or None
- ‘help’:scan_types[ms1scan], # Help describing the dependency

- dependency_type': ... } # Type of dependency see dependency_dict.dependency_type for available types

get_number_of_regions()
Get the number of available regions

get_region_selection()
Get the index of the selected region

get_regions()
Get list of all region dictionaries defining for each region the origin and extend of the region. See also self.region_dicts.

set_region_selection(region_index=None)
Define which region should be selected for local data reads.

Parameters region_index – The index of the region that should be read. The shape of the data will be adjusted accordingly. Set to None to select all regions and treat the data as a single full 3D image.

classmethod supports_regions()
Define whether the file format support multiple regions.

img_file Module

This module provides functionality for reading img mass spectrometry image files

```
class omsi.dataformat.img_file.img_file(hdr_filename=None, t2m_filename=None,
                                         img_filename=None, basename=None, requires_slicing=True)
Bases: omsi.dataformat.file_reader_base.file_reader_base
```

Interface for reading a single 2D img file

The img format consists of three different files: i) hdr header file, ii) t2m which contains the m/z data, iii) img data file.

Open an img file for data reading.

Parameters

- **hdr_filename** (*string*) – The name of the hdr header file
- **t2m_filename** (*string*) – The name of the t2m_filename
- **img_filename** (*string*) – The name of the img data file
- **basename** (*string*) – Instead of img_filename, t2m_filename, and hdr_filename one may also supply just a single basename. The basename is completed with the .img, .t2m, .hdr extension to load the data.
- **requires_slicing** (*Boolean*) – Unused here. Slicing is always supported by this reader.

Raises ValueError In case that basename and hdr_filename, t2m_filename, and img_filename are specified.

```
close_file()
Close the img file
```

classmethod get_files_from_dir(dirname)

Get a list of all basenames of all img files in a given directory. Note: The basenames include the dirname.

classmethod `is_valid_dataset` (*name*)

Check whether the given file or directory points to a img file.

Parameters `name` (*unicode*) – Name of the dir or file.

Returns Boolean indicating whether the given file or folder is a valid img file.

classmethod `size` (*name*)

Classmethod used to check the estimated size for the given file/folder.

Parameters `name` (*unicode*) – Name of the dir or file.

Returns Integer indicating the size in byte or None if unknown.

class `spectrum_iter` ()

Enable iteration over the spectra in the file

Returns tuple of ((*x* , *y*) , intensities), i.e., the tuple of (*x*, *y*) integer index of the spectrum and the numpy array of the intensities

mzml_file Module

This module provides functionality for reading mzml mass spectrometry image files.

`filename = '/Users/oruebel/Devel/openmsi-data/mzML_Data/N2A2_Serratia_spots_extract_TI.mzML'`

class `omsi.dataformat.mzml_file.mzml_file` (*basename*, *requires_slicing=True*, *resolution=5*)
Bases: `omsi.dataformat.file_reader_base.file_reader_base_multidata`

Interface for reading a single 2D mzml file with several distinct scan types.

Variables `available_mzml_types` – Dict of available mzml flavors.

Open an img file for data reading.

Parameters

- **basename** (*string*) – The name of the mzml file. If basename is a directory, then the first mzML file found in the directory will be used instead.
- **requires_slicing** (*bool*) – Should the complete data be read into memory (this makes slicing easier). (default is True)
- **resolution** (*float*) – For profile data only, the minimum m/z spacing to use for creating the “full” reprofiled data cube

_mzml_file__compute_coordinates ()

Internal helper function used to compute the coordinates for each scan.

Returns 2D numpy integer array of shape (numScans,2) indicating for each scan its x and y coordinate

classmethod _mzml_file__compute_filetype (*filename*)

Internal helper function used to compute the filetype.

classmethod _mzml_file__compute_mz_axis (*filename*, *mzml_filetype*, *scan_types*, *resolution*)

Internal helper function used to compute the mz axis of each scantype Returns a list of numpy arrays

static _mzml_file__compute_num_scans (*filename=None*)

Internal helper function used to compute the number of scans in the mzml file.

static _mzml_file__compute_scan_dependencies (*scan_types=None*, *basename=None*)

Takes a scan_types list and returns a list of tuples (x, y) indicating that scan_type[y] depends on scan_type[x]

```
_mzml_file__compute_scan_types_and_indices (filename=None)
    Internal helper function used to compute a list of unique scan types in the mzml file. Also computes a
    numpy 1d array of ints which index every scan to relevant datacube.

static _mzml_file__parse_scan_parameters ()
    Internal helper function used to parse out scan parameters from the scan filter string

_mzml_file__read_all ()
    Internal helper function used to read all data. The function directly modifies the self.data entry. Data is
    now a list of datacubes

available_mzml_types = {'unknown': 'unknown', 'bruker': 'bruker', 'thermo': 'thermo'}

close_file()
    Close the mzml file

get_dataset_dependencies()
    Get the dependencies between the current dataset and any of the other datasets stored in the current file.
    Inherited from

get_dataset_metadata()
    Get dict of additional metadata associated with the current dataset.
    Inherited from file_reader_base.file_reader_base_multidata.

    Returns Dict where keys are strings and associated values to be stored as metadata with the
    dataset.

classmethod get_files_from_dir (dirname)
    Get a list of all basenames of all img files in a given directory. Note: The basenames include the dirname.

get_number_of_datasets()
    Get the number of available datasets.

classmethod is_valid_dataset (name)
    Check whether the given file or directory points to a img file.

    Parameters name (String) – Name of the dir or file.

    Returns Boolean indicating whether the given file or folder is a valid img file.

set_dataset_selection (dataset_index)
    Define the current dataset to be read.

classmethod size (name, max_num_reads=1000)
    Classmethod used to check the estimated size for the given file/folder. For mzml this is an estimate of the
    final size of the full 3D datacube. For efficiency the number of scans is estimated based on the size of the
    first 1000 scans.

    Parameters

        • name (unicode) – Name of the dir or file.

        • max_num_reads (int) – The maximum number of spectrum reads to be performed to
            estimate the file size

    Returns Integer indicating the size in byte or None if unknown.

spectrum_iter()
    Generator function that yields a position and associated spectrum for a selected datacube type.

    Yield (xidx, yidx) a tuple of ints representing x and y position in the image
```

Yield yi, a numpy 1D-array of floats containing spectral intensities at the given position and for the selected datacube type

```
classmethod test()  
    Test method
```

bruckerflex_file Module

This module provides functionality for reading bruker flex mass spectrometry image files

Limitations:

1. Currently the reader assumes a single global m/z axis for all spectra.
2. The read of acqu files does not convert <..> entries to python values but leaves them as strings.
3. __read_spotlist__ converts the regions to start with a 0 index. This is somewhat inconsistent in the spot list file. The spotname seems to number regions starting with 0 while the region list numbers them starting with 1.
4. __read_spotlist__ computes the folder where the spots are located based on the filename of the spotlist. The question is whether this is always the case??? The advantage is that we do not rely on the regions.xml file which contains absolute paths which are in most cases invalid as the data has been copied between different machines in many cases and is stored in different locations on each of the machines.
5. __read_spotlist__ currently assumes that there is only one fid file per spot
6. __read_spotlist__ currently only looks at where the acqu and fid file is located for the spot. Other files are currently ignored.
7. __read_spotlist__ (and hence the reader at large) currently assumes that we have 2D images only.
8. __read_spotlist__ currently generates maps for the image that assume that x and y pixel indices start at 0. Not all images may record data until the border, so that this strategy may add empty spectra rather than generating a new bounding box for the image.
9. __read_spotlist__ assumes in the variable spotname_encoding a maximum of 24 characters in the spotname R01X080Y013. This should in general be more than sufficient as this allows for 7 characters for each R, X, Y entry, however, if this is not enough then this behaviour needs to be changed.
10. __getitem__ currently only works if we have read the full data into memory. An on-demand load should be supported as well.
11. We can currently only select either a single region or the full data but we cannot select multiple regions at once. E.g. if a dataset contains 3 regions then we can either select all regions at once or region 1,2, or 3 but one cannot select region 1+2, 1+3, or 2+3.

```
import brukerflex_file  
spotlist = “/Users/oruebel/Devel/msidata/Bruker_Data/UNC IMS Data/20130417 Bmycoides Paenibacillus Early SN03130/” + “2013 Bmyc Paeni Early LP/2013 Bmyc Paeni Early LP Spot List.txt”  
exppath =”/Users/oruebel/Devel/msidata/Bruker_Data/UNC IMS Data/20130417 Bmycoides Paenibacillus Early SN03130/” + “2013 Bmyc Paeni Early LP/2013 Bmyc Paeni Early LP/0_R00X012Y006/1/ISLin” f = brukerflex_file.bruckerflex_file( spotlist_filename = spotlist) f.s_read_fid( exppath+”/fid”, f.data_type ) testacqu = f.s_read_acqu( exppath+”/acqu” ) testmz = f.s_mz_from_acqu( testacqu ) testspotlist = f.s_read_spotlist(spotlist)  
  
a = brukerflex_file( dirname )  
  
class omsi.dataformat.bruckerflex_file.bruckerflex_file(basename,  
                           fid_encoding=’int32’,      re-  
                           quires_slicing=True)  
Bases: omsi.dataformat.file_reader_base.file_reader_base_with_regions  
Interface for reading a single bruker flex image file.
```

The reader supports standard array slicing for data read. I.e., to read a spectrum use [x,y,:] to read an ion image using [:,:,mz].

The reader supports multiple regions, i.e., reading of different independent regions that were imaged as part of the same dataset. Using the get_regions, get_number_of_regions, set_region_selection and get_region_selection the user can interact with the region settings. Using the set_region_selection the user can define whether the data of the complete image should be read (set_region(None), default) or whether data from a single region should be read. When a region is selected, then the reader acts as if the region were the complete dataset, i.e., the shape variable is adjusted to fit the selected region and the __get_item__ method (which is used to implement array-like slicing (e.g., [1,1,:])) behaves as if the selected region where the full data.

Open an img file for data reading.

Parameters

- **basename** (*string*) – Name of the textfile with the spotlist. Alternatively this may also be the folder with the spots.
- **requires_slicing** (*bool*) – Should the complete data be read into memory (this makes slicing easier). (default is True)
- **fid_encoding** (*string*) – String indicating in which binary format the intensity values (fid files) are stored. (default value is ‘int32’)

Variables

- **self.basename** – Name of the file with the spotlist
- **self.pixel_dict** – dictionary with the pixel array metadata (see also s_read_spotlist(...)). Some of the main keys of the dictionary are, e.g. (see also s_read_spotlist(...)) :
 - ‘spotfolder’ : String indicating the folder where all the spot-data is located
 - ‘fid’ : 2D numpy masked array of strings indicating for (x,y) pixel the fid file with the intensity values.
 - ‘acqu’ : 2D numpy masked array of strings indicating for each (x,y) pixel the acqu file with the metadata for that pixel.
 - ‘regions’ : 2D numpy masked array of integers indicating for each pixels the index of the region it belongs to.
 - ‘xpos’ : 2D numpy masked array of integers indicated for each pixel its x position.
 - ‘ypos’ : 2D numpy masked array of integers indicated for each pixel its x position.
 - ‘spotname’ : 2D masked numpy array of strings with the names of the spot corresponding to a pixel.
- **self.data_type** – the encoding used for intensity values
- **self.shape** – The 3D shape of the MSI data volume for the currently selected region.
- **self.full_shape** – Shape of the full 3D MSI dataset including all regions imaged.
- **self.metadata** – Dictionary with metadata from the acqu file
- **self.mz** – The 1D numpy array with the m/z axis information
- **self.data** – If requires_slicing is set to true then this 3D array includes the complete data of the MSI data cube. Missing data values (e.g., from regions not imaged during the aquistion processes) are completed with zero values.
- **self.region_dicts** – Dictionary with description of the imaging regions

Raises ValueError In case that no valid data is found.

close_file()

Close the img file

get_dataset_dependencies()

Get the dependencies between the current region and any of the other region datasets stored in the current file. If self.select_region is not set, then the function is expected to return a list of lists with all dependencies for all datasets.

Returns

List of dependencies (or list of lists of dependencies if self.select_dataset is None) where each dependency is a dict of the following form:

- ‘omsi_object’: None, # The omsi file API object where the data is stored. Often None.
- ‘link_name’: ms2_link_name, # Name for the dependency link to be used
- ‘basename’: basename, # Basename of the file
- ‘region’: None, # Index of the region in the dataset or None
- ‘dataset’: ind2, # Index of the dataset withing the file or None
- ‘help’: scan_types[ms1scan], # Help describing the depndency
- ‘dependency_type’: ... } # Type of dependency see dependency_dict.dependency_type for available types

classmethod is_valid_dataset(name)

Determine whether the given file or name specifies a bruckerflex file

Parameters name (string) – name of the file or dir

Returns Boolean indicating whether the name is a valid bruckerflex

static s_mz_from_acqu(acqu_dict)

Construct the m/z axis from the data stored in the acqu_dict dictionary. See also s_read_acqu

Parameters acqu_dict – Python dictionary with the complete information from the acqu file.
See s_read_acqu(...).

returns 1D Numpy array of floats with the mz axis data.

static s_read_acqu(filename)

Construct an m/z axis for the given acqu file.

Parameters filename (string) – String with the name+path for the acqu file.

Returns Return dictionary with the parsed metadata information

static s_read_fid(filename, data_type='int32', selection=slice(None, None, None))

Read data from an fid file

Parameters

- **filename (string)** – String indicating the name+path to the fid file.
- **data_type** – The numpy datatype encoding used for the fid files. (default is ‘int32’).
In the instance of this class this is encoded in the data_type variable associated with the instance.
- **selection (slice or list, i.e., a selection that numpy understands)** – This may be a python slice or a list of indecies to be read. Default value is to read all (i.e., slice(None,None,None))

Returns 1D numpy array of intensity values read from the file.

static s_read_spotlist (spotlist_filename)
Parse the given spotlist file.

Parameters `spotlist_filename` (*string*) – Name of the textfile with the spotlist

Returns

The function returns a number of different items in from of a python dictionary. Most data is stored as 2D spatial maps, indicating for each (x,y) location the corresponding data. Most data is stored as 2D masked numpy arrays. The masked of the array indicated whether data has been recorded for a given pixel or not. The dict contains the following keys:

- ‘spotfolder’ : String indicating the folder where all the spot-data is located
- ‘fid’ : 2D numpy masked array of strings with fid file name for each (x,y) pixel (intensities).
- ‘acqu’ : 2D numpy masked array of strings with acqu file name for each (x,y) (metadata).
- ‘regions’ : 2D numpy masked array of integers with region index for each (x,y) pixel.
- ‘xpos’ : 2D numpy masked array of integers indicated for each pixel its x position.
- ‘ypos’ : 2D numpy masked array of integers indicated for each pixel its x position.
- ‘spotname’ : 2D masked numpy array of strings with spot name for each (x,y) pixel.

static s_spot_from_dir (in_dir, spot_folder_only=False)

Similar to `s_read_spotlist` but instead of using a spotlist file the structure of the data is parsed directly from the structure of the directory containing all spots.

param `in_dir` Name of the directory with all spots

type `in_dir` *string*

param `spot_folder_only` If set to True, then the function only constructs the spot folders but does not check for acqu files etc. If set to True, only the spotfolder list will be returned.

returns

The function returns None in case that no valid spots were found. Returns a list of strings with the spotfolders if `spot_folder_only` is set to True. Otherwise, the function returns a number of different items in from of a python dictionary. Most data is stored as 2D spatial maps, indicating for each (x,y) location the corresponding data. Most data is stored as 2D masked numpy arrays. The masked of the array indicated whether data has been recorded for a given pixel or not. The dict contains the following keys:

- ‘spotfolder’ : String indicating the folder where all the spot-data is located
- ‘fid’ : 2D numpy masked array of strings with fid file name for each (x,y) pixel (intensities).
- ‘acqu’ : 2D numpy masked array of strings with acqu file name for each (x,y) pixel (metadata).
- ‘regions’ : 2D numpy masked array of integers with the index of the region for each (x,y) pixel.

- ‘xpos’ : 2D numpy masked array of integers indicated for each pixel its x position.
- ‘ypos’ : 2D numpy masked array of integers indicated for each pixel its x position.
- ‘spotname’ : 2D masked numpy array of strings with the name of the spot corresponding to a pixel.

set_region_selection(region_index=None)

Define which region should be selected for local data reads.

Parameters **region_index** – The index of the region that should be read. The shape of the data will be adjusted accordingly. Set to None to select all regions and treat the data as a single full 3D image.

10.1.3 datastructures Package

<code>omsi.datastructures</code>	Package with a collection of various data structures and related classes
<code>omsi.datastructures.metadata</code>	Package with metadata datastructures
<code>omsi.datastructures.metadata.metadata_data</code>	Define infrastructure for describing metadata (in memory)
<code>omsi.datastructures.metadata.metadata_ontologies</code>	Define ontologies for metadata
<code>omsi.datastructures.analysis_data</code>	Helper module with data structures for managing analysis-related data
<code>omsi.datastructures.dependency_data</code>	Define a dependency to another omsi object
<code>omsi.datastructures.run_info_data</code>	Module with helper data structures for recording runtime performance information

datastructures Package

Package with a collection of various data structures and related classes used throughout the software stack, e.g., for metadata, analysis parameter data, runtime information data etc.

analysis_data Module

Helper module with data structures for managing analysis-related data.

```
class omsi.datastructures.analysis_data.analysis_data(name='undefined', data=None, dtype='float32')
```

Bases: dict

Define an output dataset for the analysis that should be written to the omsi HDF5 file

The class can be used like a dictionary but restricts the set of keys that can be used to the following required keys which should be provided during initialization.

Required Keyword Arguments:

Parameters

- **name** – The name for the dataset in the HDF5 format
- **data** – The numpy array to be written to HDF5. The data write function `omsi_file_experiment.create_analysis` used for writing of the data to file can in principle also handle other primitive data types by explicitly converting them to numpy. However, in this case the dtype is determined based on the numpy conversion and correct behavior is not guaranteed. I.e., even single scalars should be stored as a 1D numpy array here. Default value is None which is mapped to `np.empty(shape=(0) , dtype=dtype)` in `__init__`

- **dtype** – The data type to be used during writing. For standard numpy data types this is just the dtype of the dataset, i.e., ['data'].dtype. Other allowed datatypes are:
 - For string: omsi_format.str_type (omsi_format is located in omsi.dataformat.omsi_file)
 - To generate data links: ana_hdf5link (analysis_data)

ana_hdf5link = -1

Value used to indicate that a hard link to another dataset should be created when saving an analysis object

class omsi.datastructures.analysis_data.data_dtypes

Bases: dict

Class specifying basic function for specifying common data types used as part of an analysis.

static bool_type (argument)

Implement conversion of boolean input parameters since argparse (or bool, depending on the point of view), do not handle bool as a type in an intuitive fashion.

Parameters argument – The argument to be parsed to a boolean

Returns The converted value

static get_dtypes ()

Get a list of available data type specifications

static ndarray (argument)

This dtype may be used to indicate numpy ndarrays as well as h5py arrays or omsi_dependencies

Parameters argument – The argument to be parsed to ndarray

Returns The converted ndarray

class omsi.datastructures.analysis_data.parameter_data (name, help='', dtype=None, required=False, default=None, choices=None, data=None, group=None)

Bases: dict

Define a single input parameter for an analysis.

Variables default_keys – List of allowed dictionary keys:

Required keys:

- name** : The name of the parameter
- help** : Help string describing the parameter
- type** : Optional type. Default is None, indicating a dynamically typed dataset that the analysis will convert
- required** : Boolean indicating whether the parameter is required (True) or optional (False). Default False
- default** : Optional default value for the parameter. Default None.
- choices** : Optional list of choices with allowed data values. Default None, indicating no choices set.
- data** : The data assigned to the parameter. None by default.
- ‘group’ : Optional group string used to organize parameters. This may also be a dict of {‘name’:<group>, ‘description’:<description>}

In the context of the argparse package the default keys have the following mapping:

- argparse.name = name**
- argparse.action** –> The action is constant and set to save value

- `argparse nargs` -> Left as default
- `argparse const` -> Not used as action is always save value
- `argparse type = type`
- `argparse choices = 'choices'`
- `argparse required = 'required'`
- `argparse help = 'help'`
- `argparse metavar` -> Not used. Positional arguments are not allowed for analyses
- `argparse destination` -> *Automatically determined by the 'name' of the parameter*
- `argparse.add_argument_group(...)` -> *Automatically determined based on the required parameter and the 'group' parameter if set.*

Initialize a new parameter description.

Parameters

- `name` – Required name for the parameter
- `help` – Required help string for the parameter
- `dtype` – Type argument. Default unicode.
- `required` – Boolean indicating whether the parameter is required (default=True)
- `default` – Optional default value for the parameter. Default None.
- `choices` – Optional list of choices with allowed data values. Default None, indicating no choices set.
- `data` – The data assigned to the parameter. None by default.
- `group` – The parameter group to be used. None by default.

`clear_data()`

Remove the currently assigned data.

`copy()`

Return a new parameter_data object with the same data as stored in the current object

Returns dependency_dict object

`data_ready()`

This function check if the data points to a dependency and if so, then check if the dependency can be resolved or not

`data_set()`

Check if a data has been assigned for the parameter.

`default_keys = ['name', 'default', 'dtype', 'choices', 'required', 'help', 'data', 'group']`

List of allowed keys for the parameter dict.

`get_data_or_default()`

Get the data of the parameter if set, otherwise get the default value if available.

Returns The data to be used for the parameter.

Raises KeyError is raised in case that neither 'default' nor 'data' are available. This should never be the case if the object was created properly.

`get_group_description()`

Get the description for the group if available.

Returns String with the group description or None.

get_group_name()

Get the name of the group to be used.

Returns String with the name of the group or None if not set

is_dependency()

Check whether the parameter defines a dependency.

Returns Boolean indicating whether the parameter defines a dependency.

class omsi.datastructures.analysis_data.**parameter_manager**

Bases: object

Base class for objects that manage their own parameters.

Parameters are set and their values retrieved by name using dict-like slicing. Derived classes may overwrite `__getitem__` and `__setitem__` to implement their own behavior but we expect that the functionality of the interface is preserved, i.e., others should still be able set parameter value and retrieve values via dict slicing.

add_parameter(*name*, *help*, *dtype*=<type ‘unicode’>, *required*=False, *default*=None, *choices*=None, *data*=None, *group*=None)

Add a new parameter for the analysis. This function is typically used in the constructor of a derived analysis to specify the parameters of the analysis.

Parameters

- **name** – The name of the parameter
- **help** – Help string describing the parameter
- **dtype** – Optional type. Default is string.
- **required** – Boolean indicating whether the parameter is required (True) or optional (False). Default False.
- **default** – Optional default value for the parameter. Default None.
- **choices** – Optional list of choices with allowed data values. Default None, indicating no choices set.
- **data** – The data assigned to the parameter. None by default.
- **group** – Optional group string used to organize parameters. Default None, indicating that parameters are automatically organized by driver class (e.g. in required and optional parameters)

Raises ValueError is raised if the parameter with the given name already exists.

clear_parameter_data()

Clear the list of parameter data

define_missing_parameters()

Set any required parameters that have not been defined to their respective default values.

This function may be overwritten in child classes to customize the definition of default parameter values and to apply any modifications (or checks) of parameters before the analysis is executed. Any changes applied here will be recorded in the parameter of the analysis.

get_all_dependency_data()

Get the complete list of all direct dependencies to be written to the HDF5 file

NOTE: These are only the direct dependencies as specified by the analysis itself. Use `get_all_dependency_data_recursive(..)` to also get the indirect dependencies of the analysis due to dependencies of the dependencies themselves.

Returns List of parameter_data objects that define dependencies.

get_all_parameter_data (*exclude_dependencies=False*)

Get the complete list of all parameter datasets to be written to the HDF5 file

Parameters `exclude_dependencies` – Boolean indicating whether we should exclude parameters that define dependencies from the list

get_num_dependency_data()

Return the number of dependencies defined as part of the parameters

get_num_parameter_data()

Return the number of parameter datasets to be written to the HDF5 file

get_parameter_data (*index*)

Given the index return the associated dataset to be written to the HDF5 file

:param index [Return the index entry of the private member parameters. If a] string is given, then `get_parameter_data_by_name(...)` will be used instead.

Raises IndexError is raised when the index is out of bounds

get_parameter_data_by_name (*dataname*)

Given the key name of the data return the associated parameter_data object.

Parameters `dataname` – Name of the parameter requested from the parameters member.

Returns The parameter_data object or None if not found

get_parameter_names()

Get a list of all parameter dataset names (including those that may define dependencies).

keys()

Get a list of all valid keys, i.e., a list of all parameter names.

Returns List of strings with all input parameter and output names.

set_parameter_default_value (*name, value*)

Set the default value of the parameter with the given name

Parameters

- **name** – Name of the parameter
- **value** – New value

Raises KeyError if parameter not found

dependency_data Module

Define a dependency to another omsi object

```
class omsi.datastructures.dependency_data.DependencyDict(param_name=None,
                                                       link_name=None,
                                                       omsi_object=None,
                                                       selection=None,
                                                       dataname=None,
                                                       help=None,      dependency_type=None)
```

Bases: dict

Define a dependency to another omsi file-based data object or in-memory analysis_base object

Required Keyword Arguments:

Variables

- **param_name** – The name of the parameter that has the dependency
- **link_name** – The name of for the link to be created in the HDF5 file.
- **omsi_object** – The object to which a link should be established to. This must be either an h5py.Dataset or the omsi_file_analysis or omsi_file_msidata or any of the other omsi_file API interface objects.
- **selection** – Optional string type parameter indicating a python selection for the dependency
- **dataname** – String indicating the dataset within the omsi_object. If the omsi_object is an h5py object within a managed Group, then the omsi_object is automatically split up into the parent object and dataname.
- **_data** – Private key used to store the data associated with the dependency object.

Optional Keyword arguments:

Variables dependency_type – The type of the dependency being modeled. If not defined then the default value of ‘parameter’ is assumed.

Initialize the allowed set of keys.

Parameters

- **param_name** – The name of the parameter that has the dependency
- **link_name** – The name of for the link to be created in the HDF5 file.
- **omsi_object** – The object to which a link should be established to. This must be either an h5py.Dataset or the omsi_file_analysis or omsi_file_msidata or any of the other omsi_file API interface objects.
- **selection** – Optional string type parameter indicating a python selection for the dependency
- **dataname** – String indicating the dataset within the omsi_object. If the omsi_object is an h5py object within a managed Group, then the omsi_object is automatically split up into the parent object and dataname.
- **help** – Optional string describing the object

copy()

Return a new dependency_dict object with the same data as stored in the current object

Returns dependency_dict object

dependency_types = {‘subset’: ‘subset’, ‘undefined’: None, ‘contains’: ‘contains’, ‘link’: ‘link’, ‘parameter’: ‘parameter’}

get_data()

Get the data associated with the dependency.

Returns If a selection is applied and the dependency object supports array data load (e.g., h5py.Dataset, omsi_file_msidata), then the selected data will be loaded and returned as numpy array. Otherwise the ['omsi_object'] is returned.

run_info_data Module

Module with helper data structures for recording runtime provenance data

class omsi.datastructures.run_info_data.**run_info_dict** (*args, **kwargs)
Bases: dict

Simple dictionary class for collecting runtime information

The typical use is as follows:

```
>> my_run_info = run_info_dict() >> my_run_info(my_function)(my_parameters)
```

With this, all runtime information is automatically collected in my_run_info. We can enable time-and-usage and memory profiling simply by calling enable_profile_time_and_usage(...) or enable_profile_memory(...), respectively, before we run our function.

We can also use the data structure directly and control the population ourselves, however, memory profiling is not supported by default in this case but we need to set and run the memory profiler ourselves, since memory_profiler expects that it can wrap the function

DEFAULT_TIME_FORMAT = '%Y-%m-%d %H:%M:%S.%f'

clean_up()

Clean up the runinfo object. In particular remove empty keys that either recorded None or recorded just an empty string.

This function may be overwritten to also do clean-up needed due to additional custom runtime instrumentation.

When overwriting this function we should call super(..., self).runinfo_clean_up() at the end of the function to ensure that the runinfo dictionary is clean, i.e., does not contain any empty entries.

clear()

Clear the dictionary and other internal parameters

Side Effects

- Remove all key/value pairs from the dict
- Set self.__time_and_use_profiler to None
- Set self.__memory_profiler to None
- Set self.__profile_memory to False if invalid (i.e., if set to True but memory profiling is unavailable)
- Set self.__profile_time_and_usage to False if invalid (i.e., if set to True but profiling is unavailable)

enable_profile_memory(enable=True)

Enable/disable profiling of memory usage

Parameters **enable** – boolean to enable (True) or disable (False) memory profiling

enable_profile_time_and_usage(enable=True)

Enable/disable time and usage profiling

Parameters **enable** – boolean to enable (True) or disable (False) time and usage profiling

gather()

Simple helper function to gather the runtime information—that has been collected on multiple processes when running using MPI—on a single root process

Returns If we have more than one processes then this function returns a dictionary with the same keys as usual for the run_info but the values are now lists with one entry per mpi processes.

If we only have a single process, then the run_info object will be returned without changes.

NOTE: Similar to mpi gather, the function only collects information on the root. All other processes will return just their own private runtime information.

get_profile_memory()

Check whether profiling of memory usage is enabled

Returns Boolean indicating whether memory profiling is enabled

get_profile_stats_object(consolidate=True, stream=None)

Based on the execution profile of the execute_analysis(..) function get pstats.Stats object to help with the interpretation of the data.

Parameters

- **consolidate** – Boolean flag indicating whether multiple stats (e.g., from multiple cores) should be consolidated into a single stats object. Default is True.
- **stream** – The optional stream parameter to be used fo the pstats.Stats object.

Returns A single pstats.Stats object if consolidate is True. Otherwise the function returns a list of pstats.Stats objects, one per recorded statistic. None is returned in case that the stats objects cannot be created or no profiling data is available.

get_profile_time_and_usage()

Check whether time and usage profiling is enabled

Returns Boolean indicating whether time and usage profiling is enabled

record_postexecute(execution_time=None)

Function used to record runtime information after the task we want to track is completed, e.g. the execute_analysis(...) function of a standard analysis.

The function may be overwritten in child classes to add recording of additional runtime information.

When overwriting the function we should call super(...,self).runinfo_record_postexecute(execution_time) in the custom version to ensure that the execution and end_time are properly recorded.

Parameters

- **execution_time** – The total time it took to execute the analysis. May be None, in which case the function will attempt to compute the execution time based on the start_time (if available) and the the current time.
- **comm** – Used for logging only. The MPI communicator to be used. Default value is None, in which case MPI.COMM_WORLD is used.

record_preeexecute()

Record basic runtime information in this dict before the execution is started.

Function used to record runtime information prior to executing the process we want to track, e.g., the execute_analysis(...) of a standard analysis.

The function may be overwritten in child classes to add recording of additional runtime information. All runtime data should be recorded in the main dict (i.e, self). This ensures in the case of standard analysis that the data is stored in the HDF5 file. Other data should be stored in separate variables that we may add to the object.

When overwriting the function we should typically call super(...,self).runinfo_record_pretexecuted() last in the custom version to ensure that the start_time is properly recorded right before the execution of the analysis.

static string_to_structime (*time_string*, *time_format*=*None*)
Convert a time string to a time.struct_time using time.strptime

Parameters

- **time_string** – String with the time, e.g., with the start time of a program.
- **time_format** – The time format to be used or *None* in which case run_info_dict.DEFAULT_TIME_FORMAT will be used.

static string_to_time (*time_string*, *time_format*=*None*)
Convert a time string to local time object using time.mktime.

Parameters

- **time_string** – String with the time, e.g., with the start time of a program.
- **time_format** – The time format to be used or *None* in which case run_info_dict.DEFAULT_TIME_FORMAT will be used.

Subpackages

metadata Package

metadata Package Package with metadata datastructures

metadata_data Module Define infrastructure for describing metadata (in memory)

class omsi.datastructures.metadata.metadata_data.**metadata_dict**
Bases: dict

Dictionary's for storing metadata information. The values in the dict must be of type omsi_metadata_value and the keys must be strings.

get_metadata_descriptions ()
Get a list of all metadata descriptions
get_metadata_units ()
Get a list of all metadata units
get_metadata_values ()
Get a list of all metadata values.

class omsi.datastructures.metadata.metadata_data.**metadata_value** (*name*, *value*,
description,
unit=*None*, *ontology*=*None*)

Bases: dict

A single metadata value

- *name* The name of the metadata value
- *value* The actual value associated with the metadata object
- *description* The text description of the metadata object
- *unit* The unit string

- **ontology** Optional ontology

Parameters

- **name** – The name of the metadata value. Name may be None if the metadata_value is added to a metadata_dict as it will be set (if missing) when adding it to the metadata_dict
- **value** – The actual value associated with the metadata object
- **description** – The text description of the metadata object
- **unit** – The unit string
- **ontology** – Optional ontology

metadata_ontologies Module Define ontologies for metadata

```
var METADATA_ONTOLOGIES
```

Description of simple ontologies for metadata. This is a dict where the values are the descriptions of the ontologies and the key is the commonly used name of the variable associated with the ontology, however, in practice an ontology may be associated with many different metadata values (the purpose of the ontology is to standardize the values not the names of metadata variables). Available ontologies include:

- *polarity* : Description of the polarity of the instrument
- *msn_value_of_n* : Numeric level of mass spectrometry used (e.g., 1 for MS1 etc).

An ontology can be many things. In general an ontology is a mechanism to formally name and define the types, properties, and interrelationships of entities. We here refer broadly to the concept of ontologies as a means to standardize the names of things. To define an ontology we use simple dicts with the following key/value entries:

- *name*: The name of the ontology
- *value* : Python dict describing the actual ontology. Often this is simply a dict where the keys are the allowed values and the value is the textual description of the meaning of that value. In many cases this may be a more complete description of an ontology.
- *unit* : The standard unit associated with the values (or None if no unit is available)
- *description* : Human-readable textual description of the ontology
- *version* : The version of the ontology used
- ‘uri’ : The Universal Remote Identifier (often a URL) associated with the ontology (or None)

Ontologies are stored in the OpenMSI data format as JSON attributes associated with the metadata, i.e., one main restriction is that ontologies should be JSON serializable (which in most cases should be a problem).

```
class omsi.datastructures.metadata.metadata_ontologies.metadata_ontologies
Bases: dict
```

Helper class for interacting with ontologies

10.1.4 shared Package

<code>omsi.shared</code>	Package used to implement shared functionality and helper functions.
<code>omsi.shared.data_selection</code>	Module for defining and processing data selections.
<code>omsi.shared.log</code>	Module providing functionality for logging based on the python logging module.

<code>omsi.shared.mpi_helper</code>	Module used to ease the use of MPI and distributed parallel implementations
<code>omsi.shared.omsi_web_helper</code>	Module with helper functions for interactions with the OpenMSI web infrastruc
<code>omsi.shared.spectrum_layout</code>	This module provides capabilities for computing different layouts for spectra
<code>omsi.shared.third_party</code>	Package containing shared third-party code modules included here to reduce th
<code>omsi.shared.third_party.cloudpickle</code>	This class is defined to override standard pickle functionality The goals of it fo

data_selection Module

Module for defining and processing data selections. This includes the definition of selections using strings as well as transformation and reduction of data.

TODO: We may want to expose some of the following numpy functions currently not yet

supported through the transform and reduce data operations:

- `array2string`
- `array_equal`
- `array_equiv`
- `array_repr`
- `array_split`
- `array_str`
- `asanyarray`
- `asarray`
- `asarray_chkfinite`
- `ascontiguousarray`
- `asfarray`
- `asfortranarray`
- `asmatrix`
- `asscalar`
- `atleast_1d`
- `atleast_2d`
- `atleast_3d`
- `binary_repr`
- `convolve`
- `conjugate`
- `cross`
- `dot`
- `extract`
- `fft.*`
- `histogram, histogram2D, histogramdd`
- `kron`

- linalg.*
- swapaxes(a, axis1, axis2)
- transpose

```
#Simple data transformation and reduction example from omsi.shared.omsidata_selection import *
import numpy as np
import json
t = [ { 'transformation': 'threshold', 'threshold': 60 } , { 'reduction': 'max', 'axis': 2 } ]
tj = json.dumps(t)
tj
a = np.arange(125).reshape((5,5,5))
apro = transform_and_reduce_data(data=a, operations=tj, http_error=True)
apro

#Another simple example from omsi.shared.omsidata_selection import *
import numpy as np
import json
a = np.arange(10)+5
print a # 1) subtract minimum # 2) divide by the maximum value with the maximum value converted to float
# NOTE: The conversion to float is to avoid division of integers, i.e., # 5/10 = 0, whereas 5/float(10) = 0.5
# NOTE: The specification of 'x1':'data' can be omitted as this is the default. # 'x1':'data' simply explicitly specifies that the input data should be assigned to the first operand of the arithmetic operation.
t = [ { 'transformation': 'dualDataTransform', 'operation': 'subtract', 'x1': 'data', 'x2': [ { 'reduction': 'min' } ] } ,
{ 'transformation': 'dualDataTransform', 'operation': 'divide', 'x1': 'data', 'x2': [ { 'reduction': 'max' } ],
{ 'transformation': 'astype', 'dtype': 'float' } } ]

b = transform_and_reduce_data(data=a, operations=t)
print b
t = [ { 'transformation': 'threshold' }, { 'threshold': [ { 'reduction': 'median' } ] } ]
print t
c = transform_and_reduce_data(data=a, operations=t)
print c

#Construct a JSON description of a transformation/reduction from omsi.shared.omsidata_selection import *
#Construct the different pieces of the transformation and reduction pipeline
#1) Compute the maximum data value and convert it to float
#1.1) Compute the maximum value max_value = construct_reduce_dict( reduction_type='max' , axis=None )
#1.2) Convert data to float value_as_float = construct_transform_dict( trans_type='astype' , dtype='float' )
#1.3) Merge the two steps to compute the maximum data value as float max_value_as_float = construct_transform_reduce_list( max_value, value_as_float )
#2) Normalize the data by dividing by the maximum value
divide_by_max_value = construct_transform_dict( trans_type='dualDataTransform',
operation='divide' , axes=None , x2=max_value_as_float)

#3) Project along the last axis (i.e., the mz axis) to compute a maximum project image
max_projection = construct_reduce_dict( reduction_type='max' , axis=-1 )
#4) Merge the different steps and construct the json string
json_string = transform_reduce_description_to_json( divide_by_max_value , max_projection )
#Just copy the result of the following print statement as your JSON description
print json_string
```

`omsi.shared.data_selection.check_selection_string(selection_string)`

Check whether the given selection string is valid, and indicate which type of selection the string defined. Checking the selection string is meant as a safeguard to prevent attackers from being able to insert malicious code.

Parameters `selection_string` – String given by the user with the desired selection

Returns

String indicating the type of selection as defined in `selection_type`:

- ‘indexlist’ : Selection of the form [1,2,3]
- ‘all’ : Selection of the form ‘:’
- ‘range’: Selection of the form ‘a:b’
- ‘index’: A single index selection, e.g., ‘1’
- ‘invalid’: An unsupported selection

`omsi.shared.data_selection.construct_reduce_dict(reduction_type, **kwargs)`

Helper function used to construct reduction dictionary.

Required Keyword arguments:

Parameters `reduction_type` – The reduction type to be used.

Optional Keyword arguments:

Parameters

- **axis** – Some reduction functions support the axis parameters, describing along which axis the reduction should be performed.
- **x1** – By default the reductions are performed on the output of the previous data operation ($x1='data'$). We may reference the output of, e.g., the fifth data operation by setting $x1='data5'$. $x1$ itself may also specify a separate data transformation and reduction pipeline that operates on ‘data’.
- **min_dim** – Minimum number of dimensions the input data should have in order for the reduction should be applied.

Returns Dictionary with the description of the reduction operation.

```
omsi.shared.data_selection.construct_transform_dict(trans_type, axes=None, **kwargs)
```

Helper function used to construct a dictionary describing a data transformation.

Parameters

- **trans_type** – The transformation type to be used. See transformation_type dict.
- **axes** – The axes along which the data should be split. Default is None.
- **kwargs** – Additional keyword parameters for the transformation functions.

Returns Dictionary with the description of the transformation.

Raises KeyError is raised in case that a parameter is missing. ValueError is raised in case that a given parameter value is invalid.

```
omsi.shared.data_selection.construct_transform_reduce_list(*args)
```

Merge a series of transformations and reductions into a single list describing a pipeline of transformation and reduction operations to be performed.

Args Ordered series of dictionaries describing transformation and reduction operations.

Returns List of all transformation and reduction operations

```
omsi.shared.data_selection.evaluate_transform_parameter(parameter, data=None, secondary_data=None)
```

Evaluate the given query parameter. This function is used to enable the use of data transformation and reductions as part of transformation parameters. E.g., a user may want to subtract the minimum, or divide by the maximum etc.

Parameters

- **parameter** – The parameter to be evaluated. This may be a JSON string or list/dictionary-based description of a data transformation. Or any other valid data parameter. If the parameter describes as data reduction or transformation then the transformation will be evaluated and the result is returned, otherwise the parameter itself is returned.
- **data** – The input numpy array that should be transformed.
- **secondary_data** – Other data from previous data iterations a user may reference.

Returns The evaluated parameter result.

```
omsi.shared.data_selection.is_transform_or_reduce(parameter)
```

Check if the given parameter defines a description of a data transformation or data reduction

Parameters **parameter** (JSON string, dict or list of dicts with transformation parameter.) – The parameter to be checked.

Returns Boolean

```
omsi.shared.data_selection.json_to_transform_reduce_description(json_string)
Convert the json string to the transformation/reduction dict.
```

Parameters `json_string` – The json string to be converted.

Returns Python list or dict with the description

```
omsi.shared.data_selection.perform_reduction(data, reduction, secondary_data,
                                              min_dim=None, http_error=False,
                                              **kwargs)
```

Helper function used reduce the data of a given numpy array.

Parameters

- `data` – The input numpy array that should be reduced
- `reduction` (*String*) – Data reduction to be applied to the input data. Reduction operations are defined as strings indicating the numpy function to be used for reduction. Valid reduction operations include e.g.: mins, max, mean, median, std, var etc.
- `axis` – The axis along which the reduction should be applied
- `secondary_data` – Other data from previous data iterations a user may reference.
- `http_error` – Define which type of error message the function should return. If false then None is returned in case of error. Otherwise a DJANGO HttpResponse is returned.
- `min_dim` – Minimum number of dimensions the input data must have in order for the reduction to be applied.
- `kwargs` – Additional optional keyword arguments.

Returns Reduced numpy data array or in case of error None or HttpResonse with a description of the error that occurred (see `http_error` option).

```
omsi.shared.data_selection.reduction_allowed_numpy_function = ['all', 'alltrue', 'amax', 'amin', 'angle', 'a
```

List of allowed numpy data reduction operations. Reduction operations are any single data operations that may change the shape of the data. NOTE: Some operations may have additional optional or required keyword arguments. HELP: For full documentation of the different functions see the numpy documentation.

Additional input parameters are often:

- ‘`x1`’ [The data operand specifying the data the reduction should be performed on. \] The input data will be used by default if `x1` is not specified. You may also specify ‘`data`’ to explicitly indicate that the input data should be assigned to `x1`. You may specify `data0` to indicate that the output of another data operation should be used. Note, `data0` here refers to the input to the full data operation pipeline. Data from other parts of the pipeline, are then indexed using 1-based indices. E.g., to access the output of the first data operation set `x1='data0'`]
- ‘`axis`’ [Integer indicating the axis along which the data should be reduced. \] The default behavior, if axis is not specified, depends on the behavior of the corresponding numpy function. However, in most cases (if not all cases) the data operation will be applied to the full input data if no axis is specified.
- ‘`min_dim`’ [Integer specifying the minimum number of data dimensions the input data \] must have in order for the reduction operation to be applied.

Here the list of allowed data reduction operations.

- ‘`all`’ : `out = numpy.all(data, axis)`
- ‘`amax`’ : `out = numpy.amax(data, axis)`
- ‘`amin`’ : `out = numpy.amin(data, axis)`

- ‘alltrue’ : out = numpy.alltrue(data, axis)
- ‘angle’ : out = numpy.angle(z, deg)
- ‘any’ : out = numpy.any(data, axis)
- ‘append’ : out = numpy.append(data, values, axis)
- ‘argmax’ : out = numpy.argmax(data, axis)
- ‘argmin’ : out = numpy.argmin(data, axis)
- ‘argwhere’ : out = numpy.argwhere(data)
- ‘average’ : out = numpy.average(data, axis)
- ‘bincount’ : out = numpy.bincount(x, weights=None, minlength=None)
- ‘corrcoef’ : out = numpy.corrcoef(data)
- ‘count_nonzero’ : out = numpy.count_nonzero(data)
- ‘cumprod’ : out = numpy.cumprod(data, axis)
- ‘cumproduct’ : out = numpy.cumproduct(data, axis)
- ‘cumsum’ : out = numpy.cumsum(data, axis)
- ‘diag’ : out = numpy.diag(data, k=0)
- ‘diag_indices’ : out = numpy.diag_indices(data, ndim=2)
- ‘diagflat’ : out = numpy.diagflat(data, k=0)
- ‘diagonal’ : out = numpy.diagonal(data, offset=0, axis1=0, axis2=1)
- ‘diff’ : out = numpy.diff(a, n=1, axis=-1)
- ‘max’ : out = numpy.max(data, axis)
- ‘min’ : out = numpy.min(data, axis)
- ‘median’ : out = numpy.median(data, axis)
- ‘mean’ : out = numpy.mean(data, axis)
- ‘percentile’ : out = numpy.percentile(data, q, axis)
- ‘product’ : out = numpy.product(data, axis)
- ‘prod’ : out = numpy.prod(data, axis)
- ‘ptp’ : out = numpy.ptp(data, axis)
- ‘squeeze’ : out = numpy.squeeze(data)
- ‘std’ : out = numpy.std(data, axis)
- ‘swapaxes’ : out = numpy.swapaxes(x1, axis1, axis2)
- ‘var’ : out = numpy.var(data, axis)
- ‘transpose’ : out = numpy.transpose(data)
- ‘sum’ : out = numpy.sum(data, axis)

None-numpy data reduction operations:

- ‘select_values’ : out = data[selection]

```
omsi.shared.data_selection.selection_string_to_object(selection_string,
                                                     list_to_index=False)
```

Convert the given selection string to a python selection object, i.e., either a slice, list or integer index.

Parameters

- **selection_string** – A selection string of the type indexlist
- **list_to_index** – Should we turn the list into an index if the list contains only a single value. Default value is False, i.e., the list is not modified.

Returns

- An integer index if an index selection is specified
- A python list of indices if a list specified in the string
- A python slice object if a slice operation is specified by the string

```
omsi.shared.data_selection.selection_to_indexlist(selection_string, axis_size=0)
```

Parse the indexlist selection string and return a python list of indices

Parameters

- **selection_string** – A selection string of the type indexlist
- **axis_size** – Size of the dimensions for which the selection is defined. Only needed in case that a range selection is given. This should be a list of sizes, in case that a multiaxis selection is given.

Returns

- A python list of point indices for the selection.
- None in case the list is empty or in case an error occurred.

```
omsi.shared.data_selection.selection_to_string(selection)
```

Convert the given selection, which may be either an int, a list of ints, a slice object or a tuple of the mentioned types which is used to define a selection along multiple axes. :param selection: The selection to be converted to a string :type selection: int, list, slice, or a tuple of int, list, slice objects :return: The selection string

```
omsi.shared.data_selection.selection_type = {'index': 0, 'all': 3, 'indexlist': 2, 'invalid': -1, 'range': 4, 'multiaxi
```

This an extended list of types indicated by the check_selection_string function. Indices <0 are assumed to be invalid selections.

```
omsi.shared.data_selection.transform_and_reduce_data(data, operations, secondary_data=None,
                                                    http_error=False)
```

Helper function used to apply a series of potentially multiple operations to a given numpy dataset. This function uses the transform_data_single(...) function to apply each indicated transformation to the data. This function uses the perform_reduction function to perform data reduction operations.

Parameters

- **data** – The input numpy array that should be transformed.
- **operations** – JSON string with list of dictionaries or a python list of dictionaries. Each dict specifies a single data transformation or data reduction. The operations are applied in order, i.e., operations[0] is applied first, then operations[1] and so on. The dicts must be structured according to one of the following specifications:
 - {‘transformation’:<op>} : Single transformation applied to all data at once.
 - {‘transformation’:<op>, ‘axes’:[..]} : Apply a single transformation to data chunks defined by the axes parameter. The data is split into chunks along the dimensions defined

by the axes parameter. E.g., if we have a 3D MSI dataset and we want to open ion images independently, then we need to set axes=[2]. Accordingly, if we want to open spectra individually, then we need to split the two image dimensions into chunks by setting axes=[0,1].

- {‘reduction’:<reduction>, ‘axis’:int} : Define the reduction operations to be applied and the axis along which the data should be reduced. If reduction along all axis should be done then set axis ot None (in python) or null in JSON.
- **secondary_data** – Other data from previous data iterations a user may reference.
- **http_error** – Define which type of error message the function should return. If false then None is returned in case of error. Otherwise a DJANGO HttpResponse is returned.

Returns Reduced numpy data array or HttpResonse with a description of the error that occurred.

```
omsi.shared.data_selection.transform_data_single(data, transformation='minusMinDivideMax', axes=None, secondary_data=None, http_error=False, transform_kwargs=None)
```

Helper function used to transform data of a numpy array. The function potentially splits the array into independent chunks that are normalized separately (depending on how the axes parameter is defined). The actual data transformations are implemented by transform_datachunk(...).

Parameters

- **data** – The input numpy array that should be transformed.
- **transformation** – Data transformation option to be used. Available options are: ‘minusMinDivideMax’ ,...
- **axes** – List of data axis that should be split into chunks that are treated independently during the transformation. By default transformation is applied based on the full dataset (axes=None). E.g, if transformation should be performed on a per image basis, then we need to split the m/z dimension into individual chunks and set axes=[2]. If we want to transform spectra individually, then we need to split the two image dimensions into chunks by setting axes=[0,1].
- **secondary_data** – Other data from previous data iterations a user may reference.
- **http_error** – Define which type of error message the function should return. If false then None is returned in case of error. Otherwise a DJANGO HttpResponse is returned.
- **transform_kwargs** – Dictionary of additional keyword arguments to be passed to the transform_datachunk(...) function.

Returns Reduced numpy data array or HttpResonse with a description of the error that occurred.

```
omsi.shared.data_selection.transform_datachunk(data, transformation='minusMinDivideMax', secondary_data=None, **kwargs)
```

Helper function used to transform a given data chunk. In contrast to transform_data, this function applies the transformation directly to the data provided, without consideration of axis information. This function is used by transform_data(...) to implement the actual normalization for independent data chunks that need to be normalized.

Required keyword arguments:

Parameters

- **data** – The input numpy array that should be transformed.

- **transformation** – Data transformation option to be used. For available options see the transformation_type dictionary.
- **secondary_data** – Other data from previous data iterations a user may reference.

Additional transformation-dependent keyword arguments:

Parameters kwargs – Additional keyword arguments that are specific for different data transformation. Below a list of additional keyword arguments used for different transformation options

- **transformation: ‘threshold’**

** ‘threshold’ [The threshold parameter to be used for] the threshold operation. If threshold is not specified, then the 5th %tile will be used as threshold value instead, ie., the bottom 5% of the data are set to 0.

Returns This function returns the normalized data array. If an unsupported transformation option is given, then the function simply return the unmodified input array.

`omsi.shared.data_selection.transform_reduce_description_to_json(*args)`
Convert the dictionary describing the transformation/reduction operations to a JSON string.

Parameters args – The list or dictionaries with the description of the transformation and reduction operations.

Returns JSON string

`omsi.shared.data_selection.transformation_allowed_numpy_dual_data = ['add', 'arctan2', 'bitwise_and', ...]`
List of allowed dual data transformations. Dual data transformation, are operation that operate on a two data input datasets but which do not change the shape of the data. Below a list of available numpy function options. NOTE: Some operations may have additional optional or required keyword arguments. HELP: For full documentation of the different functions see the numpy documentation.

- ‘add’ : `out = x1 + x2 = numpy.add(x1,x2)`
- ‘arctan2’ : `out = numpy.arctan2(x1,x2)`
- ‘bitwise_and’ : `out = x1 && x2 = numpy.bitwise_and(x1,x2)`
- ‘bitwise_not’ : `out = numpy.bitwise_not(x1,x2)`
- ‘bitwise_or’ : `out = x1 || x2 = numpy.bitwise_or(x1,x2)`
- ‘bitwise_xor’ : `out = numpy.bitwise_xor(x1,x2)`
- ‘corrcoef’ : `out = numpy.corrcoef(x1,x2)`
- ‘cov’ : `out = numpy.cov(x1, x2, rowvar=1, bias=0, ddof=None)`
- ‘divide’ : `out = x1 / x2 = numpy.divide(x1,x2)`
- ‘equal’ : `out = x1 == x2 = numpy.equal(x1,x2)`
- ‘fmax’ : `out = numpy.fmax(x1,x2)`
- ‘fmin’ : `out = numpy.fmin(x1,x2)`
- ‘fmod’ : `out = numpy.fmod(x1,x2)`
- ‘greater’ : `out = x1 > x2 = numpy.greater(x1,x2)`
- ‘greater_equal’ : `out = x1 >= x2 = numpy.greater_equal(x1,x2)`
- ‘left_shift’ : `out = numpy.left_shift(x1,x2)`
- ‘less’ : `out = x1 < x2 = numpy.less(x1,x2)`
- ‘less_equal’ : `out = x1 <= x2 = numpy.less_equal(x1,x2)`

- ‘logical_and’ : out = numpy.logical_and(x1,x2)
- ‘logical_not’ : See transformation_allowed_numpy_single_data instead.
- ‘logical_or’ : out = numpy.logical_or(x1,x2)
- ‘logical_xor’ : out = numpy.logical_xor(x1,x2)
- ‘mod’ : out = numpy.mod(x1,x2)
- ‘multiply’ : out = x1 * x2 = numpy.multiply(x1,x2)
- ‘not_equal’ : out = x1 != x2 = numpy.not_equal(x1,x2)
- ‘power’ : out = numpy.power(x1,x2)
- ‘subtract’ : out = x1 - x2 = numpy.subtract(x1,x2)
- ‘right_shift’ : out = np.right_shift(x1,x2)

omsi.shared.data_selection.transformation_allowed_numpy_single_data = ['abs', 'arccos', 'arccosh', 'arc
List of allowed single data transformations. Single data transformation, are operations that operate on a single
data input and which do not change the shape of the data. Below a list of available numpy options. NOTE:
Some operations may have additional optional or required keyword arguments. HELP: For full documentation
of the different functions see the numpy documentation.

- ‘abs’ : out = numpy.abs(x1)
- ‘arccos’ : out = numpy.arccos(x1)
- ‘arccosh’: out = numpy.arccosh(x1)
- ‘arcsin’ : out = numpy.arcsin(x1)
- ‘arcsinh’: out = numpy.arcsinh(x1)
- ‘arctan’ : out = numpy.arctan(x1)
- ‘arctanh’: out = numpy.arctanh1(x1)
- ‘argsort’ : out = numpy.argsort(data, axis, kind='quicksort', order=None)
- ‘around’ : out = numpy.around(x1, decimals)
- ‘ceil’ : out = numpy.ceil(x1)
- ‘cos’ : out = numpy.cos(x1)
- ‘cosh’ : out = numpy.cosh(x1)
- ‘clip’ : out = numpy.clip(x1, a_min, a_max)
- ‘deg2rad’: out = numpy.deg2rad(x1)
- ‘degrees’ : out = numpy.degrees(x1)
- ‘exp’ : out = numpy.exp(x1)
- ‘exp2’ : out = numpy.exp2(x1)
- ‘fabs’ : out = numpy.fabs(x1)
- ‘floor’ : out = numpy.floor(x1)
- ‘hypot’ : out = numpy.hypot(x1)
- ‘invert’ : out = numpy.invert(x1)
- ‘log’ [out[x1>0] = log(x1[x1>0]) \] out[x1<0] = log(x1[x1<0]*-1)*-1 out[x1==0] = 0

- ‘log2’ : out[x1>0] = log2(x1[x1>0]) out[x1<0] = log2(x1[x1<0]*-1)*-1 out[x1==0] = 0
- ‘log10’: out[x1>0] = log10(x1[x1>0]) out[x1<0] = log10(x1[x1<0]*-1)*-1 out[x1==0] = 0
- ‘logical_not’ : out = numpy.logical_not(x1)
- ‘negative’ : out = np.negative(x1)
- ‘round’ : out = numpy.round(x1, decimals)
- ‘sqrt’ [out[x1>0] = sqrt(x1[x1>0]) \] out[x1<0] = sqrt(x1[x1<0]*-1)*-1 out[x1==0] = 0
- ‘sign’ : out = numpy.sign(x1)
- ‘sin’ : out = numpy.sin(x1)
- ‘sinc’ : out = numpy.sinc(x1)
- ‘sinh’ : out = numpy.sinh(x1)
- ‘sort’ : out = numpy.sort(x1, axis=-1, kind=’quicksort’, order=None)
- ‘swapaxes: out = numpy.swapaxes(x1, axis1, axis2)
- ‘tan’ : out = numpy.tan(x1)
- ‘tanh’ : out = numpy.tanh(x1)

`omsi.shared.data_selection.transformation_type = {‘singleDataTransform’: ‘singleDataTransform’, ‘scale’: ‘sc`
Dictionary of available data transformation options. Available options are:

- ‘arithmetic’ : Same as ‘dualDataTransform’. See ‘dualDataTransform’ below for details.
- ‘divideMax’ : Divide the data by the current maximum value.
- ‘minusMinDivideMax’ [Subtract the minimum value from the data and \] then divide the data by maximum of the data (with the minimum already subtracted).
- ‘dualDataTransform’ [Apply arbitrary arithmetic operation to the data. Additional parameter \] required for this option are:
 - *operation* : String defining the arithmetic operations to be applied. Supported operations are: ‘add’, ‘divide’, ‘greater’, ‘greater_equal’, ‘multiply’, ‘subtract’
 - ‘x1’ [The first data operand of the arithmetic operation. \] The input data will be used by default if x1 is not specified. You may also specify ‘data’ to explicitly indicate that the input data should be assigned to x1. You may specify data0 to indicate that the output of another data operation should be used. Note, data0 here refers to the input to the full data operation pipeline. Data from other parts of the pipeline, are then indexed using 1-based indices. E.g., to access the output of the first data operation set x1=’data0’
 - ‘x2’ [The second data operand of the arithmetic operation. \] The input data will be used by default if x2 is not specified. You may also specify ‘data’ to explicitly indicate that the input data should be assigned to x2. You may specify data0 to indicate that the output of another data operation should be used. Note, data0 here refers to the input to the full data operation pipeline. Data from other parts of the pipeline, are then indexed using 1-based indices. E.g., to access the output of the first data operation set x2=’data0’
 - ... any additional parameters needed for the numpy function.
- ‘singleDataTransform’ [Apply scaling transformation to the data. Additional parameters \] required for this options are. NOTE: operation==’log or operation==’sqrt’: If the minimum value is 0 then the transformation is applied to positive values only and 0 values remain as is. If the minimum value is larger then 0, then the log-scale is applied as is, i.e., np.log(data). If the minimum data value is

negative, then the log scale is applied independently to the positive values and the negative values, ie.,
outdata[posvalues] = np.log(data[posvalues]) outdata[negvalues] = np.log(data[negvalues]**-1.)*-1.

- ‘operation’ : String defining the scaling operations to be applied. See the transformation_allowed_numpy_single_data list for a complete list of allowed scaling operations. Some of the more commonly used scalingoperations include: ‘abs’, ‘log’, ‘sqrt’, ‘around’ etc.
- ‘x1’ [The first data operand for the scaling.] The input data will be used by default if x1 is not specified. You may also specify ‘data’ to explicitly indicate that the input data should be assigned to x1.

Additional optional keyword arguments depending on the used operation:

- ‘decimals’ [Number of decimal places to round to when using numpy.around or numpy.round \] (default: 0). If decimals is negative, it specifies the number of positions to the left of the decimal point.
 - ‘a_min’, ‘a_max’ : Lower and upper bound when using numpy.clip.
 - ‘axis’, ‘kind’, ‘order’ : Additional optional arguments for numpy.argsort and numpy.sort.
 - ...
- ‘scale’ : Same as ‘singleDataTransform’. See ‘singleDataTransform’ for details.
 - ‘threshold’ [Threshold the data. Set all values that are smaller than threshold \] to 0. Additional parameters required for this option are:
 - ‘threshold’ . If threshold is missing, then the threshold will be set of the 5%’ile so that the bottom 5% of the data will be set to 0.
 - ‘astype’ : Change the type of the data. Additional required parameters are:
 - ‘dtype’ : The numpy data type to be used. Default dtype=‘float’.

omsi_web_helper Module

Module with helper functions for interactions with the OpenMSI web infrastructure, e.g. update job status, explicitly add a file to the OpenMSI database, update file permissions so that Apache can access it etc.

```
class omsi.shared.omsi_web_helper.UserInput
Bases: object
```

Collection of helper functions used to collect user input

```
static userinput_with_timeout(timeout, default='')
```

Read user input. Return default value given after timeout. This function decides which platform-dependent version should be used to retrieve the user input.

Parameters

- **timeout** – Number of seconds till timeout
- **default (String)** – Default string to be returned after timeout

Returns String

```
static userinput_with_timeout_default(timeout, default='')
```

Read user input. Return default value given after timeout.

Parameters

- **timeout** – Number of seconds till timeout
- **default** (*String*) – Default string to be returned after timeout

Returns String

```
static userinput_with_timeout_windows (timeout, default='')
```

Read user input. Return default value given after timeout. This function is used when running on windows-based systems.

Parameters

- **timeout** – Number of seconds till timeout
- **default** (*String*) – Default string to be returned after timeout

Returns String

```
class omsi.shared.omsi_web_helper.WebHelper
```

Bases: object

Class providing a collection of functions for web-related file conversion tasks, e.g., i) adding files to the web database, ii) notifying users via email, iii) setting file permissions for web-access.

```
allowed_nersc_locations = ['/project/projectdirs/openmsi/omsi_data_private', '/global/project/projectdirs/openmsi/omsi_data_private']
default_db_server_url = 'https://openmsi.nersc.gov/'

static register_file_with_db (filepath, db_server, file_user_name, jobid=None,
                             check_add_nersc=True)
```

Function used to register a given file with the database

Parameters

- **filepath** – Path of the file to be added to the database
- **db_server** – The database server url
- **file_user_name** – The user to be used, or None if the user should be determined based on the file URL.
- **jobid** – Optional input parameter defining the jobid to be updated. If the jobid is given then the job will be updated with the database instead of adding the file explicitly. I.e., instead of register_filer_with_db the update_job_status call is executed.

Returns Boolean indicating whether the operation was successful

```
static send_email (subject, body, sender='convert@openmsi.nersc.gov', email_type='success',
                  email_success_recipients=None, email_error_recipients=None)
```

Send email notification to users.

Parameters

- **subject** – Subject line of the email
- **body** – Body text of the email.
- **sender** – The originating email address
- **email_type** – One of ‘success’, ‘error’, ‘warning’. Error messages are sent to ConvertSettings.email_error_recipients, success messages to ConvertSettings.email_success_recipients and warning messages are sent to both lists.
- **email_success_recipients** – List of user that should receive an email if the status is success or warning.

- **email_error_recipients** – List of users that should receive an email if the status is error or warning.

static set_apache_acl (filepath)

Helper function used to set acl permissions for apache to make the given file accessible to Apache at NERSC. This necessary to make the file readable for adding it to the database.

super_users = ['bpb', 'oruebel']

static update_job_status (filepath, db_server, jobid, status='complete')

Function used to update the status of the job on the server

Parameters

- **filepath** – Path of the file to be added to the database (only needed update file permissions)
- **db_server** – The database server url
- **jobid** – The id of the current job.
- **status** – One of ‘running’, ‘complete’ or ‘error’

spectrum_layout Module

This module provides capabilities for computing different layouts for spectra

`omsi.shared.spectrum_layout.compute_hilbert_spectrum(original_coords, original_intensities, left=0, right=0)`

Given a 1D spectrum, interpolate the spectrum onto the closest 2D hilbert curve.

Parameters

- **original_coords** (*1D numpy array in increasing order.*) – The original coordinate values (m/z). Values must be increasing.
- **original_intensities** (*1D numpy array of same length as original_coords*) – The original intensity values. Same length as original_coords.
- **left** – Optional. Value to be used for padding data at the lower bound during interpolation
- **right** – Optional. Value to be used for padding data at the upper bound during interpolation

Type float

Type float

Returns 2D numpy array with the coordinate (m/z) values for the hilbert spectrum and separate 2D numpy array for the interpolated intensity values.

Raises ValueError If original_coords and original_intensities have different length.

`omsi.shared.spectrum_layout.hilbert_curve (order=2)`

Compute a 2D hilbert curve.

Parameters **order** (*Integer that defines a power of 2 (>=2)*) – The order of the hilber curve. This is the length of the sides of the square, i.e., the number of points in x and y.

Returns Returns two numpy arrays of integers x,y, indicating the locations of the vertices of the hilbert curve.

```
omsi.shared.spectrum_layout.plot_2d_spectrum_as_image(hilbert_intensities,  
                                                    show_plot=False,  
                                                    show_axis=False)
```

Plot image with pixels colored according to hilbert_intensities.

Parameters

- **hilbert_intensities** (*2D numpy array*) – 2D numpy array with the intensity values for the spectrum.
- **show_plot** (*Boolean*) – Show the generated plot in a window.
- **show_axis** (*Boolean*) – Show x,y axis for the plot. Default is False.

Returns matplotlib image plot or None in case that the plotting failed.

```
omsi.shared.spectrum_layout.reinterpolate_spectrum(coords, original_coords, original_intensities, left=0, right=0)
```

Given a 1D spectrum, interpolate the spectrum onto a new axis.

Parameters

- **coords** – The coordinate values (m/z) for which intensities should be computed.
- **original_coords** – The original coordinate values (m/z). Values must be increasing.
- **original_intensities** – The original intensity values. Same length as original_coords.
- **left** – Optional. Value to be used if coords < original_coords
- **right** – Optional. Value to be used if coords > original_coords

Returns y : {float, ndarray} The interpolated values, same shape as coords.

Raises ValueError If original_coords and original_intensities have different length.

log Module

Module providing functionality for logging based on the python logging module. The module is intended to ease the use of logging while a developer can still access the standard python logging mechanism if needed.

```
class omsi.shared.log.log_helper
```

Bases: object

BASTet helper module to ease the use of logging

Class Variables:

Variables `log_levels` – Dictionary describing the different available logging levels.

```
classmethod critical(module_name, message, root=0, comm=None, *args, **kwargs)
```

Create a critical log entry. This function is typically called as:

```
log_helper.critical(module_name=__name__, message="your message")
```

Parameters

- **module_name** – __name__ of the calling module or None in case the ROOT logger should be used.
- **message** – The message to be added to the log
- **root** – The root process to be used for output when running in parallel. If None, then all calling ranks will perform logging. Default is 0.

- **comm** – The MPI communicator to be used to determin the MPI rank. None by default, in which case mpi.comm_world is used.
- **args** – Additional positional arguments for the python logger.debug function. See the python docs.
- **kwargs** – Additional keyword arguments for the python logger.debug function. See the python docs.

classmethod debug (*module_name*, *message*, *root*=0, *comm*=None, **args*, ***kwargs*)

Create a debug log entry. This function is typically called as:

```
log_helper.debug(module_name=__name__, message="your message")
```

Parameters

- **module_name** – __name__ of the calling module or None in case the ROOT logger should be used.
- **message** – The message to be added to the log
- **root** – The root process to be used for output when running in parallel. If None, then all calling ranks will perform logging. Default is 0.
- **comm** – The MPI communicator to be used to determin the MPI rank. None by default, in which case mpi.comm_world is used.
- **args** – Additional positional arguments for the python logger.debug function. See the python docs.
- **kwargs** – Additional keyword arguments for the python logger.debug function. See the python docs.

classmethod error (*module_name*, *message*, *root*=0, *comm*=None, **args*, ***kwargs*)

Create a error log entry. This function is typically called as:

```
log_helper.error(module_name=__name__, message="your message")
```

Parameters

- **module_name** – __name__ of the calling module or None in case the ROOT logger should be used.
- **message** – The message to be added to the log
- **root** – The root process to be used for output when running in parallel. If None, then all calling ranks will perform logging. Default is 0.
- **comm** – The MPI communicator to be used to determin the MPI rank. None by default, in which case mpi.comm_world is used.
- **args** – Additional positional arguments for the python logger.debug function. See the python docs.
- **kwargs** – Additional keyword arguments for the python logger.debug function. See the python docs.

classmethod exception (*module_name*, *message*, *root*=0, *comm*=None, **args*, ***kwargs*)

Create a exception log entry. This function is typically called as:

```
log_helper.exception(module_name=__name__, message="your message")
```

Parameters

- **module_name** – __name__ of the calling module or None in case the ROOT logger should be used.

- **message** – The message to be added to the log
- **root** – The root process to be used for output when running in parallel. If None, then all calling ranks will perform logging. Default is 0.
- **comm** – The MPI communicator to be used to determin the MPI rank. None by default, in which case mpi.comm_world is used.
- **args** – Additional positional arguments for the python logger.debug function. See the python docs.
- **kwargs** – Additional keyword arguments for the python logger.debug function. See the python docs.

classmethod get_default_format ()

Get default formatting string.

classmethod get_logger (module_name)

Get the logger for a particular module. The module_name should always be set to the __name__ variable of the calling module.

Parameters **module_name** – __name__ of the calling module or None in case the ROOT logger should be used.

Returns Python logging.Logger retrieved via logging.getLogger.

global_log_level = 20**classmethod info (module_name, message, root=0, comm=None, *args, **kwargs)**

Create a info log entry. This function is typically called as:

```
log_helper.info(module_name=__name__, message="your message")
```

Parameters

- **module_name** – __name__ of the calling module or None in case the ROOT logger should be used.
- **message** – The message to be added to the log
- **root** – The root process to be used for output when running in parallel. If None, then all calling ranks will perform logging. Default is 0.
- **comm** – The MPI communicator to be used to determin the MPI rank. None by default, in which case mpi.comm_world is used.
- **args** – Additional positional arguments for the python logger.debug function. See the python docs.
- **kwargs** – Additional keyword arguments for the python logger.debug function. See the python docs.

initialized=False**classmethod log (module_name, message, root=0, comm=None, level=None, *args, **kwargs)**

Convenience function used to select the log message level using an input parameter rathern than by selecting the approbiate function.

Parameters

- **module_name** – __name__ of the calling module or None in case the ROOT logger should be used.
- **message** – The message to be added to the log

- **root** – The root process to be used for output when running in parallel. If None, then all calling ranks will perform logging. Default is 0.
- **comm** – The MPI communicator to be used to determine the MPI rank. None by default, in which case mpi.comm_world is used.
- **level** – To which logging level should we send the message
- **args** – Additional positional arguments for the python logger.debug function. See the python docs.
- **kwargs** – Additional keyword arguments for the python logger.debug function. See the python docs.

log_levels = {'INFO': 20, 'WARNING': 30, 'CRITICAL': 50, 'ERROR': 40, 'DEBUG': 10, 'NOTSET': 0}

classmethod log_var (module_name, root=0, comm=None, level=None, **kwargs)

Log one or more variable values

Parameters

- **module_name** – __name__ of the calling module or None in case the ROOT logger should be used.
- **message** – The message to be added to the log
- **root** – The root process to be used for output when running in parallel. If None, then all calling ranks will perform logging. Default is 0.
- **comm** – The MPI communicator to be used to determin the MPI rank. None by default, in which case mpi.comm_world is used.
- **kwargs** – Variables+values to be logged

classmethod set_log_level (level)

Set the logging level for all BASTet loggers

Parameters level – The logging levels to be used, one of the values specified in log_helper.log_levels.

classmethod setup_logging (level=None)

Call this function at the beginning of your code to initiate logging.

Parameters level – The default log level to be used. One of log_helper.log_level.

classmethod warning (module_name, message, root=0, comm=None, *args, **kwargs)

Create a warning log entry. This function is typically called as:

log_helper.warning(module_name=__name__, message="your message")

Parameters

- **module_name** – __name__ of the calling module or None in case the ROOT logger should be used.
- **message** – The message to be added to the log
- **root** – The root process to be used for output when running in parallel. If None, then all calling ranks will perform logging. Default is 0.
- **comm** – The MPI communicator to be used to determin the MPI rank. None by default, in which case mpi.comm_world is used.
- **args** – Additional positional arguments for the python logger.debug function. See the python docs.

- **kwargs** – Additional keyword arguments for the python logger.debug function. See the python docs.

mpi_helper Module

Module used to ease the use of MPI and distributed parallel implementations using MPI

`omsi.shared.mpi_helper.barrier(comm=None)`
MPI barrier operation or no-op when running without MPI

Parameters `comm` – MPI communicator. If None, then MPI.COMM_WORLD will be used.

`omsi.shared.mpi_helper.broadcast(data, comm=None, root=0)`
MPI broadcast operation to broadcast data from one rank to all other ranks

Parameters

- `data` – The data to be gathered
- `comm` – MPI communicator. If None, then MPI.COMM_WORLD will be used.
- `root` – The rank where the data is sned from

Returns The data object

`omsi.shared.mpi_helper.gather(data, comm=None, root=0)`
MPI gather operation or return a list with just [data,] if MPI is not available

Parameters

- `data` – The data to be gathered
- `comm` – MPI communicator. If None, then MPI.COMM_WORLD will be used.
- `root` – The rank where the data should be collected to. Default value is 0

Returns List of data objects from all the ranks

`omsi.shared.mpi_helper.get_comm_world()`
Get MPI.COMM_WORLD :return: mpi communicator or None if MPI is not available

`omsi.shared.mpi_helper.get_rank(comm=None)`
Get the current process rank :param comm: MPI communicator. If None, then MPI.COMM_WORLD will be used. :return: The integer index of the rank

`omsi.shared.mpi_helper.get_size(comm=None)`
Get the size of the current communication domain/ :param comm: MPI communicator. If None, then MPI.COMM_WORLD will be used. :return: The integer index of the rank

`omsi.shared.mpi_helper.imports_mpi(python_object)`
Check whether the given class import mpi

The implementation inspects the source code of the analysis to see if MPI is imported by the code.

`omsi.shared.mpi_helper.is_mpi_available()`
Check if MPI is available. Same as MPI_AVAILABLE :return: bool indicating whether MPI is available

`omsi.shared.mpi_helper.mpi_type_from_dtype(dtype)`
Ge the the corresponding MPI type for the given basic numpy dtype

Parameters `dtype` – Basic numpy dtype to be mapped to the MPI type

Returns The MPI type or None if not found

```
class omsi.shared.mpi_helper.parallel_over_axes(task_function,      task_function_params,
                                                main_data,                  split_axes,
                                                main_data_param_name,      sched-
                                                ule='STATIC_ID', root=0, comm=None)
```

Bases: object

Helper class used to parallelize the execution of a function using MPI by splitting the input data into sub-blocks along a given set of axes.

Variables

- **task_function** – The function we should run.
- **task_function_params** – Dict with the input parameters for the function. may be None or {} if no parameters are needed.
- **main_data** – Dataset over which we should parallelize
- **split_axes** – List of integer axis indicies over which we should parallelize
- **main_data_param_name** – The name of data input parameter of the task function
- **root** – The master MPI rank (Default=0)
- **schedule** – The task scheduling schema to be used (see parallel_over_axes.SCHEDULES
- **collect_output** – Should we collect all the output from the ranks on the master rank?
- **schedule** – The parallelization schedule to be used. See also parallel_over_axes.schedule
- **result** – The result form the task_function. If self.__data_collected is set and we are the root then this will a list with the the output of all tasks
- **blocks** – List with tuples describing the selected subset of data processed by the given block task. If self.__data_collected is set and we are the root rank then this is a list of all the blocks processed by each rank.
- **block_times** – List of times in seconds used to process the data block with the given index. NOTE: The block times include also any required communications and other operations to initialize and complete the task, and not just the execution of the task function itself.
- **run_time** – Float time in seconds for executing the run function.
- **comm** – The MPI communicator used for the parallelization. Default value is MPI.COMM_WORLD

Parameters

- **task_function** – The function we should run.
- **task_function_params** – Dict with the input parameters for the function. May be None or {} if no parameters are needed.
- **main_data** – Dataset over which we should parallelize
- **split_axes** – List of integer axis indicies over which we should parallelize
- **main_data_param_name** – The name of data input parameter of the task function
- **root** – The master MPI rank (Default=0)
- **schedule** – The task scheduling schema to be used (see parallel_over_axes.SCHEDULES
- **comm** – The MPI communicator used for the parallelization. Default value is None, in which case MPI.COMM_WORLD is used

```
MPI_MESSAGE_TAGS = {'BLOCK_MSG': 12, 'COLLECT_MSG': 13, 'RANK_MSG': 11}
SCHEDULES = {'DYNAMIC': 'DYNAMIC', 'STATIC_1D': 'STATIC_1D', 'STATIC': 'STATIC'}
collect_data(force_collect=False)
    Collect the results from the parallel execution to the self.root rank.

NOTE: On the root the self.result, self.blocks, and self.block_times variables are updated with the collected data as well and self.__data_collected will be set

NOTE: If the data has already been collected previously (ie., collect_data has been called before), then the collection will not be performed again, unless force_collect is set.
```

Parameters **force_collect** – Set this parameter to force that data collection is performed again. By default the collect_data is performed only once for each time the run(..) function is called and the results are reused to ensure consistent data structures. We can force that collect will be reexecuted anyways by setting force_collect.

Returns On worker ranks (i.e., MPI_RANK!=self.root) this is simply the self.result and self.blocks containing the result created by run function. On the root rank (i.e., MPI_RANK!=self.root) this is a tuple of two lists containing the combined data of all self.result and self.blocks from all ranks respectively.

run()

Call this function to run the function in parallel.

Returns

Tuple with the following elements:

1. List with the results from the local execution of the task_function. Each entry is the result from one return of the task_function. In the case of static execution, this is always a list of length 1.
2. List of block_indexes. Each block_index is a tuple with the selection used to divide the data into sub-blocks. In the case of static decomposition we have a range slice object along the axes used for decomposition whereas in the case of dynamic scheduling we usually have single integer point selections for each task.

omsi.shared.mpi_helper.test_mpi_available()

This function import MPI in a separate process to safely check if MPI is available. This precaution is necessary as on Cray systems importing MPI can lead to a crash on, e.g., login nodes where the use of MPI is not permitted. By executing the import in a separate process we avoid crashing the main process and we can safely check whether the process aborted or not.

Returns False if the import failed, otherwise return True

10.1.5 workflow Package

<i>omsi.workflow</i>	Package with modules for specification and execution of analysis tasks
<i>omsi.workflow.common</i>	Module defining basic data structures used by workflows.
<i>omsi.workflow.driver</i>	Package with drivers for analyses and workflows.
<i>omsi.workflow.driver.base</i>	Module with base classes for workflow drivers.
<i>omsi.workflow.driver.cl_analysis_driver</i>	Module used to help with driving the execution of omsi-based analyses.
<i>omsi.workflow.driver.cl_workflow_driver</i>	Module used to help with driving the execution of analysis workflows
<i>omsi.workflow.executor</i>	Package with executors of analysis workflows.

Table 10.13 – continued from previous page

<code>omsi.workflow.executor.base</code>	Module containing base classes for workflow executors.
<code>omsi.workflow.executor.greedy_executor</code>	Module used to help with the execution of complex analyses workflows

workflow Package

Package with modules for specification and execution of analysis tasks and complex analysis workflows.

common Module

Module defining basic data structures used by workflows.

```
class omsi.workflow.common.RawDescriptionDefaultHelpArgParseFormatter(prog, indent_increment=2, max_help_position=24, width=None)
```

Bases: argparse.ArgumentParserHelpFormatter, argparse.RawDescriptionHelpFormatter

Simple derived formatter class for use with argparse used by the cl_analysis_driver class. This formatter combines the default argparse.ArgumentParserHelpFormatter and argparse.RawDescriptionHelpFormatter for formatting arguments and help descriptions.

```
class omsi.workflow.common.analysis_task_list(analysis_objects=None)
```

Bases: list

Define a python list of analyses to be executed as a workflow. The list allows only for storage of analysis_base objects and ensures uniqueness of elements in the list.

Initialize the set of analysis tasks to be performed as part of the workflow

Parameters `analysis_objects` – Set or list of unique analysis objects to be added. Duplicates will be removed.

add (`analysis_object`)

Same as append

add_all ()

Add all known analyses to the workflow list

Returns The updated analysis_task_list with all analyses added

add_analysis_dependencies ()

Add the dependencies of all analyses to the workflow list in case they are missing.

This function is recursive, step-by-step adding all dependencies of the workflow to the list of tasks to be executed, until no more dependencies are found.

Usually this function is called by the workflow executor itself before running the analysis and should not need to be called by the user.

Returns Integer indicating the number of dependencies added to the list of tasks

classmethod all ()

Get an analysis_task_list of all current analysis_base objects

Returns New analysis_task_list of all current analysis objects

analysis_identifiers_unique ()

Check whether all identifiers of the analyses in the this list are unique. :return: bool

append(*analysis_object*)

Add a given analysis to the set of object to be executed by the workflow

This is the same as set.add() but we ensure that only analysis_base objects are added.

Parameters **analysis_object** (`omsi.analysis.base.analysis_base`) – Analysis object to be added to the execution. All dependencies of the analysis will also be executed as part of the execution.

Raises ValueError is raised if the given analysis_object is invalid

clear()

Remove all elements from the list

enable_memory_profiling(*enable=True*)

Enable or disable line-by-line profiling of memory usage of execute_analysis.

Parameters **enable_memory** (*bool*) – Enable (True) or disable (False) line-by-line profiling of memory usage

Raises ImportError is raised if a required package for profiling is not available.

enable_time_and_usage_profiling(*enable=True*)

Enable or disable profiling of time and usage of code parts of execute_analysis for all analyses.

Parameters **enable** (*bool*) – Enable (True) or disable (False) profiling

Raises ImportError is raised if a required package for profiling is not available.

classmethod from_script_files(*script_files*)

Same as from_script, but the script is read from the given files.

Parameters **script_files** – List of strings with the paths to the script files. If only a single script is used, then a single string may be used as well.

Returns An instance of workflow_base with the specification of the workflow to be executed

classmethod from_scripts(*scripts*)

Evaluate the workflow script to extract all analyses to be run.

NOTE: This function executes using eval(..), i.e., there are NO safeguards against malicious codes.

Parameters **scripts** – The script with the setup of the workflow. This should only include the definition of analyses and their inputs.

Returns An instance of workflow_base with the specification of the workflow to be executed

get_additional_analysis_dependencies()

Compute a list of all dependencies of the current list of analyses (excluding analyses that are already in the the list of tasks.

Returns analysis_task_list of all analysis dependencies

get_all_analysis_data()

Get a list of all output data objects for all analysis

Returns List of `omsi.analysis.analysis_data.analysis_data` objects, one for each analysis

get_all_analysis_identifiers()

Get a list of all analysis identifiers

Returns List of strings with the analysis identifier of each analysis

get_all_dependency_data()

Get the complete list of all direct and indirect dependencies of all analysis tasks.

NOTE: These are only the direct dependencies as specified by the analysis itself. Use `get_all_dependency_data_recursive(..)` to also get the indirect dependencies of the analysis due to dependencies of the dependencies themselves.

Returns List of parameter_data objects that define dependencies.

get_all_parameter_data (*exclude_dependencies=False*)

Get the complete list of all parameters

Parameters `exclude_dependencies` – Boolean indicating whether we should exclude parameters that define dependencies from the list

Returns List of omsi.analysis.analysis_data.parameter_data objects with the description of the parameters

get_all_run_info()

Get a list of dict with the complete info about the last run of each of the analysis analysis

Returns List of run_info_dict objects, one for each analysis

insert (*index, analysis_object*)

Insert a given analysis object at the given location

Parameters

- `index` – Location where the obejct should be inserted
- `analysis_object` – The analysis object to be inserted

make_analysis_identifiers_unique()

Update analysis identifiers to be unique.

Side effects: This function updates the analysis tasks stored in the set

Returns self, i.e., the modified object with identifiers updated

set_undefined_analysis_identifiers()

Check that all analysis descriptors are set to a value different than “undefined” and set the descriptor based on their index in the list if necessary.

update (*analysis_objects*)

Return the set with elements added from the given set of analysis_objects.

This is the same as `set.update()` but we ensure that only analysis_base objects are added.

Parameters `analysis_objects` – List or set of analysis_base objects to be added to workflow set

Raise ValueError is raised in case that objects that are not instances of analysis_base are to be added.

Returns self with elements added to self.

Subpackages

driver Package

driver Package Package with drivers for analyses and workflows. Drivers are intened to control the set up—i.e., creation and initialization—of workflows. The execution of workflows itself is typically performed by a workflow executor.

base Module Module with base classes for workflow drivers.

Workflow drivers are responsible for the creation and initialization of workflows. The execution of workflows is then controlled by the workflow executor.

class omsi.workflow.driver.base.**analysis_driver_base** (*analysis_class*)
Bases: *omsi.workflow.driver.base.driver_base*

Base class defining the minimal interface for drivers of a single analysis based on the type/class of the analysis.

This is a class-based execution, i.e, the user defines only the type of analysis and inputs but does not actually create the analysis.

Derived classes must implement the main(...) function where the analysis is created and executed.

Variables **analysis_class** – The analysis class for which we want to execute the analysis. The analysis class must derive from omsi.analysis.analysis_base. May be None in case that we use other means to set the analysis_class, e.g., via the command-line.

Initialize the analysis driver

Variables **analysis_class** – The analysis class for which we want to execute the analysis. The analysis class must derive from omsi.analysis.analysis_base. May be None in case that we use other means to set the analysis_class, e.g., via the command-line.

main()

The main function for running the analysis.

class omsi.workflow.driver.base.**driver_base**
Bases: object

Primitve base class for driving the execution of an object

execute()

Same as main

main()

The main function for running the analysis.

class omsi.workflow.driver.base.**workflow_driver_base** (*workflow_executor*)
Bases: object

Base class defining the minimal interface for drivers of complex analysis workflows.

Workflows may be specified via scripts or given via a set of analysis objects.

Derived classes must implement the main(...) function where the analysis is created and executed.

Variables **workflow_executor** – The executor of the workflow.

Initialize the workflow driver

Parameters **workflow_executor** – The executor of the workflow we want to drive.

main()

The main function for running the analysis.

cl_analysis_driver Module Module used to help with driving the execution of omsi-based analyses.

class omsi.workflow.driver.cl_analysis_driver.**cl_analysis_driver** (*analysis_class*,
add_analysis_class_arg=False,
add_output_arg=True,
add_log_level_arg=True)
Bases: *omsi.workflow.driver.base.analysis_driver_base*

Command-line analysis driver.

Variables

- **`analysis_class_arg_name`** – The name for the argument where the positional argument for defining the analysis class should be stored.
- **`output_save_arg_name`** – Name of the optional keyword argument for specifying the name and target for the analysis
- **`analysis_class_arg_name`** – Name of the optional first positional argument to be used to define the analysis class to be used.
- **`log_level_arg_name`** – Name of the keyword cl argument to define the level of logging to be used.
- **`analysis_class`** – The class (subclass of `analysis_base`) defining the analysis to be executed
- **`analysis_object`** – Instance of the analysis object to be executed
- **`add_analysis_class_arg`** – Boolean indicating whether an optional positional command line argument should be used to determine the analysis class (or whether the analysis class will be set explicitly)
- **`add_output_arg`** – Boolean indicating whether an optional keyword argument should be added to define the output target for the analysis.
- **`add_log_level_arg`** – Boolean indicating whether the `-loglevel` argument should be added to the command line
- **`parser`** – The `argparse.ArgumentParser` instance used for defining command-line arguments
- **`required_argument_group`** – `argparse.ArgumentParser` argument group used to define required command line arguments
- **`custom_argument_groups`** – Dict of custom `argparse.ArgumentParser` argument groups specified by the analysis
- **`output_target`** – Specification of the output target where the analysis result should be stored
- **`analysis_arguments`** – Dictionary defining the input arguments to be used for the analysis
- **`mpi_root`** – Integer indicating the root rank when running using MPI
- **`mpi_comm`** – Integer indicating the MPI communicator to be used when running in parallel using MPI

Parameters

- **`analysis_class`** (`omsi.analysis.base.analysis_base`) – The analysis class for which we want to execute the analysis. The analysis class must derive from `omsi.analysis.analysis_base`. May be `None` in case that we use the command-line to define the analysis class via the optional positional argument for the command class (i.e., set `add_analysis_class_arg` to `True`).
- **`add_analysis_class_arg`** – Boolean indicating whether we will use the positional command-line argument to determine the analysis class name
- **`add_output_arg`** – Boolean indicating whether we should add the optional keyword argument for defining the output target for the analysis.

- **add_log_level_arg** – Boolean indicating whether we should add the option keyword argument to specify the logging level via the command line.

Raises A ValueError is raised in the case of conflicting inputs, i.e., if i) analysis_class==None and add_analysis_class_arg=False, i.e., the analysis class is not determined or ii) analysis_class!=None and add_analysis_class_arg=False, i.e., the analysis class is determined via two separate mechanisms.

add_and_parse_analysis_arguments()

The function assumes that the command line parser has been setup using the initialize_argument_parser(..)

This function is responsible for adding all command line arguments that are specific to the analysis and to then parse those arguments and save the relevant data in the self.analysis_arguments dictionary. Command-line arguments that are specific to the command line driver are removed, so that only arguments that can be consumed by the analysis are handed to the analysis.

Side effects: The function sets self.analysis_arguments

analysis_class_arg_name = ‘_analysis_class’

The name where the positional argument for defining the analysis class will be stored.

create_analysis_object()

Initialize the analysis object, i.e., set self.analysis_object

get_analysis_class_from_cl()

Internal helper function used to get the analysis class object based on the analysis_class_arg_name positional argument from the command line.

Side effects: The function sets “self.analysis_class”

Raises ImportError in case that the analysis module cannot be loaded

Raises AttributeError in case that the analysis class cannot be extracted from the module

initialize_argument_parser()

Internal helper function used to initialize the argument parser. NOTE: self.analysis_class must be set before calling this function.

Side effects: The function sets self.parser and self.required_argument_group

log_level_arg_name = ‘loglevel’

Name of the keyword argument used to specify the level of logging to be used

main()

Default main function for running an analysis from the command line. The default implementation exposes all specified analysis parameters as command line options to the user. The default implementation also provides means to print a help text for the function.

Raises ValueError is raised in case that the analysis class is unknown

output_save_arg_name = ‘save’

Name of the key-word argument used to define

parse_cl_arguments()

The function assumes that the command line parser has been setup using the initialize_argument_parser(..)

This function parses all arguments that are specific to the command-line parser itself. Analysis arguments are added and parsed later by the add_and_parse_analysis_arguments(...) function. The reason for this is two-fold: i) to separate the parsing of analysis arguments and arguments of the command-line driver and ii) if the same HDF5 file is used as input and output target, then we need to open it first here in append mode before it gets opened in read mode later by the arguments.

Side effects: The function sets self.output_target and self.profile_analysis

print_settings()
Print the analysis settings.

remove_output_target()

This function is used to delete any output target files created by the command line driver. This is done in case that an error occurred and we do not want to leave garbage files left over.

Side effects The function modifies self.output_target

Returns Boolean indicating whether we successfully cleaned up the output

reset_analysis_object()

Clear the analysis object and recreate it, i.e., delete self.analysis_object and set it again.

cl_workflow_driver Module Module used to help with driving the execution of analysis workflows

```
class omsi.workflow.driver.cl_workflow_driver(workflow_executor=None,  
                                              add_script_arg=False,  
                                              add_output_arg=True,  
                                              add_log_level_arg=True,  
                                              add_profile_arg=False,  
                                              add_mem_profile_arg=False)
```

Bases: *omsi.workflow.driver.base.workflow_driver_base*

Command-line workflow driver.

Variables

- **script_arg_name** – Name of the optional keyword cl argument for defining workflow scripts to be executed
- **output_save_arg_name** – Name of the optional keyword argument for specifying the name and target for the workflow. This may be a folder or an HDF5 file ending with .h5
- **profile_arg_name** – Name of the keyword argument used to enable profiling of the analysis
- **profile_mem_arg_name** – Name of the keyword argument used to enable profiling of memory usage of an analysis
- **log_level_arg_name** – Name of the keyword cl argument to define the level of logging to be used.
- **workflow_executor** – The workflow executor object used to execute the analysis workflow. The workflow executor must derive from omsi.workflow.executor.base.workflow_executor_base. May be None in case that we use the command-line to define workflow executor or if the default executor should be used. The default executor class is defined by omsi.workflow.executor.base.workflow_executor_base.
- **script_files** – List of strings with the paths to files with workflow scripts to be executed.
- **add_script_arg** – Boolean indicating whether the –script keyword argument should be added to the command-line, to define the workflow scripts via the CL (or whether the scripts will be set explicitly)
- **add_output_arg** – Boolean indicating whether an optional keyword argument should be added to define the output target for the analysis.
- **add_profile_arg** – Add the optional –profile keyword argument for profiling the analysis

- **add_mem_profile_arg** – Boolean indicating whether we should add the optional keyword argument for enabling memory profiling of the analysis.
- **add_log_level_arg** – Boolean indicating whether we should add the option keyword argument to specify the logging level via the command line.
- **parser** – The argparse.ArgumentParser instance used for defining command-line arguments
- **required_argument_group** – argparse.ArgumentParser argument group used to define required command line arguments
- **optional_argument_group** – argparse.ArgumentParser argument group used to define optional command line arguments
- **custom_argument_groups** – Dict of custom argparse.ArgumentParser argument groups specified by the analysis
- **identifier_argname_separator** – String used to separate the analysis identifier and argument name when creating custom command-line options for the individual analyses of the workflow
- **output_target** – Specification of the output target where the analysis result should be stored
- **profile_analyses** – Boolean indicating whether we should profile the analysis for time and usage
- **profile_analyses_mem** – Boolean indicating whether we should profile the memory usage of the individual analyses
- **analysis_arguments** – Dictionary defining the custom input arguments to be used for the analysis
- **workflow_executor_arguments** – Dictionary defining the custom input arguments routed to the workflow executor
- **__output_target_self** – Private member variable used to store the output files created by this object.
- **user_log_level** – The custom logging level specified by the user (or None)
- **mpi_root** – The root rank used when running in parallel
- **mpi_comm** – The mpit communicator to be used when running in parallel

Parameters

- **workflow_executor** (`omsi.analysis.base.analysis_base`) – The workflow executor object used to execute the analysis workflow. The workflow executor must derive from `omsi.workflow.executor.base.workflow_executor_base`. May be None in case that we use the command-line to define workflow executor or if the default executor should be used. The default executor class is defined by `omsi.workflow.executor.base.workflow_executor_base`.
- **add_script_arg** – Boolean indicating whether the `--script` keyword argument should be added to the command-line, to define the workflow scripts via the CL (or whether the scripts will be set explicitly)
- **add_output_arg** – Boolean indicating whether we should add the optional keyword argument for defining the output target for the analysis.
- **add_log_level_arg** – Boolean indicating whether we should add the option keyword argument to specify the

logging level via the command line. :param add_profile_arg: Boolean indicating whether we should add the optional keyword

argument for enabling profiling of the analysis.

Parameters `add_mem_profile_arg` – Boolean indicating whether we should add the optional keyword argument for enabling memory profiling of the analysis.

Raises A ValueError is raised in the case of conflicting inputs, i.e., if i) workflow_executor==None and add_script_arg=False, i.e., the analysis class is not determined or ii) workflow_executor!=None and add_script_arg=False, i.e, the analysis class is determined via two separate mechanisms.

`add_and_parse_workflow_arguments()`

The function assumes that the command line parser has been setup using the `initialize_argument_parser(..)`

This function is responsible for adding all command line arguments that are specific to the workflow and to then parse those arguments and save the relevant data in the `self.analysis_arguments` dictionary. Command-line arguments that are specific to the command line driver are removed, so that only arguments that can be consumed by the analysis are handed to the analysis.

Side effects: The function sets `self.analysis_arguments` and updates the analysis parameters of the analyses stored in `self.workflow_executor.analysis_tasks`

`create_workflow_executor_object()`

Initialize the workflow executor object, i.e., set `self.workflow_executor`

Side effects This function potentially modifies `self.workflow_executor`

`initialize_argument_parser()`

Internal helper function used to initialize the argument parser.

Side effects: The function sets:

- `self.parser`
- `self.required_argument_group`
- `self.optional_argument_group`

`log_level_arg_name = 'loglevel'`

Name of the keyword argument used to specify the level of logging to be used

`main()`

Default main function for running an analysis from the command line. The default implementation exposes all specified analysis parameters as command line options to the user. The default implementation also provides means to print a help text for the function.

Raises ValueError is raised in case that the analysis class is unknown

`output_save_arg_name = 'save'`

Name of the key-word argument used to define

`parse_cl_arguments()`

The function assumes that the command line parser has been setup using the `initialize_argument_parser(..)`

This function parses all arguments that are specific to the command-line parser itself. Analysis workflow arguments are added and parsed later by the `add_and_parse_workflow_arguments(...)` function. The reason for this is two-fold: i) to separate the parsing of analysis arguments and arguments of the command-line driver and ii) if the same HDF5 file is used as input and output target, then we need to open it first here in append mode before it gets opened in read mode later by the arguments.

Side effects: The function sets:

```
    • self.output_target
    • self.profile_analyses

print_memory_profiles()
    Print the memory profiles if available

print_settings()
    Print the analysis settings.

print_time_and_usage_profiles()
    Print the profiling data for time and usage if available

profile_arg_name = ‘profile’
    Name of the keyword argument used to enable profiling of the analysis

profile_mem_arg_name = ‘memprofile’
    Name of the keyword argument used to enable profiling of memory usage of an analysis

remove_output_target()
    This function is used to delete any output target files created by the command line driver. This is done in case that an error occurred and we do not want to leave garbage files left over.

    Side effects The function modifies self.output_target

    Returns Boolean indicating whether we successfully cleaned up the output

reset_workflow_executor_object()
    Remove and recreate the workflow executor object

script_arg_name = ‘script’
    The name where the positional argument for defining the analysis class will be stored.
```

executor Package

executor Package Package with executors of analysis workflows. Executors perform and control the execution of workflows. The setup of workflows is often performed by the user or via dedicated workflow drivers.

base Module Module containing base classes for workflow executors.

Workflow executors control the execution of workflows. The setup of workflows is often controlled either by a workflow driver or the user.

```
class omsi.workflow.executor.base.workflow_executor_base(analysis_objects=None)
Bases: omsi.datastructures.analysis_data.parameter_manager
```

Base class used to execute a workflow of one or many analyses. This is an object-based execution, i.e., the user defines a set of analyses to be executed.

We are given a set of existing analysis objects for which we need to coordinate the execution.

Variables

- **analysis_objects** – Private set of analysis objects to be executed
- **DEFAULT_EXECUTOR_CLASS** – Define the derived workflow_executor_base class to be used as default executor. The default value is None, in which case the greedy_workflow_executor is used. This variable is used by the get_default_executor function to instantiate a default workflow executor on request. Using this variable we can change the default executor to our own preferred executor, e.g., to change the executor used by the omsi.analysis.base.analysis_base functions execute_all(...) and execute_recursive(...)

To implement a derived workflow executor, we need to implement a derived class that implements the main() function.

Initialize the workflow executor

Parameters `analysis_objects` – A list of analysis objects to be executed

`DEFAULT_EXECUTOR_CLASS = None`

The default executor class to be used

`add_analysis(analysis_object)`

Add a given analysis to the set of object to be executed by the workflow

Shorthand for: `self.analysis_tasks.add(analysis_object)`

`add_analysis_all()`

Add all known analyses to the workflow.

Shorthand for: `self.analysis_tasks.add_analysis_all()`

`add_analysis_dependencies()`

Add the dependencies of all analyses to the workflow in case they are missing.

This function is recursive, step-by-step adding all dependencies of the workflow to the list of tasks to be executed, until no more dependencies are found.

Usually this function is called by the workflow executor itself before running the analysis and should not need to be called by the user.

Returns Integer indicating the number of dependencies added to the list of tasks

`add_analysis_from_scripts(script_files)`

Evaluate the list of scripts and add all (i.e., zero, one, or multiple) analyses to this workflow

NOTE: This function executes scripts using exec(..), i.e., there are NO safeguards against malicious codes.

Parameters `script_files` – List of strings with the paths to the script files. If only a single script is used, then a single string may be used as well.

`clear()`

Remove all analyses from the workflow.

Shorthand for: `self.analysis_tasks.clear()`

`execute()`

Execute the workflow. This uses the main() function to run the actual workflow.

`classmethod from_script_files(script_files)`

Same as from_script, but the scripts are read from the given list of files.

NOTE: This function executes scripts using exec(..), i.e., there are NO safeguards against malicious codes.

Parameters `script_files` – List of strings with the paths to the script files. If only a single script is used, then a single string may be used as well.

Returns Instance of the current workflow executor class for running the given workflow

`classmethod from_scripts(scripts)`

Create and initialize a workflow executor of the current class type to execute the workflow defined in the given set of scripts.

This function uses `analysis_task_list.from_scripts` to evaluate the workflow scripts to extract all analyses to be created.

NOTE: This function executes scripts using exec(..), i.e., there are NO safeguards against malicious codes.

Parameters **scripts** – The script with the setup of the workflow. This should only include the definition of analyses and their inputs.

Returns Instance of the current workflow executor class for running the given workflow

get_analyses()

Get the list of analyses to be run.

Shorthand for: self.analysis_tasks

get_analysis(index)

Get the analysis with the given index

Shorthand for: self.analysis_tasks[index]

Parameters **index** – Integer index of the analysis

Returns omsi.analysis.base.analysis_base object

Raises IndexError in case that the index is invalid

classmethod get_default_executor(analysis_objects=None)

Create an instance of the default workflow executor to be used.

Parameters **analysis_objects** – A set or unique list of analysis objects to be executed by the workflow

Returns Instance of the default workflow executor

classmethod get_default_executor_class()

Get the default executor class

Returns Derived class of workflow_executor_base

main()

Implement the execution of the workflow. We should always call execute(..) or __call__(..) to run the workflow. This function is intended to implement the executor-specific execution behavior and must be implemented in child classes.

greedy_executor Module Module used to help with the execution of complex analyses workflows

class omsi.workflow.executor.greedy_executor.**greedy_executor(analysis_objects=None)**

Bases: *omsi.workflow.executor.base.workflow_executor_base*

Execute a set of analysis objects and their dependencies

Variables

- **run_info** – The runtime information dictionary for the overall workflow
- **mpi_comm** – The MPI communicator to be used when running in parallel
- **mpi_root** – The MPI root rank when running in parallel

Additional parameters:

Parameters **reduce_memory_usage** – Boolean indicating whether we should reduce memory usage by pushing analysis data to file after an analysis has been completed. This reduces the amount of data we keep in memory but results in additional overhead for I/O and temporary disk storage.

Initialize the workflow driver

Parameters **analysis_objects** – A list of analysis objects to be executed

```
main()  
Execute the analysis workflow
```

10.1.6 tools Package

<code>omsi.tools</code>	Package for collecting tools (e.g.,
<code>omsi.tools.convertToOMSI</code>	Tool used to convert img files to OpenMSI HDF5 files.
<code>omsi.tools.run_analysis</code>	Simple helper tool to run an analysis.
<code>omsi.tools.run_workflow</code>	Simple helper tool to run a workflow.
<code>omsi.tools.misc</code>	Collection of miscellaneous tools.
<code>omsi.tools.misc.create_peak_cube_overview</code>	Simple helper tool used to generate a set of PNG images for a global
<code>omsi.tools.misc.make_thumb</code>	Simple script to generate thumbnail images
<code>omsi.tools.experimental</code>	Collection of experimental tools and tools under development.

convertToOMSI Module

Tool used to convert img files to OpenMSI HDF5 files.

For usage information execute: `python convertToOMSI --help`

```
class omsi.tools.convertToOMSI.ConvertFiles  
Bases: object
```

Class providing a number of functions for converting various file types to OMSI, including a number of helper functions related to the data conversion.

```
static check_format(name, format_type)
```

Helper function used to determine the file format that should be used

Parameters

- **name** – Name of the folder/file that we should read
- **format_type** – String indicating the format-option given by the user. If the format is not determined (i.e., “auto”) then this function tries to determine the appropriate format. Otherwise this option is returned as is, as the user explicitly said which format should be used.

Returns String indicating the appropriate format. Returns None in case no valid option was found.

```
static convert_files()
```

Convert all files in the given list of files with their appropriate conversion options

```
static create_dataset_list(input_filenames, format_type=None,  
                           data_region_option='split+merge')
```

Based on the list of input_filenames, generate the ConvertSettings.dataset_list, which contains a dictionary describing each conversion job

Parameters

- **input_filenames** – List of names of files to be converted.
- **format_type** – Define which file-format should be used. Default value is ‘auto’ indicating the function should determine for each file the format to be used. See also ConvertSettings.available_formats parameter.

- **data_region_option** – Define how different regions defined for a file should be handled. E.g., one may want to split all regions into individual datasets ('split'), merge all regions into a single dataset ('merge'), or do both ('split+merge'). See also the ConvertSettings.available_region_options parameter for details. By default the function will do 'split+merge'.

Returns

List of dictionaries describing the various conversion jobs. Each job is described by a dict with the following keys:

- 'basename' : The base name of the file or directory with the data
- 'format' : The data format to be used
- 'dataset' : The index of the dataset to be converted if the input stores multiple data cubes
- 'region' : The index of the region to be converted if the input defines multiple regions
- 'exp' : One of 'previous' or 'new', defining whether a new experiment should be created or whether the experiment from the previous conversion(s) should be reused.

static suggest_chunking (xsize, ysize, mzsize, dtype, print_results=False)

Helper function used to suggest good chunking strategies for a given data cube

Parameters

- **xsize** – Size of the dataset in x.
- **ysize** – Size of the dataset in y.
- **mzsize** – Size of the dataset in mz.
- **print_results** – Print the results to the console.

Returns

Three tuples:

- spectrum_chunk : The chunking to be used to optimize selection of spectra.
- slice_chunk : The chunking to be used to optimize selection of image slices.
- balanced_chunk : The chunking that would provide a good balance in performance for different selection strategies.

static suggest_chunkings_for_files (in_dataset_list)

Helper function used to suggest good chunking strategies for a given set of files.

Parameters **in_dataset_list** – Python list of dictionaries describing the settings to be used for the file conversion

Returns This function simply prints results to standard-out but does not return anything.

static write_data (input_file, data, data_io_option='spectrum', chunk_shape=None, write_progress=True)

Helper function used to implement different data write options.

Parameters

- **input_file** – The input data file
- **data** – The output dataset (either an h5py dataset or omsi_file_msidata object).
- **data_io_option** – String indicating the data write method to be used. One of:
 - spectrum: Write the data one spectrum at a time

- `all` : Write the complete dataset at once.
- `chunk` : Write the data one chunk at a time.
- `chunk_shape` – The chunking used by the data. Needed to decide how the data should be written when a chunk-aligned write is requested.
- `write_progress (bool)` – Write progress in % to standard out while data is being written.

```
class omsi.tools.convertToOMSI.ConvertSettings
Bases: object
```

This class is used specify the settings for the data conversion

```
add_file_to_db = True
auto_chunk = True
available_error_options = ['terminate-and-cleanup', 'terminate-only', 'continue-on-error']
available_formats = {'imzml_file': <class 'omsi.dataformat.imzml_file.imzml_file'>, 'bruckerflex_file': <class 'omsi.
available_io_options = ['chunk', 'spectrum', 'all']
available_region_options = ['split', 'merge', 'split+merge']
check_add_nersc = True
chunks = (4, 4, 2048)
compression = 'gzip'
compression_opts = 4
dataset_list = []
```

Parameters `dataList` – List of python dictionaries describing specific conversion settings for each conversion task. Each dictionary contains the following keys:

- ‘basename’ : Name of the file to be converted
- ‘format’ : File format to be used (see `ConvertSettings.available_formats`)
- ‘exp’ : Indicate the experiment the dataset should be stored with. Valid values are
 - ‘new’ : Generate a new experiment for the dataset
 - ‘previous’ : Use the same experiment as used for the previous dataset
 - 1, 2,3... : Integer value indicating the index of the experiment to be used.
- ‘region’ : Optional key with index of the region to be converted. None to merge all regions.
- ‘dataset’ : Optional key with index of the dataset to be converted.
- ‘omsi_object’ : Optional key used to save a pointer to the omsi data object with the converted data
- ‘dependencies’ : Additional dependencies that should be added for the dataset

```
db_server_url = 'https://openmsi.nersc.gov/'
email_error_recipients = []
email_success_recipients = []
error_handling = 'terminate-and-cleanup'
execute_fpg = True
```

```
execute_fpl = False
execute_nmf = True
execute_ticnorm = False
file_user = 'oruebel'
format_option = None
generate_thumbnail = False
generate_xdmf = False
io_block_size_limit = 524288000
io_option = 'spectrum_to_image'
job_id = None
metadata = {}
nmf_num_component = 20
nmf_num_iter = 2000
nmf_timeout = 600
nmf_tolerance = 0.0001
nmf_use_raw_data = False
omsi_output_file = None
```

classmethod parse_input_args (argv)

Process input parameters and define the script settings.

Parameters **argv** – The list of input arguments

Returns

This function returns the following four values:

- ‘input_error’ : Boolean indicating whether an error has occurred during the processing of the inputs
- ‘inputWarning’ : Boolean indicating whether a warning occurred during the processing of the inputs
- ‘output_filename’ : Name for the output HDF5 file
- ‘input_filenames’ : List of strings indicating the list of input filenames

classmethod print_help ()

Function used to print the help for this script

```
recorded_warnings = []
region_option = 'split+merge'
suggest_file_chunkings = False
user_additional_chunks = []
```

omsi.tools.convertToOMSI.main (argv=None)

The main function defining the control flow for the conversion

run_analysis Module

Simple helper tool to run an analysis. This is essentially just a short-cut to the omsi/workflow/analysis_driver/omsi_cl_driver module

run_workflow Module

Simple helper tool to run an analysis. This is essentially just a short-cut to the omsi/workflow/analysis_driver/omsi_cl_driver module

Subpackages**tools.experimental Package**

tools.experimental Package Collection of experimental tools and tools under development.

tools.misc Package

tools.misc Package Collection of miscellaneous tools.

make_thumb Module Simple script to generate thumbnail images

`omsi.tools.misc.make_thumb.main(argv=None)`

Then main function

create_peak_cube_overview Module Simple helper tool used to generate a set of PNG images for a global peak analysis (one per global peak) as well as a LaTeX document that summarizes all the images in a single document.

NOTE: The module will try to build the LaTeX document using pdflatex, i.e, it is assumed that pdflatex is available.

`omsi.tools.misc.create_peak_cube_overview.main(argv=None)`

Then main function

`omsi.tools.misc.create_peak_cube_overview.print_help()`

Print the user help information to standard out.

10.1.7 examples Package

`omsi.examples` Package with a collection of various misc.

simple_viewer Module

Simple viewer for OpenMSI data

class `omsi.examples.simple_viewer.MyViewer(data, mzdata)`

Create a simple viewer with image of the data and a cruve plot for a spectrum.

Parameters

- **data** – Reference to the hdf5 dataset of the image

- **mzdata** – mz values of the instrument to be displayed as axis in the curve plot. may be None in case the mz data is unknown

```
omsi.examples.simple_viewer.main(argv=None)
    Then main function
```

testHDF5Optimization Module

Simple test script used to test the performance of different HDF5 optimizations (using chunking) to improve the performance of hyperslap selections

```
omsi.examples.testHDF5Optimization.generateTestFile(omsiOutFile, xdim, ydim, zdim,
                                                    xchunk, ychunk, zchunk)
```

```
omsi.examples.testHDF5Optimization.main(argv=None)
    Then main function
```

```
omsi.examples.testHDF5Optimization.printHelp()
    Print the help explaining the usage of testHDF5Optimation
```

testHDF5Optimization_alignedWrite Module

```
omsi.examples.testHDF5Optimization_alignedWrite.generateTestFile(omsiOutFile,
                                                                xdim, ydim,
                                                                zdim, xchunk,
                                                                ychunk,
                                                                zchunk)
```

```
omsi.examples.testHDF5Optimization_alignedWrite.main(argv=None)
    Then main function
```

```
omsi.examples.testHDF5Optimization_alignedWrite.printHelp()
    Print the help explaining the usage of testHDF5Optimation
```

test_multiprocess_slice Module

```
omsi.examples.test_multiprocess_slice.create_process(argv)
```

```
omsi.examples.test_multiprocess_slice.generateBaseTestFile(omsiOutFile, xdim,
                                                          ydim, zdim)
```

```
omsi.examples.test_multiprocess_slice.generateChunkedTestFile(omsiOutFile,
                                                               xdim, ydim, zdim,
                                                               xchunk, ychunk,
                                                               zchunk, compress=False,
                                                               donor-
                                                               File='/project/projectdirs/openmsi/omsi_d
```

```
omsi.examples.test_multiprocess_slice.main(argv=None)
    Then main function
```

```
omsi.examples.test_multiprocess_slice.sliceSelect(args)
```

```
omsi.examples.test_multiprocess_slice.spectraSelect(args)
```

test_par Module

```
omsi.examples.test_par.create_process(argv)
omsi.examples.test_par.generateBaseTestFile(omsiOutFile, xdim, ydim, zdim)
omsi.examples.test_par.generateChunkedTestFile(omsiOutFile, xdim, ydim, zdim, xchunk,
                                              ychunk, zchunk, compress=False, donor-
                                              File='/project/projectdirs/openmsi/omsi_data/old/TEST.h5')
omsi.examples.test_par.main(argv=None)
    Then main function
omsi.examples.test_par.sliceSelect(args)
omsi.examples.test_par.spectraSelect(args)
```

test_peakcube Module

```
omsi.examples.test_peakcube.main(argv=None)
    Then main function
omsi.examples.test_peakcube.printHelp()
```

testhdf5_file_read Module

Simple test script used to test the performance of different HDF5 optimizations (using chunking) to improve the performance of hyperslab selections

```
omsi.examples.testhdf5_file_read.main(argv=None)
    Then main function
omsi.examples.testhdf5_file_read.printHelp()
    Print the help explaining the usage of testHDF5Optimiation
```

10.1.8 templates Package

<code>omsi.templates</code>	This package provides a collection of code templates to ease the development of additional components, e.g., analysis modules.
<code>omsi.templates.analysis_template</code>	Template intended to help with the development of new analysis modules.

templates Package

This package provides a collection of code templates to ease the development of additional components, e.g., analysis modules. As such, this package is NOT intended for direct usage but is rather just a library of code templates.

analysis_template Module

Template intended to help with the development of new analysis modules.

class `omsi.templates.analysis_template.analysis_template(name_key='undefined')`
Bases: `omsi.analysis.base.analysis_base`

Template intended to help with the development of new analysis classes.

Search for EDIT_ME to find locations that need to be changed.

EDIT_ME Search for analysis_template and replace it with your classname throughout

EDIT_ME Replace this doc-string with your class documentation

Initialize the basic data members

execute_analysis()

EDIT_ME Implement this function to implement the execution of the actual analysis.

This function may not require any input parameters. All input parameters are recoded in the parameters and dependencies lists and should be retrieved from there, e.g, using basic slicing self[paramName]

EDIT_ME Remove this comment and replace it with your own documentation. Describe what your analysis does and how a user can use it. Note, a user will call the function execute(...) which takes care of storing parameters, collecting execution data etc., so that you only need to implement your analysis, the rest is taken care of by analysis_base.

Keyword Arguments:

Parameters mydata – ...

Returns This function may return any developer-defined data. Note, all output that should be recorded must be put into the data list.

groups = None

EDIT_ME

Add a list of names of input parameters for your analysis using the self.add_add_parameter.

For parameters that define n-dimension arrays you should specify the dtypes['ndarray'] as dtype. This will allow discovery of dependencies and proper function with the analysis drivers. Other available dtypes include standard built-ins, e.g, int, float etc. See self.get_default_dtypes() for details.

It is also recommended to organize parameters into groups using the default set of groups, e.g., groups['input'], groups['settings'], groups['stop'].

classmethod v_qmz (analysis_object, qslice_viewer_option=0, qspectrum_viewer_option=0)

Get the mz axes for the analysis

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **qslice_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qslice URL pattern.
- **qspectrum_viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them for the qspectrum URL pattern.

Returns

The following four arrays are returned by the analysis:

- mz_spectra : Array with the static mz values for the spectra.
- label_spectra : Lable for the spectral mz axis
- mz_slice : Array of the static mz values for the slices or None if identical to the mz_spectra.
- label_slice : Lable for the slice mz axis or None if identical to label_spectra.

classmethod v_qslice (analysis_object, z, viewer_option=0)

Get 3D analysis dataset for which z-slices should be extracted for presentation in the OMSI viewer

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **z** – Selection string indicating which z values should be selected.
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns numpy array with the data to be displayed in the image slice viewer. Slicing will be performed typically like [::,zmin:zmax].

classmethod v_qslice_viewer_options (analysis_object)

Get a list of strings describing the different default viewer options for the analysis for qslice. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

Parameters **analysis_object** – The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

Returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qslice requests (i.e., v_qslice(...) is not available).

classmethod v_qspectrum (analysis_object, x, y, viewer_option=0)

Get from which 3D analysis spectra in x/y should be extracted for presentation in the OMSI viewer

Developer Note: h5py currently supports only a single index list. If the user provides an index-list for both x and y, then we need to construct the proper merged list and load the data manually, or if the data is small enough, one can load the full data into a numpy array which supports multiple lists in the selection.

Parameters

- **analysis_object** – The omsi_file_analysis object for which slicing should be performed
- **x** – x selection string
- **y** – y selection string
- **viewer_option** – If multiple default viewer behaviors are available for a given analysis then this option is used to switch between them.

Returns

The following two elements are expected to be returned by this function :

1. 1D, 2D or 3D numpy array of the requested spectra. NOTE: The mass (m/z) axis must be the last axis. For index selection x=1,y=1 a 1D array is usually expected. For indexList selections x=[0]&y=[1] usually a 2D array is expected. For range selections x=0:1&y=1:2 we one usually expects a 3D array.
2. None in case that the spectra axis returned by v_qmz are valid for the returned spectrum. Otherwise, return a 1D numpy array with the m/z values for the spectrum (i.e., if custom m/z values are needed for interpretation of the returned spectrum). This may be needed, e.g., in cases where a per-spectrum peak analysis is performed and the peaks for each spectrum appear at different m/z values.

classmethod v_qspectrum_viewer_options (*analysis_object*)

Get a list of strings describing the different default viewer options for the analysis for qspectrum. The default implementation tries to take care of handling the spectra retrieval for all the dependencies but can naturally not decide how the qspectrum should be handled by a derived class. However, this implementation is often called at the end of custom implementations to also allow access to data from other dependencies.

param **analysis_object** The omsi_file_analysis object for which slicing should be performed. For most cases this is not needed here as the support for slice operations is usually a static decision based on the class type, however, in some cases additional checks may be needed (e.g., ensure that the required data is available).

returns List of strings indicating the different available viewer options. The list should be empty if the analysis does not support qspectrum requests (i.e., v_qspectrum(...) is not available).

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