romancal

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Roman calibration pipeline developers

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CHAPTER

ONE

INTRODUCTION

This document provides instructions on running the Roman Science Calibration Pipeline (referred to as "the pipeline") and individual pipeline steps.

CHAPTER

TWO

REFERENCE FILES

Many pipeline steps rely on the use of reference files that contain different types of calibration data or information necessary for processing the data. The reference files are instrument-specific and are periodically updated as the data processing evolves and the understanding of the instruments improves. They are created, tested, and validated by the Roman Instrument Teams. They ensure all the files are in the correct format and have all required attributes. The files are then delivered to the Reference Data for Calibration and Tools (ReDCaT) Management Team. The result of this process is the files being ingested into the Roman Calibration Reference Data System (CRDS), and made available to the pipeline team and any other ground subsystem that needs access to them.

Information about all the reference files used by the Calibration Pipeline can be found at *Reference File Information*, as well as in the documentation for each Calibration Step that uses a reference file.

CHAPTER

THREE

CRDS

CRDS reference file mappings are usually set by default to always give access to the most recent reference file deliveries and selection rules. On occasion it might be necessary or desirable to use one of the non-default mappings in order to, for example, run different versions of the pipeline software or use older versions of the reference files. This can be accomplished by setting the environment variable `CRDS_CONTEXT` to the desired project mapping version, e.g.

```
$ export CRDS_CONTEXT='roman_0017.pmap'
```

Within STScI, the current storage location for all Roman CRDS reference files is:

```
/grp/crds/roman/references/roman/
```

CHAPTER

FOUR

RUNNING FROM THE COMMAND LINE

Individual steps and pipelines (consisting of a series of steps) can be run from the command line using the `strun` command:

```
$ strun <pipeline_name, class_name, or input_file>
```

The first argument to `strun` must be one of either a pipeline name, python class of the step or pipeline to be run. The second argument to `strun` is the name of the input data file to be processed.

For example, the Stage 1 pipeline is implemented by the class *romancal.pipeline.ExposurePipeline*. The command to run this pipeline is:

```
$ strun romancal.pipeline.ExposurePipeline r0008308002010007027_06311_0019_WFI01_uncal.
↪asdf
```

Pipeline classes also have a **pipeline name**, or **alias**, that can be used instead of thefull class specification. For example, `calroman.pipeline.ExposurePipeline` has the alias `roman_elp` and can be run as

```
$ strun roman_elp r0008308002010007027_06311_0019_WFI01_uncal.asdf
```

4.1 Exit Status

`strun` produces the following exit status codes:

- 0: Successful completion of the step/pipeline
- 1: General error occurred
- 64: No science data found

CHAPTER

FIVE

INPUT AND OUTPUT FILE CONVENTIONS

5.1 Input Files

There are two general types of input to any step or pipeline: references files and data files. The references files, unless explicitly overridden, are provided through CRDS.

Data files are the science input, such as exposure ASDF files. All files are assumed to be co-resident in the directory where the primary input file is located.

5.2 Output Files

Output files will be created either in the current working directory, or where specified by the *output_dir* parameter.

File names for the outputs from pipelines and steps come from three different sources:

- The name of the input file
- As specified by the *output_file* parameter

Regardless of the source, each pipeline/step uses the name as a base name, onto which several different suffixes are appended, which indicate the type of data in that particular file. A list of the main suffixes can be *found below*.

The pipelines do not manage versions. When re-running a pipeline, previous files will be overwritten.

5.2.1 Individual Step Outputs

If individual steps are executed without an output file name specified via the `output_file` parameter, the `stpipe` infrastructure automatically uses the input file name as the root of the output file name and appends the name of the step as an additional suffix to the input file name. If the input file name already has a known suffix, that suffix will be replaced. For example:

```
$ strun romancal.dq_init.DQInitStep r0008308002010007027_06311_0019_WFI01_uncal.asdf
```

produces an output file named `r0008308002010007027_06311_0019_WFI01_dq_init.asdf`.

See *Pipeline/Step Suffix Definitions* for a list of the more common suffixes used.

CHAPTER

SIX

PARAMETERS

All pipelines and steps have **parameters** that can be set to change various aspects of how they execute. To see what parameters are available for any given pipeline or step, use the -h option on strun. Some examples are:

```
$ strun roman_elp -h
$ strun calroman.dq_init.DQInitStep -h
```

To set a parameter, simply specify it on the command line. For example, to have *roman_elp* save the calibrated ramp files, the strun command would be as follows:

```
$ strun roman_elp r0008308002010007027_06311_0019_WFI01_uncal.asdf --save_calibrated_
↪ramp=true
```

To specify parameter values for an individual step when running a pipeline use the syntax `--steps.<step_name>.<parameter>=value`. For example, to override the default selection of a dark current reference file from CRDS when running a pipeline:

```
$ strun roman_elp r0008308002010007027_06311_0019_WFI01_uncal.asdf
      --steps.dark_current.override_dark='my_dark.asdf'
```

6.1 Universal Parameters

The set of parameters that are common to all pipelines and steps are referred to as **universal parameters** and are described below.

6.1.1 Output Directory

By default, all pipeline and step outputs will drop into the current working directory, i.e., the directory in which the process is running. To change this, use the output_dir parameter. For example, to have all output from roman_elp, including any saved intermediate steps, appear in the sub-directory calibrated, use

```
$ strun roman_elp r0008308002010007027_06311_0019_WFI01_uncal.asdf
    --output_dir=calibrated
```

output_dir can be specified at the step level, overriding what was specified for the pipeline. From the example above, to change the name and location of the dark_current step, use the following

```
$ strun roman_elp r0008308002010007027_06311_0019_WFI01_uncal.asdf
    --output_dir=calibrated
```

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```
    --steps.dark_current.output_file='dark_sub.asdf'
    --steps.dark_current.output_dir='dark_calibrated'
```

6.1.2 Output File

When running a pipeline, the `stpipe` infrastructure automatically passes the output data model from one step to the input of the next step, without saving any intermediate results to disk.

6.2 Pipeline/Step Suffix Definitions

However the output file name is determined (*see above*), the various pipeline modules will use that file name, along with a set of predetermined suffixes, to compose output file names. The output file name suffix will always replace any known suffix of the input file name. Each pipeline module uses the appropriate suffix for the product(s) it is creating. The list of suffixes is shown in the following table. Replacement occurs only if the suffix is one known to the calibration code. Otherwise, the new suffix will simply be appended to the basename of the file.

Product	Suffix
Uncalibrated raw input	uncal
DQ initialization	dq_init
Saturation detection	saturation
Linearity correction	linearity
Dark current	dark_current
Jump detection	jump
Corrected ramp data	rampfit
Optional fitting results from ramp_fit step	fitopt
Assign WCS	assign_wcs
Flat field	flat
Photometric calibration	phot
Calibrated image	cal

CHAPTER

SEVEN

PACKAGE DOCUMENTATION

7.1 Package Index

7.1.1 Assign WCS

Description

romancal.assign_wcs is the first step run on an image, after romancal.ramp_fitting. It associates a World Coodrinate System (WCS) object with each science exposure. The WCS object transforms positions in the detector frame to positions in the world coordinate frame - ICRS. The WCS can be accessed as an attribute of the meta object when the file is opened as a data model. The forward direction of the transforms is from detector to world coordinates and the input positions are 0-based.

romancal.assign_wcs uses GWCS - a package for managing the World Coordinate System of astronomical data. It expects to find the basic WCS keywords in the model.meta.wcsinfo structure. Distortions are stored in reference files in the ASDF format.

assign_wcs retrieves reference files from CRDS and creates a pipeline of transforms from input frame detector to a frame v2v3. This part of the WCS pipeline may include intermediate coordinate frames. The basic WCS keywords are used to create the transform from frame v2v3 to frame world.

Note: in earlier builds of the pipeline the distortions are not available.

Basic WCS keywords and the transform from v2v3 to world

The following attributes in meta.wcsinfo are used to define the transform from v2v3 to world:

RA_REF, DEC_REF - a fiducial point on the sky, ICRS, [deg]

V2_REF, V3_REF - a point in the V2V3 system which maps to RA_REF, DEC_REF, [arcsec]

ROLL_REF - local roll angle associated with each aperture, [deg]

RADESYS - standard coordinate system [ICRS]

These quantities are used to create a 3D Euler angle rotation between the V2V3 spherical system, associated with the telescope, and a standard celestial system.

Using the WCS interactively

Once a science file is opened as a `DataModel` the WCS can be accessed as an attribute of the meta object. Calling it as a function with detector positions as inputs returns the corresponding world coordinates:

```
>>> from roman_datamodels import datamodels as rdm
>>> image = rdm.open('roman_assign_wcs.asdf')
>>> ra, dec = image.meta.wcs(x, y)
```

The WCS provides access to intermediate coordinate frames and transforms between any two frames in the WCS pipeline in forward or backward direction:

```
>>> image.meta.wcs.available_frames
    ['detector', 'v2v3', 'world']
>>> v2world = image.meta.wcs.get_transform('v2v3', 'world')
>>> ra, dec = v2world(v2, v3)
>>> x1, y1 = image.meta.wcs.invert(ra, dec)
```

There are methods which allow the result of evaluating the WCS object to be an `astropy.SkyCoord` objext (as opposed to numbers) which allows further transformation of coordinates to different coordinate frames.

romancal.assign_wcs Package

Classes

AssignWcsStep([name, parent, config_file, ...])	Assign a gWCS object to a science image.

AssignWcsStep

class `romancal.assign_wcs.`**`AssignWcsStep`**(*name=None*, *parent=None*, *config_file=None*, *_validate_kwds=True*, ***kws*)

Bases: `RomanStep`

Assign a gWCS object to a science image.

Create a `Step` instance.

Parameters

- **name** (*str, optional*) – The name of the Step instance. Used in logging messages and in cache filenames. If not provided, one will be generated based on the class name.
- **parent** (*Step instance, optional*) – The parent step of this step. Used to determine a fully-qualified name for this step, and to determine the mode in which to run this step.
- **config_file** (*str path, optional*) – The path to the config file that this step was initialized with. Use to determine relative path names of other config files.
- ****kws** (*dict*) – Additional parameters to set. These will be set as member variables on the new Step instance.

Attributes Summary

reference_file_types

Methods Summary

process(input)	This is where real work happens.

Attributes Documentation

reference_file_types = ['distortion']

Methods Documentation

process(*input*)

This is where real work happens. Every Step subclass has to override this method. The default behaviour is to raise a NotImplementedError exception.

Class Inheritance Diagram

7.1.2 Data Models

About datamodels

The purpose of the data model is to abstract away the peculiarities of the underlying file format. The same data model may be used for data created from scratch in memory, or loaded from ASDF files or some future file format.

The detailed datamodel structure and specifics are contained in the documentation included with the roman_datamodels package found here (TBD).

Each model instance is created to contain a variety of attributes and data that are needed for analysis or to propagate information about the file and the contents of the file. For example, the `ImageModel` class has the following arrays associated with it:

- `data`: The science data
- `dq`: The data quality array
- `err`: The error array

Along with data arrays the datamodel also contains information about the observation that can include the observation program, exposure information, pointing information and processing steps.

Working with models

Reading a data model

If you have an existing data file it is straightforward to access the file using python.

```
from roman_datamodels import datamodels as rdm
fn = 'r0019106003005004023_03203_0034_WFI01_cal.asdf'
data_file = rdm.open(fn)
type(data_file)
```

<class 'roman_datamodels.datamodels.ImageModel'>

Where the output of the type command tells you that you have imported an ImageModel from roman_datamodels,

Creating a data model from scratch

To create a new `ImageModel`, you can just:

```
from roman_datamodels import datamodels as rdm
from roman_datamodels.testing.factories import create_wfi_image
import numpy as np

image_node = create_wfi_image()
image_model = rdm.ImageModel(image_node)
type(image_model)
#<class 'roman_datamodels.datamodels.ImageModel'>
```

Warning: The values in the file generated by create_wfi_image are intended to be clearly incorrect and should be replaced if the file is intended to be used for anything besides a demonstration.

Creating a data model from a file

The `roman_datamodels.open` function is a convenient way to create a model from a file on disk. It may be passed any of the following:

- a path to an ASDF file
- a readable file-like object

The file will be opened, and based on the nature of the data in the file, the correct data model class will be returned. For example, if the file contains 2-dimensional data, an `ImageModel` instance will be returned. You will generally want to instantiate a model using a `with` statement so that the file will be closed automatically when exiting the `with` block.

```
from roman_datamodels import datamodels
with datamodels.open("myimage.asdf") as im:
    assert isinstance(im, datamodels.ImageModel)
```

If you know the type of data stored in the file, or you want to ensure that what is being loaded is of a particular type, use the constructor of the desired concrete class. For example, if you want to ensure that the file being opened contains 2-dimensional image data:

```
from roman_datamodels.datamodels import ImageModel
with ImageModel("myimage.asdf") as im:
    # raises exception if myimage.asdf is not an image file
    pass
```

This will raise an exception if the file contains data of the wrong type.

Saving a data model to a file

Simply call the save method on the model instance. The format to save into will be deduced from the filename.:

```
im.save("myimage.asdf")
```

Note: This save always clobbers the output file.

Copying a model

To create a new model based on another model, simply use its copy method. This will perform a deep-copy: that is, no changes to the original model will propagate to the new model:

```
new_model = old_model.copy()
```

Looking at the contents of a model

You can examine the contents of your model from within python using:

```
print("\n".join("{: >20}\t{}".format(k, v) for k, v in im.items()), "\n")
```

which will list the contents of the ImageModel im:

```
meta.aperture.name  Aperture name c1d861ddaebdb859f619fb2b79ea7bdf
meta.aperture.position_angle       115.33996998457596
meta.cal_step.flat_field    SKIPPED

area        <array (unloaded) shape: [4096, 4096] dtype: float32>
history.description HISTORY of this file
history.time        2021-12-29 14:03:57.465551
history.software.name       roman_datamodels
history.software.author     STSCI
history.software.homepage   https://github.com/spacetelescope/roman_datamodels
history.software.version    0.8
```

or you can print specifics:

```
print("\n".join("{: >20}\t{}".format(k, v) for k, v in im.meta.wcsinfo.items()), "\n")
             v2_ref  1312.9491452484797
             v3_ref  -1040.7853726755036
            vparity  -1
           v3yangle  -60.0
             ra_ref  84.49289366006334
            dec_ref  -69.14101326380924
           roll_ref  0.0
           s_region  NONE
```

Note: These will be incorporated as methods in the data models in a future release.

Metadata

Metadata information associated with a data model is accessed through its `meta` member. For example, to access the date that an observation was made:

```
print(model.meta.observation.start_time)
```

Metadata values are automatically type-checked against the schema when they are set. Therefore, setting a attribute which expects a number to a string will raise an exception.

```
from roman_datamodels.testing.factories import create_wfi_image
from roman_datamodels import datamodels as rdmfrom romancal.datamodels import ImageModel
model = rdm.ImageModel(create_wfi_image())
model.meta.target.ra = "foo"
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
  File "/Users/ddavis/miniconda3/envs/rcal_dev/lib/python3.9/site-packages/roman_
↪datamodels/stnode.py", line 183, in __setattr__
    if schema is None or _validate(key, value, schema, self.ctx):
  File "/Users/ddavis/miniconda3/envs/rcal_dev/lib/python3.9/site-packages/roman_
↪datamodels/stnode.py", line 97, in _validate
    return _value_change(attr, tagged_tree, schema, False, strict_validation, ctx)
  File "/Users/ddavis/miniconda3/envs/rcal_dev/lib/python3.9/site-packages/roman_
↪datamodels/stnode.py", line 68, in _value_change
    raise jsonschema.ValidationError(errmsg)
jsonschema.exceptions.ValidationError: While validating ra the following error occurred:
'foo' is not of type 'number'

Failed validating 'type' in schema:
    {'$schema': 'http://stsci.edu/schemas/asdf-schema/0.1.0/asdf-schema',
     'archive_catalog': {'datatype': 'float',
                         'destination': ['ScienceCommon.ra']},
     'sdf': {'source': {'origin': 'PSS:fixed_target.ra_computed'},
             'special_processing': 'VALUE_REQUIRED'},
     'title': 'Target RA at mid time of exposure',
     'type': 'number'}

On instance:
    'foo'
```

The set of available metadata elements is defined in a YAML Schema that is installed with roman_datamodels from

the RAD (Roman Attribute Dictionary).

There is also a utility method for finding the schema associated with a given model.

```
from roman_datamodels import datamodels as rdm
from roman_datamodels.testing.factories import create_wfi_science_raw
# Create a model of the desired type
raw = create_wfi_science_raw()
raw_science = rdm.ScienceRawModel(raw)
# find the associated Schema
raw_science.schema_uri
'asdf://stsci.edu/datamodels/roman/schemas/wfi_science_raw-1.0.0'
```

An alternative method to get and set metadata values is to use a dot-separated name as a dictionary lookup. This is useful for databases, such as CRDS, where the path to the metadata element is most conveniently stored as a string. The following two lines are equivalent:

```
print(raw_science.meta['observation']['start_time'])
print(raw_science.meta.observation.start_time)
```

In addtion the times are stored as Astropy time objects and so the date can be displayed using various formats:

```
print(raw_science.meta.observation.start_time.iso)
2028-12-22 05:17:56.203
print(raw_science.meta.observation.start_time.mjd)
62127.22078938165
print(raw_science.meta.observation.start_time.yday)
2028:357:05:17:56.203
```

Working with Roman datamodels and ASDF files

If you've installed the roman calibration pipeline you should also have access to the standalone tool asdfinfo which allows access to asdf (and roman) files from the terminal prompt,:

```
asdftool info r0000101001001001001_01101_0001_WFI16_cal.asdf
root (AsdfObject)
├─asdf_library (Software)
│ ├─author (str): The ASDF Developers
...
```

also useful is:

```
asdftool help
usage: asdftool [-h] [--verbose] {help,explode,implode,extract,defragment,diff,edit,
↪remove-hdu,info,extensions,tags,to_yaml} ...

Commandline utilities for managing ASDF files.

optional arguments:
  -h, --help            show this help message and exit
  --verbose, -v         Increase verbosity

subcommands:
```

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```
  {help,explode,implode,extract,defragment,diff,edit,remove-hdu,info,extensions,tags,to_
↪yaml}
    help                Display usage information
    explode             Explode a ASDF file.
    implode             Implode a ASDF file.
    extract             Extract ASDF extensions in ASDF-in-FITS files into pure ASDF␣
↪files
    defragment          Defragment an ASDF file..
    diff                Report differences between two ASDF files
    remove-hdu          Remove ASDF extension from ASDF-in-FITS file
    info                Print a rendering of an ASDF tree.
    extensions          Show information about installed extensions
    tags                List currently available tags
    to_yaml             Convert as ASDF file to pure YAML.
```

which gives a list of possible actions one of the more useful can be:

```
asdftool edit file.asdf
```

Which will open the file in an editor you have set via the EDITOR environment variable. A more complete description of the options can be found in the asdftool documentation.

To access the files via a python session,

```
import roman_datamodels as rdm
import asdf
with rdm.open('r0000101001001001001_01101_0001_WFI16_cal.asdf') as model:
    <Manipulate the files>

with asdf.open('r0000101001001001001_01101_0001_WFI16_cal.asdf', copy_arrays=True) as␣
↪model:
    <Manipulate the files>
```

Once the files are loaded you can access various attributes. Below is a table showing how to access various properties using the roman_datamodels and the asdf.open methods,

Roman Datamodels	ASDF

`rdm_a.meta`
`rdm_a.meta.aperture`
`rdm_a.meta.aperture.position_angle`
`120`
	`asdf_a.tree['roman']['meta']`
	`asdf_a.tree['roman']['meta']['aperture']`
	`asdf_a.tree['roman']['meta']['aperture'][`
	`↪'position_angle']`
	`120`

You can also update or modify the metadata in Roman datamodels

```
rdm_a.meta.aperture.position_angle = 120.21
rdm_a.meta.aperture.position_angle
120.21
```

The ASDF equivalent is

```
asdf_a.tree['roman']['meta']['aperture']['position_angle'] = 120.05
asdf_a.tree['roman']['meta']['aperture']['position_angle']
120.05
```

Hint: If you trigger an error, "ValueError: assignment destination is read-only" make sure the asdf file was opened with copy_arrays=True, or with mode='rw'

You can also access and modify the data arrays

Listing 1: Roman Datamodels

```
rdm_a.data
<array (unloaded) shape: [4096, 4096] dtype: float32>

rdm_a.data[10,11]
0.0

rdm_a.data[10,11] = 122.1
rdm_a.data[10,11]
122.1
```

or by modifying the ASDF tree,

Listing 2: ASDF

```
asdf_a.tree['roman']['data']
<array (unloaded) shape: [4096, 4096] dtype: float32>

asdf_a.tree['roman']['data'][10,11]
0.0

asdf_a.tree['roman']['data'][10,11] = 3.14159
asdf_a.tree['roman']['data'][10,11]
3.14159
```

Using the info method

You can examine a roman data model using the info and search methods provided from the asdf package. The info fuction will print a representation of the asdf tree.

```
>>> from roman_datamodels import datamodels as rdm
>>> d_uncal = rdm.open('r0000101001001001001_01101_0001_WFI01_uncal.asdf')
>>> d_uncal.info()
root (AsdfObject)
├─asdf_library (Software)
│ ├─author (str): The ASDF Developers
│ ├─homepage (str): http://github.com/asdf-format/asdf
│ ├─name (str): asdf
│ └─version (str): 2.8.1
├─history (dict)
│ └─extensions (list)
```

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```
│    ├─[0] (ExtensionMetadata) ...
│    ├─[1] (ExtensionMetadata) ...
│    └─[2] (ExtensionMetadata) ...
└─roman (WfiScienceRaw)
  ├─meta (dict)
  │ ├─aperture (Aperture) ...
  │ ├─cal_step (CalStep) ...
  │ ├─calibration_software_version (str): 0.4.3.dev89+gca5771d
  │ ├─coordinates (Coordinates) ...
  │ ├─crds_context_used (str): roman_0020.pmap
  │ ├─crds_software_version (str): 11.5.0
  │ ├─ephemeris (Ephemeris) ...
  │ ├─exposure (Exposure) ...
  │ └─17 not shown
  └─data (NDArrayType): shape=(8, 4096, 4096), dtype=uint16
Some nodes not shown.
```

The info command also gives you control over the number of lines displayed by passing the argument `max_rows`. As an integer, `max_rows` will be interpreted as an overall limit on the number of displayed lines. If `max_rows` is a tuple, then each member limits lines per node at the depth corresponding to its tuple index. For example, to show all top-level nodes and 5 of each's children:

```
>>> d_uncal.info(max_rows=(None,5))
root (AsdfObject)
├─asdf_library (Software)
│ ├─author (str): The ASDF Developers
│ ├─homepage (str): http://github.com/asdf-format/asdf
│ ├─name (str): asdf
│ └─version (str): 2.8.1
├─history (dict)
│ └─extensions (list) ...
└─roman (WfiScienceRaw)
  ├─meta (dict) ...
  └─data (NDArrayType): shape=(8, 4096, 4096), dtype=uint16
Some nodes not shown.
```

Or you can use the asdf.info method to view the contents of the tree

```
import asdf
asdf.info(d_uncal)
```

Will print the same information as the above `d_uncal.info` command but also gives you enhanced capabilities. For instance you can display the first three lines for each of the meta entries,

```
>>> asdf.info(d_uncal.meta,max_rows=(None, 3))
root (DNode)
├─aperture (Aperture)
│ ├─name (str): WFI_CEN
│ └─position_angle (int): 120
├─cal_step (CalStep)
│ ├─assign_wcs (str): INCOMPLETE
│ ├─flat_field (str): INCOMPLETE
│ └─6 not shown
```

(continues on next page)

(continued from previous page)

```
├─calibration_software_version (str): 0.4.3.dev89+gca5771d
├─coordinates (Coordinates)
│ └─reference_frame (str): ICRS
├─crds_context_used (str): roman_0020.pmap
├─crds_software_version (str): 11.5.0
├─ephemeris (Ephemeris)
│ ├─earth_angle (float): 3.3161255787892263
│ ├─moon_angle (float): 3.3196162372932148
│ └─10 not shown
...
```

or you can concentrate on a given attribute. To list all the attributes in `cal_step` without listing the values,

```
>>> asdf.info(d_uncal.meta.cal_step,max_rows=(None, 3),show_values=False)
root (CalStep)
├─assign_wcs (str)
├─flat_field (str)
├─dark (str)
├─dq_init (str)
├─jump (str)
├─linearity (str)
├─ramp_fit (str)
└─saturation (str)
```

More information on the info method can be found in the ASDF documentation at rendering the ASDF trees.

Using the search method

You can also use the search method to find attributes,

```
>>> d_uncal.search('cal_step')
root (AsdfObject)
└─roman (WfiScienceRaw)
  └─meta (dict)
    └─cal_step (CalStep)
```

or a a general search for all attributes with cal in the name

```
>>> d_uncal.search('cal')
root (AsdfObject)
└─roman (WfiScienceRaw)
 └─meta (dict)
   ├─cal_step (CalStep)
   ├─calibration_software_version (str): 0.4.3.dev89+gca5771d
   ├─instrument (WfiMode)
   │ └─optical_element (str): F158
   └─velocity_aberration (VelocityAberration)
     └─scale_factor (float): 0.9999723133902021
```

This will do a regular expression search for `cal` in the attribute name. More information on using regular expressions in the search method can be found in the ASDF documentation linked below.

To search only within the meta tree,

```
>>> d_uncal.search('cal_')['roman']['meta']
meta (dict)
├─cal_step (CalStep)
└─instrument (WfiMode)
  └─optical_element (str): F158
```

You can also use the search method to find attributes by type in the asdf tree. For instance, you can find all integers, floats, or booleans by using the type keyword,

```
>>> d_uncal.search(type=bool)
root (AsdfObject)
└─roman (WfiScienceRaw)
  └─meta (dict)
    ├─exposure (Exposure)
    │ └─data_problem (bool): False
    └─visit (Visit)
      ├─internal_target (bool): False
      └─target_of_opportunity (bool): False

d_uncal.search(type=bool, value=True)
No results found.
```

More information and options for the search method can be found in the ASDF documentation here.

7.1.3 Dark Current Subtraction

Description

Assumptions

It is assumed that the input science data have had the zero group (or bias) subtracted. Accordingly, the dark reference data should have their own group zero subtracted from all groups.

Algorithm

The dark current step removes dark current from a Roman exposure by subtracting dark current data stored in a dark reference file.

The current implementation uses dark reference files that are matched to the MA table entry in the exposure metadata. The dark data are then subtracted, group-by-group, from the science exposure groups, in which each SCI group of the dark data is subtracted from the corresponding SCI group of the science data.

The ERR arrays of the science data are not modified.

The DQ flags from the dark reference file are propagated into science exposure PIXELDQ array using a bitwise OR operation.

Upon successful completion of the dark subtraction the cal_step attribute is set to “COMPLETE”.

Special Handling

Any pixel values in the dark reference data that are set to NaN will have their values reset to zero before being subtracted from the science data, which will effectively skip the dark subtraction operation for those pixels.

Step Arguments

The dark current step has one step-specific argument:

- `--dark_output`

If the `dark_output` argument is given with a filename for its value, the frame-averaged dark data that are created within the step will be saved to that file.

Reference File

The `dark` step uses a DARK reference file.

DARK Reference File

REFTYPE
DARK

Data models
`DarkRefModel`

The DARK reference file contains pixel-by-pixel and frame-by-frame dark current values for a given detector readout mode.

Reference Selection Keyword Attributes for DARK

CRDS selects appropriate DARK references based on the following keyword attributes. DARK is not applicable for instruments not in the table.

Instrument	Keyword Attributes
WFI	instrument, detector, date, time

Standard ASDF metadata

The following table lists the attributes that are *required* to be present in all reference files. The first column shows the attribute in the ASDF reference file headers, which is the same as the name within the data model meta tree (second column). The second column gives the roman data model name for each attribute, which is useful when using data models in creating and populating a new reference file.

Attribute	Fully Qualified Path
author	model.meta.author
model_type	model.meta.model_type
date	model.meta.date
description	model.meta.description
instrument	model.meta.instrument.name
reftype	model.meta.reftype
telescope	model.meta.telescope
useafter	model.meta.useafter

NOTE: More information on standard required attributes can be found here: *Standard ASDF metadata*

Type Specific Keyword Attributes for DARK

In addition to the standard reference file keyword attributes listed above, the following keyword attributes are *required* in DARK reference files, because they are used as CRDS selectors (see *Reference Selection Keyword Attributes for DARK*):

Attribute	Fully qualified path	Instruments
detector	model.meta.instrument.detector	WFI

Reference File Format

DARK reference files are ASDF format, with 3 data arrays. The format and content of the file is as follows (see `DarkRefModel`):

Data	Array Type	Dimensions	Data type
data	NDArray	4096 x 4096 x ngroups	float32
err	NDArray	4096 x 4096 x ngroups	float32
dq	NDArray	4096 x 4096	uint32

The ASDF file contains a single set of data, err, and dq arrays.

romancal.dark_current Package

Classes

`DarkCurrentStep`([name, parent, config_file, ...])	DarkCurrentStep: Performs dark current correction by subtracting dark current reference data from the input science data model.

DarkCurrentStep

class romancal.dark_current.**DarkCurrentStep**(*name=None*, *parent=None*, *config_file=None*, *_validate_kwds=True*, ***kws*)

Bases: `RomanStep`

DarkCurrentStep: Performs dark current correction by subtracting dark current reference data from the input science data model.

Create a `Step` instance.

Parameters

- **name** (*str, optional*) – The name of the Step instance. Used in logging messages and in cache filenames. If not provided, one will be generated based on the class name.
- **parent** (*Step instance, optional*) – The parent step of this step. Used to determine a fully-qualified name for this step, and to determine the mode in which to run this step.
- **config_file** (*str path, optional*) – The path to the config file that this step was initialized with. Use to determine relative path names of other config files.
- ****kws** (*dict*) – Additional parameters to set. These will be set as member variables on the new Step instance.

Attributes Summary

reference_file_types
spec

Methods Summary

process(input)	This is where real work happens.

Attributes Documentation

reference_file_types = ['dark']

spec = '\n dark_output = output_file(default = None) # Dark corrected model\n '

Methods Documentation

process(*input*)

This is where real work happens. Every Step subclass has to override this method. The default behaviour is to raise a NotImplementedError exception.

Class Inheritance Diagram

7.1.4 Data Quality (DQ) Initialization

Description

The Data Quality (DQ) initialization step in the calibration pipeline populates the DQ mask for the input dataset. Flag values from the appropriate static mask ("MASK") reference file in CRDS are copied into the "PIXELDQ" array of the input dataset, because it is assumed that flags in the mask reference file pertain to problem conditions that affect all groups for a given pixel.

The actual process consists of the following steps:

- Determine what MASK reference file to use via the interface to the bestref utility in CRDS.
- Copy the input product into a RampModel (if it isn't already) for processing through pipeline. This will create "pixeldq" and "groupdq" arrays (if they don't already exist).
- Propagate the DQ flags from the reference file DQ array to the science data "PIXELDQ" array using numpy's `bitwise_or` function.

Note that when applying the `dq_init` step to guide star data, the flags from the MASK reference file are propagated into the guide star dataset "dq" array, instead of the "pixeldq" array. The step identifies guide star data based on the following exposure type (exposure.type keyword attribute) values: WFI_WIM_ACQ, WFI_WIM_TRACK, WFI_WSM_ACQ1, WFI_WSM_ACQ2, WFI_WSM_TRACK.

Step Arguments

The Data Quality Initialization step has no step-specific arguments.

Reference Files

The `dq_init` step uses a MASK reference file.

MASK Reference File

reftype
MASK

Data model
`MaskRefModel`

The MASK reference file contains pixel-by-pixel DQ flag values that indicate problem conditions.

Reference Selection Keywords for MASK

CRDS selects appropriate MASK references based on the following keywords. MASK is not applicable for instruments not in the table.

Instrument	Metadata
WFI	instrument, detector, date, time

Standard ASDF metadata

The following table lists the attributes that are *required* to be present in all reference files. The first column shows the attribute in the ASDF reference file headers, which is the same as the name within the data model meta tree (second column). The second column gives the roman data model name for each attribute, which is useful when using data models in creating and populating a new reference file.

Attribute	Fully Qualified Path
author	model.meta.author
model_type	model.meta.model_type
date	model.meta.date
description	model.meta.description
instrument	model.meta.instrument.name
reftype	model.meta.reftype
telescope	model.meta.telescope
useafter	model.meta.useafter

NOTE: More information on standard required attributes can be found here: *Standard ASDF metadata*

Type Specific Keywords for MASK

In addition to the standard reference file keyword attributes listed above, the following keyword attributes are *required* in MASK reference files, because they are used as CRDS selectors (see *Reference Selection Keywords for MASK*):

Attribute	Fully qualified path	Instruments
detector	model.meta.instrument.detector	WFI

Reference File Format

MASK reference files are ASDF format, with one data object. The format and content of the file is as follows:

Data	Object Type	Dimensions	Data type
dq	NDArray	4096 x 4096	uint32

The values in the `dq` array give the per-pixel flag conditions that are to be propagated into the science exposure's `pixeldq` array. The dimensions of the `dq` array should be equal to the number of columns and rows in a full-frame readout of a given detector, including reference pixels.

The ASDF file contains a single dq array.

romancal.dq_init Package

Classes

DQInitStep([name, parent, config_file, ...])	Initialize the Data Quality extension from the mask reference file.

DQInitStep

class `romancal.dq_init.`**`DQInitStep`**(*name=None*, *parent=None*, *config_file=None*, *_validate_kwds=True*, ***kws*)

Bases: `RomanStep`

Initialize the Data Quality extension from the mask reference file.

The dq_init step initializes the pixeldq attribute of the input datamodel using the MASK reference file. For some Guiding and Image model types, initalize the dq attribute of the input model instead. The dq attribute of the MASK model is bitwise OR'd with the pixeldq (or dq) attribute of the input model.

Create a `Step` instance.

Parameters

- **name** (*str, optional*) – The name of the Step instance. Used in logging messages and in cache filenames. If not provided, one will be generated based on the class name.
- **parent** (*Step instance, optional*) – The parent step of this step. Used to determine a fully-qualified name for this step, and to determine the mode in which to run this step.
- **config_file** (*str path, optional*) – The path to the config file that this step was initialized with. Use to determine relative path names of other config files.
- ****kws** (*dict*) – Additional parameters to set. These will be set as member variables on the new Step instance.

Attributes Summary

reference_file_types	

Methods Summary

process(input)	Perform the dq_init calibration step

Attributes Documentation

reference_file_types = ['mask']

Methods Documentation

process(*input*)

Perform the dq_init calibration step

Parameters

input (*Roman datamodel*) – input roman datamodel

Returns

output_model – result roman datamodel

Return type

Roman datamodel

Class Inheritance Diagram

7.1.5 Flatfield Correction

Description

At its basic level this step flat-fields an input science data set by dividing by a flat-field reference image. In particular, the SCI array from the flat-field reference file is divided into both the SCI and ERR arrays of the science data set, and the flat-field DQ array is combined with the science DQ array using a bitwise OR operation.

Upon completion of the step, the cal_step attribute "flat_field" gets set to "COMPLETE" in the output science data.

Imaging Data

Imaging data use a straight-forward approach that involves applying a single flat-field reference file to the science image. The processing steps are:

- Find pixels that have a value of NaN or zero in the FLAT reference file SCI array and set their DQ values to "NO_FLAT_FIELD."
- Reset the values of pixels in the flat that have DQ="NO_FLAT_FIELD" to 1.0, so that they have no effect when applied to the science data.
- Apply the flat by dividing it into the science exposure SCI and ERR arrays.
- Propagate the FLAT reference file DQ values into the science exposure DQ array using a bitwise OR operation.

Error Propagation

The VAR_POISSON and VAR_RNOISE variance arrays of the science exposure are divided by the square of the flat-field value for each pixel. A flat-field variance array, VAR_FLAT, is created from the science exposure and flat-field reference file data using the following formula:

$$SCI_{science} = SCI_{science}/SCI_{flat}$$

$$VAR_POISSON_{science} = VAR_POISSON_{science}/SCI_{flat}^2$$

$$VAR_RNOISE_{science} = VAR_RNOISE_{science}/SCI_{flat}^2$$

$$VAR_FLAT_{science} = (SCI_{science}^2/SCI_{flat}^2) * ERR_{flat}^2$$

$$ERR_{science} = \sqrt{VAR_POISSON + VAR_RNOISE + VAR_FLAT}$$

The total ERR array in the science exposure is updated as the square root of the quadratic sum of VAR_POISSON, VAR_RNOISE, and VAR_FLAT.

Reference Files

The `flat_field` step uses a FLAT reference file.

FLAT Reference File

REFTYPE
FLAT

Data model
`roman_datamodels.datamodels.FlatRefModel`

The FLAT reference file contains pixel-by-pixel detector response values. It is used.

Reference Selection Keywords for FLAT

CRDS selects appropriate FLAT references based on the following attributes. FLAT is not applicable for instruments not in the table. Non-standard attributes used for file selection are *required*.

Instrument	Metadata
WFI	instrument, detector, optical_element, date, time

Standard ASDF metadata

The following table lists the attributes that are *required* to be present in all reference files. The first column shows the attribute in the ASDF reference file headers, which is the same as the name within the data model meta tree (second column). The second column gives the roman data model name for each attribute, which is useful when using data models in creating and populating a new reference file.

Attribute	Fully Qualified Path
author	model.meta.author
model_type	model.meta.model_type
date	model.meta.date
description	model.meta.description
instrument	model.meta.instrument.name
reftype	model.meta.reftype
telescope	model.meta.telescope
useafter	model.meta.useafter

NOTE: More information on standard required attributes can be found here: *Standard ASDF metadata*

Type Specific Keywords for FLAT

In addition to the standard reference file attributes listed above, the following attributes are *required* in FLAT reference files, because they are used as CRDS selectors (see *Reference Selection Keywords for FLAT*):

Attribute	Fully qualified path	Instruments
detector	model.meta.instrument.detector	WFI
exptype	model.meta.exposure.type	
optical_element	model.meta.instrument.optical_element	

Reference File Format

FLAT reference files are ASDF format, with 3 data arrays. The format and content of the file is as follows:

Data	Array Type	Dimensions	Data type
data	NDArray	4096 x 4096	float32
err	NDArray	4096 x 4096	float32
dq	NDArray	4096 x 4096	uint32

The ASDF file contains a single set of data, err, and dq arrays.

romancal.flatfield Package

Classes

FlatFieldStep([name, parent, config_file, ...])	Flat-field a science image using a flatfield reference image.

FlatFieldStep

class romancal.flatfield.**FlatFieldStep**(*name=None*, *parent=None*, *config_file=None*, *_validate_kwds=True*, ***kws*)

Bases: `RomanStep`

Flat-field a science image using a flatfield reference image.

Create a `Step` instance.

Parameters

- **name** (*str, optional*) – The name of the Step instance. Used in logging messages and in cache filenames. If not provided, one will be generated based on the class name.
- **parent** (*Step instance, optional*) – The parent step of this step. Used to determine a fully-qualified name for this step, and to determine the mode in which to run this step.
- **config_file** (*str path, optional*) – The path to the config file that this step was initialized with. Use to determine relative path names of other config files.
- ****kws** (*dict*) – Additional parameters to set. These will be set as member variables on the new Step instance.

Attributes Summary

reference_file_types

Methods Summary

process(step_input)	This is where real work happens.

Attributes Documentation

reference_file_types = ['flat']

Methods Documentation

process(*step_input*)

This is where real work happens. Every Step subclass has to override this method. The default behaviour is to raise a NotImplementedError exception.

Class Inheritance Diagram

7.1.6 Jump Detection

Description

Assumptions

We assume that the `saturation` step has already been applied to the input science exposure, so that saturated values are appropriately flagged in the input GROUPDQ array. We also assume that steps such as the reference pixel correction (`refpix`) and non-linearity correction (`linearity`) have been applied, so that the input data ramps do not have any non-linearities or noise above the modeled Poission and read noise due to instrumental effects. The absence of any of these preceding corrections or residual non-linearities or noise can lead to the false detection of jumps in the ramps, due to departure from linearity.

The `jump` step will automatically skip execution if the input data contain fewer than 3 groups in the integration, because the baseline algorthim requires two first differences to work.

Algorithm

This routine detects jumps in an exposure by looking for outliers in the up-the-ramp signal for each pixel in the integration within an input exposure. On output, the GROUPDQ array is updated with the DQ flag "JUMP_DET" to indicate the location of each jump that was found. In addition, any pixels that have non-positive or NaN values in the gain reference file will have DQ flags "NO_GAIN_VALUE" and "DO_NOT_USE" set in the output PIXELDQ array. The SCI and ERR arrays of the input data are not modified.

The current implementation uses the two-point difference method described in Anderson&Gordon2011_.

Two-Point Difference Method

The two-point difference method is applied to the integration as follows:

- Compute the first differences for each pixel (the difference between adjacent groups)
- Compute the clipped (dropping the largest difference) median of the first differences for each pixel.
- Use the median to estimate the Poisson noise for each group and combine it with the read noise to arrive at an estimate of the total expected noise for each difference.
- Compute the "difference ratio" as the difference between the first differences of each group and the median, divided by the expected noise.
- If the largest "difference ratio" is greater than the rejection threshold, flag the group corresponding to that ratio as having a jump.
- If a jump is found in a given pixel, iterate the above steps with the jump-impacted group excluded, looking for additional lower-level jumps that still exceed the rejection threshold.
- Stop iterating on a given pixel when no new jumps are found or only one difference remains.
- If the there are only three differences (four groups), the standard median is used rather than the clipped median.
- If there are only two differences (three groups), the smallest one is compared to the larger one and if the larger one is above a threshold, it is flagged as a jump.

Note that any ramp values flagged as SATURATED in the input GROUPDQ array are not used in any of the above calculations and hence will never be marked as containing a jump.

Multiprocessing

This step has the option of running in multiprocessing mode. In that mode it will split the input data cube into a number of row slices based on the number of available cores on the host computer and the value of the max_cores input parameter. By default the step runs on a single processor. At the other extreme if max_cores is set to 'all', it will use all available cores (real and virtual). Testing has shown a reduction in the elapsed time for the step proportional to the number of real cores used. Using the virtual cores also reduces the elasped time but at a slightly lower rate than the real cores.

If multiprocessing is requested the input cube will be divided into a number of slices in the row dimension (with the last slice being slightly larger, if needed). The slices are then sent to twopoint_difference.py by detect_jumps. After all the slices have finished processing, detect_jumps assembles the output group_dq cube from the slices.

Arguments

The `jump` step has five optional arguments that can be set by the user:

- `--rejection_threshold`: A floating-point value that sets the sigma threshold for jump detection for ramps having 5 or more groups.. In the code sigma is determined using the read noise from the read noise reference file and the Poisson noise (based on the median difference between samples, and the gain reference file). Note that any noise source beyond these two that may be present in the data will lead to an increase in the false positive rate and thus may require an increase in the value of this parameter. The default value of 4.0 for the rejection threshold will yield 6200 false positives for every million pixels, if the noise model is correct.
- `--three_group_rejection_threshold`: A floating-point value that sets the sigma threshold for jump detection for ramps having exactly 3 groups. The default value is 6.0
- `--four_group_rejection_threshold`: A floating-point value that sets the sigma threshold for jump detection for ramps having exactly 4 groups. The default value is 5.0

- `--maximum_cores`: The fraction of available cores that will be used for multi-processing in this step. The default value is 'none' which does not use multi-processing. The other options are 'quarter', 'half', and 'all'. Note that these fractions refer to the total available cores and on most CPUs these include physical and virtual cores. The clock time for the step is reduced almost linearly by the number of physical cores used on all machines. For example, on an Intel CPU with six real cores and 6 virtual cores setting maximum_cores to 'half' results in a decrease of a factor of six in the clock time for the step to run. Depending on the system the clock time can also decrease even more with maximum_cores is set to 'all'.
- `--flag_4_neighbors`: If set to True (default is True) it will cause the four perpendicular neighbors of all detected jumps to be flagged as a jump. This is needed because of the inter-pixel capacitance (IPC) causing a small jump in the neighbors. The small jump might be below the rejection threshold but will affect the slope determination of the pixel. The step will take about 40% longer to run when this is set to True.
- `--max_jump_to_flag_neighbors`: A floating point value in units of sigma that limits the flagging of neighbors. Any jump above this cutoff will not have its neighbors flagged. The concept is that the jumps in neighbors will be above the rejection-threshold and thus be flagged as primary jumps. The default value is 1000.
- `--min_jump_to_flag_neighbors`: A floating point value in units of sigma that limits the flagging of neighbors of marginal detections. Any primary jump below this value will not have its neighbors flagged. The goal is to prevent flagging jumps that would be too small to significantly affect the slope determination. The default value is 10.

Reference File Types

The `jump` step uses two reference files: GAIN and READNOISE. The GAIN reference file is used to temporarily convert pixel values in the `jump` step from units of DN to electrons. The READNOISE reference file is used in estimating the expected noise in each pixel. Both are necessary for proper computation of noise estimates within the `jump` step.

GAIN

READNOISE

romancal.jump Package

Classes

JumpStep([name, parent, config_file, ...])	JumpStep: Performs CR/jump detection.

JumpStep

class `romancal.jump.`**`JumpStep`**(*name=None*, *parent=None*, *config_file=None*, *_validate_kwds=True*, ***kws*)

Bases: `RomanStep`

JumpStep: Performs CR/jump detection. The 2-point difference method is applied.

Create a `Step` instance.

Parameters

- **name** (*str, optional*) – The name of the Step instance. Used in logging messages and in cache filenames. If not provided, one will be generated based on the class name.
- **parent** (*Step instance, optional*) – The parent step of this step. Used to determine a fully-qualified name for this step, and to determine the mode in which to run this step.

- **config_file** (*str path, optional*) – The path to the config file that this step was initialized with. Use to determine relative path names of other config files.
- ****kws** (*dict*) – Additional parameters to set. These will be set as member variables on the new Step instance.

Attributes Summary

reference_file_types	
spec	

Methods Summary

process(input)	This is where real work happens.

Attributes Documentation

reference_file_types = ['gain', 'readnoise']

spec = "\n rejection_threshold = float(default=4.0,min=0) # CR sigma rej thresh\n three_group_rejection_threshold = float(default=6.0,min=0) # CR sigma rej thresh\n four_group_rejection_threshold = float(default=5.0,min=0) # CR sigma rej thresh\n maximum_cores = option('none', 'quarter', 'half', 'all', default='none') # max number of processes to create\n flag_4_neighbors = boolean(default=True) # flag the four perpendicular neighbors of each CR\n max_jump_to_flag_neighbors = float(default=1000) # maximum jump sigma that will trigger neighbor flagging\n min_jump_to_flag_neighbors = float(default=10) # minimum jump sigma that will trigger neighbor flagging\n "

Methods Documentation

process(*input*)

This is where real work happens. Every Step subclass has to override this method. The default behaviour is to raise a NotImplementedError exception.

Class Inheritance Diagram

7.1.7 Linearity Correction

Description

Assumptions

It is assumed that the saturation step has already been applied to the input data, so that saturation flags are set in the GROUPDQ array of the input science data.

Algorithm

The linearity step applies the "classic" linearity correction adapted from the HST WFC3/IR linearity correction routine, correcting science data values for detector non-linearity. The correction is applied pixel-by-pixel, group-by-group, integration-by-integration within a science exposure.

The correction is represented by an nth-order polynomial for each pixel in the detector, with n+1 arrays of coefficients read from the linearity reference file.

The algorithm for correcting the observed pixel value in each group of an integration is currently of the form:

$$F_\text{c} = c_0 + c_1 F + c_2 F^2 + c_3 F^3 + ... + c_n F^n$$

where F is the observed counts (in DN), c_n are the polynomial coefficients, and F_c is the corrected counts. There is no limit to the order of the polynomial correction; all coefficients contained in the reference file will be applied.

Upon successful completion of the linearity correction, "cal_step" in the metadata is set to "COMPLETE".

Special Handling

- Pixels having at least one correction coefficient equal to NaN will not have the linearity correction applied and the DQ flag "NO_LIN_CORR" is added to the science exposure PIXELDQ array.
- Pixels that have the "NO_LIN_CORR" flag set in the DQ array of the linearity reference file will not have the correction applied and the "NO_LIN_CORR" flag is added to the science exposure PIXELDQ array.
- Pixel values that have the "SATURATED" flag set in a particular group of the science exposure GROUPDQ array will not have the linearity correction applied to that group. Any groups for that pixel that are not flagged as saturated will be corrected.

The ERR array of the input science exposure is not modified.

The flags from the linearity reference file DQ array are propagated into the PIXELDQ array of the science exposure using a bitwise OR operation.

Arguments

The linearity correction has no step-specific arguments.

Reference File Types

The `linearity` step uses a LINEARITY reference file.

LINEARITY Reference File

REFTYPE
LINEARITY

Data model
`LinearityModel`

The LINEARITY reference file contains pixel-by-pixel polynomial correction coefficients.

Reference Selection Keywords for LINEARITY

CRDS selects appropriate LINEARITY references based on the following keyword attributes. All keyword attributes used for file selection are *required*.

Instrument	Keyword Attributes
WFI	instrument, detector, date, time

Standard ASDF metadata

The following table lists the attributes that are *required* to be present in all reference files. The first column shows the attribute in the ASDF reference file headers, which is the same as the name within the data model meta tree (second column). The second column gives the roman data model name for each attribute, which is useful when using data models in creating and populating a new reference file.

Attribute	Fully Qualified Path
author	model.meta.author
model_type	model.meta.model_type
date	model.meta.date
description	model.meta.description
instrument	model.meta.instrument.name
reftype	model.meta.reftype
telescope	model.meta.telescope
useafter	model.meta.useafter

NOTE: More information on standard required attributes can be found here: *Standard ASDF metadata*

Type Specific Attributes for LINEARITY

In addition to the standard reference file attributes listed above, the following attributes are *required* in LINEARITY reference files, because they are used as CRDS selectors (see linearity_selectors):

Attribute	Fully qualified path	Instruments
detector	model.meta.intstrument.detector	WFI

Reference File Format

LINEARITY reference files are ASDF format, with 2 data arrays. The format and content of the file is as follows:

Data	Array Type	Dimensions	Data type
coeffs	NDArray	ncols x nrows x ncoeffs	float32
dq	NDArray	ncols x nrows	uint32

Each plane of the COEFFS data cube contains the pixel-by-pixel coefficients for the associated order of the polynomial. There can be any number of planes to accommodate a polynomial of any order.

romancal.linearity Package

Classes

LinearityStep([name, parent, config_file, ...])	LinearityStep: This step performs a correction for non-linear detector response, using the "classic" polynomial method.

LinearityStep

class romancal.linearity.**LinearityStep**(*name=None*, *parent=None*, *config_file=None*, *_validate_kwds=True*, ***kws*)

Bases: RomanStep

LinearityStep: This step performs a correction for non-linear detector response, using the “classic” polynomial method.

Create a Step instance.

Parameters

- **name** (*str, optional*) – The name of the Step instance. Used in logging messages and in cache filenames. If not provided, one will be generated based on the class name.
- **parent** (*Step instance, optional*) – The parent step of this step. Used to determine a fully-qualified name for this step, and to determine the mode in which to run this step.
- **config_file** (*str path, optional*) – The path to the config file that this step was initialized with. Use to determine relative path names of other config files.
- ****kws** (*dict*) – Additional parameters to set. These will be set as member variables on the new Step instance.

Attributes Summary

reference_file_types	

Methods Summary

process(input)	This is where real work happens.

Attributes Documentation

reference_file_types = ['linearity']

Methods Documentation

process(*input*)

This is where real work happens. Every Step subclass has to override this method. The default behaviour is to raise a NotImplementedError exception.

Class Inheritance Diagram

7.1.8 Pipeline Modules

Pipeline Stages

End-to-end calibration of Roman data is divided into stages of processing:

- Stage 2 consists of detector-level corrections that are performed on a group-by-group basis, followed by ramp fitting. The output of stage 1 processing is a count rate image per exposure, or per integration for some modes. Details of this pipeline can be found at:
  - *exposure_pipeline: Exposure Level Detector Processing*
  - Stage 2 processing consists of additional instrument-level and observing-mode corrections and calibrations to produce fully calibrated exposures. The details differ for imaging and spectroscopic exposures, and there are some corrections that are unique to certain instruments or modes. Details are at: TBD

  The table below represents the same information as described above, but alphabetically ordered by pipeline class.

Pipeline Class | Alias	Used For
ExposurePipeline | roman_elp	Stage 2:

Pipelines and Exposure Type

The data from different observing modes needs to be processed with the proper pipeline stages listed above. The proper pipeline selection is usually based solely on the exposure type (exposure.type attribute).

exposure_pipeline: Exposure Level Detector Processing

Class
romancal.pipeline.ExposurePipeline

Alias
exposure_pipeline

The ExposurePipeline applies detector-level corrections to given exposure types (imaging, prism, and grism.). It is applied to one exposure at a time. It is sometimes referred to as "ramps-to-slopes" processing, because the input raw data are in the form of ramps containing accumulating counts from the non-destructive detector readouts and the output is a corrected countrate (slope) image.

The list of steps applied by the ExposurePipeline pipeline is shown in the table below.

Step	WFI-Image	WFI-Prism	WFI-Grism
dq_init	✓	✓	✓
saturation	✓	✓	✓
linearity	✓	✓	✓
dark_current	✓	✓	✓
jump	✓	✓	✓
ramp_fitting	✓	✓	✓
assign_wcs	✓	✓	✓
flatfield	✓		

Arguments

The exposure pipeline has one optional argument:

```
--save_calibrated_ramp  boolean  default=False
```

If set to True, the pipeline will save intermediate data to a file as it exists at the end of the *jump* step (just before ramp fitting). The data at this stage of the pipeline are still in the form of the original 3D ramps (ngroups x ncols x nrows) and have had all of the detector-level correction steps applied to it, including the detection and flagging of Cosmic-Ray (CR) hits within each ramp (integration). If created, the name of the intermediate file will be constructed from the root name of the input file, with the new product type suffix "_ramp" appended, e.g. "r0008308002010007027_06311_0019_WFI01_ramp.asdf".

Inputs

3D raw data

Data model
: `RampModel`

File suffix
: _uncal

The input to the `ExposurePipeline` is a single raw exposure, e.g. "r0008308002010007027_06311_0019_WFI01_uncal.asdf", which contains the original raw data from all of the detector readouts in the exposure (ngroups x ncols x nrows).

Note that in the operational environment, the input will be in the form of a `RawScienceModel`, which only contains the 3D array of detector pixel values, along with some optional extensions. When such a file is loaded into the pipeline, it is immediately converted into a `RampModel`, and has all additional data arrays for errors and Data Quality flags created and initialized to zero.

Outputs

2D Image model

Data model
: `ImageModel`

File suffix
: _cal

Result of applying all pipeline steps up through the *flatfield* step, to produce corrected flatfield data which is 2D image data, which will have one less data dimensions as the input raw 3D data (ngroups x ncols x nrows). In addition to being a 2-dimensional image the output from the pipeline has the *reference pixels* removed from the edges of the science array.

romancal.pipeline Package

This module collects all of the stpipe.Pipeline subclasses made available by this package.

Classes

`ExposurePipeline`(*args, **kwargs)	ExposurePipeline: Apply all calibration steps to raw Roman WFI ramps to produce a 2-D slope product.

ExposurePipeline

class romancal.pipeline.**ExposurePipeline**(**args*, ***kwargs*)

Bases: `RomanPipeline`

ExposurePipeline: Apply all calibration steps to raw Roman WFI ramps to produce a 2-D slope product. Included steps are: dq_init, saturation, linearity, dark current, jump detection, ramp_fit, and assign_wcs. The flat field step is only applied to WFI imaging data.

See `Step.__init__` for the parameters.

Attributes Summary

class_alias	
spec	
step_defs	

Methods Summary

create_fully_saturated_zeroed_image(input_model)	Create zeroed-out image file
process(input)	Process the Roman WFI data
setup_output(input)	Determine the proper file name suffix to use later

Attributes Documentation

```
class_alias = 'roman_elp'
```

```
spec = '\n save_calibrated_ramp = boolean(default=False)\n save_results =
boolean(default=False)\n '
```

```
step_defs = {'assign_wcs': <class
'romancal.assign_wcs.assign_wcs_step.AssignWcsStep'>, 'dark_current': <class
'romancal.dark_current.dark_current_step.DarkCurrentStep'>, 'dq_init': <class
'romancal.dq_init.dq_init_step.DQInitStep'>, 'flatfield': <class
'romancal.flatfield.flat_field_step.FlatFieldStep'>, 'jump': <class
'romancal.jump.jump_step.JumpStep'>, 'linearity': <class
'romancal.linearity.linearity_step.LinearityStep'>, 'photom': <class
'romancal.photom.photom_step.PhotomStep'>, 'rampfit': <class
'romancal.ramp_fitting.ramp_fit_step.RampFitStep'>, 'saturation': <class
'romancal.saturation.saturation_step.SaturationStep'>}
```

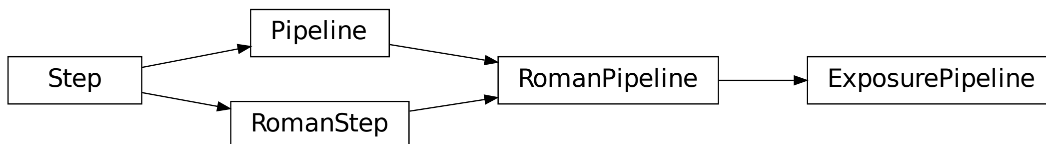
Methods Documentation

create_fully_saturated_zeroed_image(*input_model*)
Create zeroed-out image file

process(*input*)
Process the Roman WFI data

setup_output(*input*)
Determine the proper file name suffix to use later

Class Inheritance Diagram



7.1.9 Photometric Calibration

Description

Algorithm

The `photom` step adds flux (photometric) calibrations to the metadata of a data product. The calibration information is read from a photometric reference file, and the exact nature of the calibration information loaded from the reference file is described below. This step does not affect the pixel values of the data product.

Upon successful completion of the photometric correction, the "photom" keyword in "cal_step" in the metadata is set to "COMPLETE".

Photom and Pixel Area Data

The photom reference file contains a table of exposure parameters that define the flux conversion and pixel area data for each optical element. The table contains one row for each optical_element, and the photom step searches the table for the row that matches the parameters of the science exposure and then loads the calibration information from that row of the table.

For these table-based PHOTOM reference files, the calibration information in each row includes a scalar flux conversion constant, the conversion uncertainty, and the nominal pixel area.

The scalar conversion constant is copied to the header keyword "conversion_megajanskys", which gives the conversion from DN/s to megaJy/steradian, and converted to microJy/square arcseconds and saved to the header keyword "conversion_microjanskys". The same process is performed for the uncertainty, with the values saved in "conversion_megajanskys_uncertainty" and "conversion_microjanskys_uncertainty", respectively.

The step also populates the metadata keywords "pixelarea_steradians" and "pixelarea_arcsecsq" in the science data product, which give the average pixel area in units of steradians and square arcseconds, respectively.

Step Arguments

The photometric calibration step has one step-specific argument:

- `--photom`

If the `photom` argument is given with a filename for its value, the photometric calibrated data that are created within the step will be saved to that file.

Reference Files

The `photom` step uses *PHOTOM* reference files.

PHOTOM Reference File

REFTYPE
PHOTOM

Data models
`WfiImgPhotomRefModel`

The PHOTOM reference file contains conversion factors for putting pixel values into physical units.

Reference Selection Keywords for PHOTOM

CRDS selects appropriate PHOTOM reference based on the following keyword. PHOTOM is not applicable for instruments not in the table. All keywords used for file selection are *required*.

Instrument	Keyword Attributes
WFI	instrument, date, time

Standard ASDF metadata

The following table lists the attributes that are *required* to be present in all reference files. The first column shows the attribute in the ASDF reference file headers, which is the same as the name within the data model meta tree (second column). The second column gives the roman data model name for each attribute, which is useful when using data models in creating and populating a new reference file.

Attribute	Fully Qualified Path
author	model.meta.author
model_type	model.meta.model_type
date	model.meta.date
description	model.meta.description
instrument	model.meta.instrument.name
reftype	model.meta.reftype
telescope	model.meta.telescope
useafter	model.meta.useafter

NOTE: More information on standard required attributes can be found here: *Standard ASDF metadata*

Type Specific Keywords for PHOTOM

In addition to the standard reference file keywords listed above, the following keywords are *required* in PHOTOM reference files. The first (detector) is needed because it is used as a CRDS selector. The second (optical_element) is used to select the appropriate set of photometric parameters. (see *Reference Selection Keywords for PHOTOM*):

Attribute	Fully qualified path	Instruments
detector	model.meta.instrument.detector	WFI
optical_element	model.meta.instrument.optical_element	WFI

Tabular PHOTOM Reference File Format

PHOTOM reference files are ASDF format, with data in the phot_table attribute. The format and content of the file is as follows (see `WfiImgPhotomRefModel`):

Data is stored in a 2D table, with optical elements for the row names:

Instrument	Row names
WFI	F062, F087, F106, F129, F146, F158, F184, F213, GRISM, PRISM, DARK

And the variable attributes for the columns (with data type):

Instrument	Column name	Data type	Dimensions	Units
WFI	photmjsr	quantity	scalar	MJy/steradian
	uncertainty	quantity	scalar	MJy/steradian
	pixelareasr	quantity	scalar	steradian

The pixelareasr variable attribute gives the average pixel area in units of steradians.

romancal.photom Package

Classes

PhotomStep([name, parent, config_file, ...])	PhotomStep: Module for loading photometric conversion information from

PhotomStep

class romancal.photom.**PhotomStep**(*name=None*, *parent=None*, *config_file=None*, *_validate_kwds=True*, ***kws*)

Bases: `RomanStep`

PhotomStep: Module for loading photometric conversion information from
reference files and attaching to the input science data model

Create a `Step` instance.

Parameters

- **name** (*str, optional*) – The name of the Step instance. Used in logging messages and in cache filenames. If not provided, one will be generated based on the class name.
- **parent** (*Step instance, optional*) – The parent step of this step. Used to determine a fully-qualified name for this step, and to determine the mode in which to run this step.
- **config_file** (*str path, optional*) – The path to the config file that this step was initialized with. Use to determine relative path names of other config files.
- ****kws** (*dict*) – Additional parameters to set. These will be set as member variables on the new Step instance.

Attributes Summary

reference_file_types	

Methods Summary

process(input)	Perform the photometric calibration step

Attributes Documentation

reference_file_types = ['photom']

Methods Documentation

process(*input*)

Perform the photometric calibration step

Parameters

input (*Roman level 2 image datamodel (wfi_image-1.x.x)*) – input roman datamodel

Returns

output_model – output roman datamodel

Return type

Roman level 2 image datamodel (wfi_image-1.x.x)

Class Inheritance Diagram

7.1.10 Ramp Fitting

Description

This step determines the mean count rate, in units of counts per second, for each pixel by performing a linear fit to the data in the input file. The fit is done using the "ordinary least squares" method. The fit is performed independently for each pixel. There can be up to two output files created by the step. The primary output file ("rate") contains the slope at each pixel. A second, optional output product is also available, containing detailed fit information for each pixel. The two types of output files are described in more detail below.

The count rate for each pixel is determined by a linear fit to the cosmic-ray-free and saturation-free ramp intervals for each pixel; hereafter this interval will be referred to as a "segment." The fitting algorithm uses an 'optimal' weighting scheme, as described by Fixsen et al, PASP, 112, 1350. Segments are determined using the 3-D GROUPDQ array of the input data set, under the assumption that the jump step will have already flagged CR's. Segments are terminated where saturation flags are found. Pixels are processed simultaneously in blocks using the array-based functionality of numpy. The size of the block depends on the image size and the number of groups.

The ramp fitting step is also where the *reference pixels* are trimmed, resulting in a smaller array being passed to the subsequent steps.

Multiprocessing

This step has the option of running in multiprocessing mode. In that mode it will split the input data cube into a number of row slices based on the number of available cores on the host computer and the value of the max_cores input parameter. By default the step runs on a single processor. At the other extreme if max_cores is set to 'all', it will use all available cores (real and virtual). Testing has shown a reduction in the elapsed time for the step proportional to the number of real cores used. Using the virtual cores also reduces the elasped time but at a slightly lower rate than the real cores.

Special Cases

If the input dataset has only a single group, the count rate for all unsaturated pixels will be calculated as the value of the science data in that group divided by the group time. If the input dataset has only two groups, the count rate for all unsaturated pixels will be calculated using the differences between the two valid groups of the science data.

For datasets having more than a single group, a ramp having a segment with only a single group is processed differently depending on the number and size of the other segments in the ramp. If a ramp has only one segment and that segment contains a single group, the count rate will be calculated to be the value of the science data in that group divided by the group time. If a ramp has a segment having a single group, and at least one other segment having more than one good group, only data from the segment(s) having more than a single good group will be used to calculate the count rate.

The data are checked for ramps in which there is good data in the first group, but all first differences for the ramp are undefined because the remainder of the groups are either saturated or affected by cosmic rays. For such ramps, the first differences will be set to equal the data in the first group. The first difference is used to estimate the slope of the ramp, as explained in the 'segment-specific computations' section below.

If any input dataset contains ramps saturated in their second group, the count rates for those pixels will be calculated as the value of the science data in the first group divided by the group time.

All Cases

For all input datasets, including the special cases described above, arrays for the primary output (rate) product are computed as follows.

After computing the slopes for all segments for a given pixel, the final slope is determined as a weighted average from all segments, and is written as the primary output product. In this output product, the 3-D GROUPDQ is collapsed into 2-D, merged (using a bitwise OR) with the input 2-D PIXELDQ, and stored as a 2-D DQ array.

A second, optional output product is also available and is produced only when the step parameter 'save_opt' is True (the default is False). This optional product contains 3-D arrays called SLOPE, SIGSLOPE, YINT, SIGYINT, WEIGHTS, VAR_POISSON, and VAR_RNOISE that contain the slopes, uncertainties in the slopes, y-intercept, uncertainty in the y-intercept, fitting weights, the variance of the slope due to poisson noise only, and the variance of the slope due to read noise only for each segment of each pixel, respectively. The y-intercept refers to the result of the fit at an effective exposure time of zero. This product also contains a 2-D array called PEDESTAL, which gives the signal at zero exposure time for each pixel, and the 3-D CRMAG array, which contains the magnitude of each group that was flagged as having a CR hit. By default, the name of this output file will have the suffix "_fitopt". In this optional output product, the pedestal array is calculated by extrapolating the final slope (the weighted average of the slopes of all ramp segments) for each pixel from its value at the first group to an exposure time of zero. Any pixel that is saturated on the first group is given a pedestal value of 0. Before compression, the cosmic ray magnitude array is equivalent to the input SCI array but with the only nonzero values being those whose pixel locations are flagged in the input GROUPDQ as cosmic ray hits. The array is compressed, removing all groups in which all the values are 0 for pixels having at least one group with a non-zero magnitude. The order of the cosmic rays within the ramp is preserved.

Slope and Variance Calculations

Slopes and their variances are calculated for each segment, and for the entire exposure. As defined above, a segment is a set of contiguous groups where none of the groups are saturated or cosmic ray-affected. The appropriate slopes and variances are output to the primary output product, and the optional output product. The following is a description of these computations. The notation in the equations is the following: the type of noise (when appropriate) will appear as the superscript 'R', 'P', or 'C' for readnoise, Poisson noise, or combined, respectively; and the form of the data will appear as the subscript: 's', 'o' for segment, or overall (for the entire dataset), respectively.

Optimal Weighting Algorithm

The slope of each segment is calculated using the least-squares method with optimal weighting, as described by Fixsen et al. 2000, PASP, 112, 1350; Regan 2007, JWST-STScI-001212. Optimal weighting determines the relative weighting of each sample when calculating the least-squares fit to the ramp. When the data have low signal-to-noise ratio S, the data are read noise dominated and equal weighting of samples is the best approach. In the high signal-to-noise regime, data are Poisson-noise dominated and the least-squares fit is calculated with the first and last samples. In most practical cases, the data will fall somewhere in between, where the weighting is scaled between the two extremes.

The signal-to-noise ratio S used for weighting selection is calculated from the last sample as:

$$S = \frac{data \times gain}{\sqrt{(read_noise)^2 + (data \times gain)}} \,,$$

The weighting for a sample i is given as:

$$w_i = (i - i_{midpoint})^P \, ,$$

where $i_{midpoint}$ is the the sample number of the midpoint of the sequence, and P is the exponent applied to weights, determined by the value of S. Fixsen et al. 2000 found that defining a small number of P values to apply to values of S was sufficient; they are given as:

Minimum S	Maximum S	P
0	5	0
5	10	0.4
10	20	1
20	50	3
50	100	6
100		10

Segment-specific Computations:

The variance of the slope of a segment due to read noise is:

$$var^R_s = \frac{12 \ R^2 }{ (ngroups_s^3 - ngroups_s)(group_time^2) } \, ,$$

where R is the noise in the difference between 2 frames, $ngroups_s$ is the number of groups in the segment, and $group_time$ is the group time in seconds (from the exposure.group_time).

The variance of the slope in a segment due to Poisson noise is:

$$var^P_s = \frac{ slope_{est} }{ tgroup \times gain\ (ngroups_{s} -1)} \, ,$$

where $gain$ is the gain for the pixel (from the GAIN reference file), in e/DN. The $slope_{est}$ is an overall estimated slope of the pixel, calculated by taking the median of the first differences of the groups that are unaffected by saturation and cosmic rays. This is a more robust estimate of the slope than the segment-specific slope, which may be noisy for short segments.

The combined variance of the slope of a segment is the sum of the variances:

$$var^C_s = var^R_s + var^P_s$$

Exposure-level computations:

The variance of the slope due to read noise is:

$$var^R_o = \frac{1}{ \sum_{s} \frac{ 1}{ var^R_s }}$$

where the sum is over all segments.

The variance of the slope due to Poisson noise is:

$$var^P_o = \frac{1}{ \sum_{s} \frac{ 1}{ var^P_s }}$$

The combined variance of the slope is the sum of the variances:

$$var^C_o = var^R_o + var^P_o$$

The square root of the combined variance is stored in the ERR array of the primary output.

The overall slope depends on the slope and the combined variance of the slope of all segments, so is a sum over segments:

$$slope_o = \frac{\sum_s \frac{slope_s}{var^C_s}}{\sum_s \frac{1}{var^C_s}}$$

Upon successful completion of this step, the status attribute ramp_fit will be set to "COMPLETE".

Error Propagation

Error propagation in the ramp fitting step is implemented by storing the square-root of the exposure-level combined variance in the ERR array of the primary output product. This combined variance of the exposure-level slope is the sum of the variance of the slope due to the Poisson noise and the variance of the slope due to the read noise. These two variances are also separately written to the arrays VAR_POISSON and VAR_RNOISE in the asdf output.

For the optional output product, the variance of the slope due to the Poisson noise of the segment-specific slope is written to the VAR_POISSON array. Similarly, the variance of the slope due to the read noise of the segment-specific slope is written to the VAR_RNOISE array.

Arguments

The ramp fitting step has three optional arguments that can be set by the user:

- `--save_opt`: A True/False value that specifies whether to write the optional output product. Default if False.
- `--opt_name`: A string that can be used to override the default name for the optional output product.
- `--maximum_cores`: The fraction of available cores that will be used for multi-processing in this step. The default value is 'none' which does not use multi-processing. The other options are 'quarter', 'half', and 'all'. Note that these fractions refer to the total available cores and on most CPUs these include physical and virtual cores. The clock time for the step is reduced almost linearly by the number of physical cores used on all machines. For example, on an Intel CPU with six real cores and 6 virtual cores setting maximum_cores to 'half' results in a decrease of a factor of six in the clock time for the step to run. Depending on the system the clock time can also decrease even more with maximum_cores is set to 'all'.

Reference Files

The `ramp_fit` step uses two reference file types: GAIN and READNOISE. During ramp fitting, the GAIN values are used to temporarily convert the pixel values from units of DN to electrons, and convert the results of ramp fitting back to DN. The READNOISE values are used as part of the noise estimate for each pixel. Both are necessary for proper computation of noise estimates.

GAIN

READNOISE

romancal.ramp_fitting Package

Classes

RampFitStep([name, parent, config_file, ...])	This step fits a straight line to the value of counts vs.

RampFitStep

class romancal.ramp_fitting.**RampFitStep**(*name=None*, *parent=None*, *config_file=None*, *_validate_kwds=True*, ***kws*)

Bases: RomanStep

This step fits a straight line to the value of counts vs. time to determine the mean count rate for each pixel.

Create a Step instance.

Parameters

- **name** (*str, optional*) – The name of the Step instance. Used in logging messages and in cache filenames. If not provided, one will be generated based on the class name.
- **parent** (*Step instance, optional*) – The parent step of this step. Used to determine a fully-qualified name for this step, and to determine the mode in which to run this step.
- **config_file** (*str path, optional*) – The path to the config file that this step was initialized with. Use to determine relative path names of other config files.
- ****kws** (*dict*) – Additional parameters to set. These will be set as member variables on the new Step instance.

Attributes Summary

algorithm
reference_file_types
spec
weighting

Methods Summary

process(input)	This is where real work happens.

Attributes Documentation

`algorithm = 'ols'`

`reference_file_types = ['readnoise', 'gain']`

`spec = "\n opt_name = string(default='')\n maximum_cores = option('none','quarter','half','all',default='none') # max number of processes to create\n save_opt = boolean(default=False) # Save optional output\n "`

`weighting = 'optimal'`

Methods Documentation

process(*input*)

This is where real work happens. Every Step subclass has to override this method. The default behaviour is to raise a NotImplementedError exception.

Class Inheritance Diagram

7.1.11 Reference File Information

Introduction

This document is intended to be a core reference guide to the formats, naming convention and data quality flags used by the reference files for pipeline steps requiring them, and is not intended to be a detailed description of each of those pipeline steps. It also does not give details on pipeline steps that do not use reference files. The present manual is the living document for the reference file specifications.

Reference File Naming Convention

Before reference files are ingested into CRDS, they are renamed following a convention used by the pipeline. As with any other changes undergone by the reference files, the previous names are kept in header, so the Instrument Teams can easily track which delivered file is being used by the pipeline in each step.

The naming of reference files uses the following syntax:

```
roman_<instrument>_<reftype>_<version>.<extension>
```

where

- `instrument` is currently “WFI”

- `reftype` is one of the type names listed in the table below
- `version` is a 4-digit version number (e.g. 0042)
- `extension` gives the file format, "asdf"

An example WFI FLAT reference file name would be "roman_wfi_flat_0042.asdf".

Reference File Types

Most reference files have a one-to-one relationship with calibration steps, e.g. there is one step that uses one type of reference file. Some steps, however, use several types of reference files and some reference file types are used by more than one step. The tables below show the correspondence between pipeline steps and reference file types. The first table is ordered by pipeline step, while the second is ordered by reference file type. Links to the reference file types provide detailed documentation on each reference file.

Pipeline Step	Reference File Type (reftype)
assign_wcs	DISTORTION
dark_current	*DARK*
dq_init	*MASK*
flatfield	*FLAT*
jump_detection	GAIN
	READNOISE
linearity	LINEARITY
photom	*PHOTOM*
ramp_fitting	GAIN
	READNOISE
saturation	*SATURATION*

Reference File Type (reftype)	Pipeline Step
DARK	*dark_current*
DISTORTION	*assign_wcs*
FLAT	*flatfield*
GAIN	*jump_detection*
	ramp_fitting
LINEARITY	*linearity*
MASK	*dq_init*
PHOTOM	*photom*
READNOISE	*jump_detection*
	ramp_fitting
SATURATION	*saturation*

Standard ASDF metadata

Al Roman science and reference files are ASDF files.

The required attributes Documenting Contents of Reference Files are:

Attribute	Comment
reftype	FLAT Required values are listed in the discussion of each pipeline step.
description	Summary of file content and/or reason for delivery.
author	Fred Jones Person(s) who created the file.
useafter	YYYY-MM-DDThh:mm:ss Date and time after the reference files will be used. The T is required. Time string may NOT be omitted; use T00:00:00 if no meaningful value is available. Astropy Time objects are allowed.
pedigree	Options are 'SIMULATION' 'GROUND' 'DUMMY' 'INFLIGHT YYYY-MM-DD YYYY-MM-DD'
history	Description of Reference File Creation.
telescope	ROMAN Name of the telescope/project.
instrument	WFI Instrument name.

Observing Mode Attributes

A pipeline module may require separate reference files for each instrument, detector, optical element, observation date, etc. The values of these parameters must be included in the reference file attributes. The observing-mode attributes are vital to the process of ingesting reference files into CRDS, as they are used to establish the mapping between observing modes and specific reference files. Some observing-mode attributes are also used in the pipeline processing steps.

The Keywords Documenting the Observing Mode are:

Keyword	Sample Value	Comment
detector	WFI01	Allowed values WFI01, WFI02, … WFI18
optical element	F158	Name of the filter element and includes PRISM and GRISM
exposure type	WFI_IMAGE	Allowed values WFI_IMAGE, WFI_GRATING, WFI_PRISM, WFI_DARK, WFI_FLAT, WFI_WFSC

Tracking Pipeline Progress

As each pipeline step is applied to a sciece data product, it will record a status indicator in a cal_step attribute of the science data product. These statuses may be included in the primary header of reference files, in order to maintain a history of the data that went into creating the reference file. Allowed values for the status Attribute are 'INCOMPLETE', 'COMPLETE' and 'SKIPPED'. The default value is set to 'INCOMPLETE'. The pipeline modules will set the value to 'COMPLETE' or 'SKIPPED'. If the pipeline steps are run manually and you skip a step the cal_step will remain 'INCOMPLETE'.

Data Quality Flags

Within science data files, the PIXELDQ flags are stored as 32-bit integers; the GROUPDQ flags are 8-bit integers. All calibrated data from a particular instrument and observing mode have the same set of DQ flags in the same (bit) order. The table below lists the allowed DQ flags. Only the first eight entries in the table below are relevant to the GROUPDQ array.

Flags for the DQ, PIXELDQ, and GROUPDQ Arrays.

Bit	Value	Name	Description
0	1	DO_NOT_USE	Bad pixel. Do not use.
1	2	SATURATED	Pixel saturated during exposure
2	4	JUMP_DET	Jump detected during exposure
3	8	DROPOUT	Data lost in transmission
4	16	RESERVED_1	
5	32	PERSISTENCE	High persistence (was RESERVED_2)
6	64	AD_FLOOR	Below A/D floor (0 DN, was RESERVED_3)
7	128	RESERVED_4	
8	256	UNRELIABLE_ERROR	Uncertainty exceeds quoted error
9	512	NON_SCIENCE	Pixel not on science portion of detector
10	1024	DEAD	Dead pixel
11	2048	HOT	Hot pixel
12	4096	WARM	Warm pixel
13	8192	LOW_QE	Low quantum efficiency
15	32768	TELEGRAPH	Telegraph pixel
16	65536	NONLINEAR	Pixel highly nonlinear
17	131072	BAD_REF_PIXEL	Reference pixel cannot be used
18	262144	NO_FLAT_FIELD	Flat field cannot be measured
19	524288	NO_GAIN_VALUE	Gain cannot be measured
20	1048576	NO_LIN_CORR	Linearity correction not available
21	2097152	NO_SAT_CHECK	Saturation check not available
22	4194304	UNRELIABLE_BIAS	Bias variance large
23	8388608	UNRELIABLE_DARK	Dark variance large
24	16777216	UNRELIABLE_SLOPE	Slope variance large (i.e., noisy pixel)
25	33554432	UNRELIABLE_FLAT	Flat variance large
26	67108864	RESERVED_5	
27	134217728	RESERVED_6	
28	268435456	UNRELIABLE_RESET	Sensitive to reset anomaly
29	536870912	RESERVED_7	
30	1073741824	OTHER_BAD_PIXEL	A catch-all flag
31	2147483648	REFERENCE_PIXEL	Pixel is a reference pixel

7.1.12 Saturation Detection

Description

The `saturation` step flags pixels at or below the A/D floor or above the saturation threshold. Pixels values are flagged as saturated if the pixel value is larger than the defined saturation threshold. Pixel values are flagged as below the A/D floor if they have a value of zero DN.

This step examines the data group-by-group, comparing the pixel values in the data array with defined saturation thresholds for each pixel. When it finds a pixel value in a given group that is above the saturation threshold (high

saturation), it sets the "SATURATED" flag in the corresponding location of the "groupdq" array in the science exposure. When it finds a pixel in a given group that has a zero or negative value (below the A/D floor), it sets the "AD_FLOOR" and "DO_NOT_USE" flags in the corresponding location of the "groupdq" array in the science exposure For the saturation case, it also flags all subsequent groups for that pixel as saturated. For example, if there are 10 groups and group 7 is the first one to cross the saturation threshold for a given pixel, then groups 7 through 10 will all be flagged for that pixel.

Pixels with thresholds set to NaN or flagged as "NO_SAT_CHECK" in the saturation reference file have their thresholds set to the 16-bit A-to-D converter limit of 65535 and hence will only be flagged as saturated if the pixel reaches that hard limit in at least one group. The "NO_SAT_CHECK" flag is propagated to the PIXELDQ array in the output science data to indicate which pixels fall into this category.

Step Arguments

The `saturation` step has no step-specific arguments.

Reference Files

The `saturation` step uses a SATURATION reference file.

SATURATION Reference File

REFTYPE
SATURATION

Data model
`SaturationRefModel`

The SATURATION reference file contains pixel-by-pixel saturation threshold values.

Reference Selection Keywords for SATURATION

CRDS selects appropriate SATURATION references based on the following metadata attributes. All attributes used for file selection are *required*.

Instrument	Keywords
WFI	instrument, detector, date, time

Standard ASDF metadata

The following table lists the attributes that are *required* to be present in all reference files. The first column shows the attribute in the ASDF reference file headers, which is the same as the name within the data model meta tree (second column). The second column gives the roman data model name for each attribute, which is useful when using data models in creating and populating a new reference file.

Attribute	Fully Qualified Path
author	model.meta.author
model_type	model.meta.model_type
date	model.meta.date
description	model.meta.description
instrument	model.meta.instrument.name
reftype	model.meta.reftype
telescope	model.meta.telescope
useafter	model.meta.useafter

NOTE: More information on standard required attributes can be found here: *Standard ASDF metadata*

Type Specific Keywords for SATURATION

In addition to the standard reference file keywords listed above, the following keywords are *required* in SATURATION reference files, because they are used as CRDS selectors (see *Reference Selection Keywords for SATURATION*):

Keyword	Data Model Name	Instrument
detector	model.meta.instrument.detector	WFI

Reference File Format

SATURATION reference files are ASDF format, with two data objects. The format and content of the file is as follows:

Data	Object Type	Dimensions	Data type
data	NDArray	4096 x 4096	float32
dq	NDArray	4096 x 4096	uint32

The values in the `data` array give the saturation threshold in units of DN for each pixel.

The ASDF file contains two data arrays.

romancal.saturation Package

Classes

SaturationStep([name, parent, config_file, ...])	This Step sets saturation flags.

SaturationStep

class romancal.saturation.**SaturationStep**(*name=None*, *parent=None*, *config_file=None*, *_validate_kwds=True*, ***kws*)

Bases: RomanStep

This Step sets saturation flags.

Create a Step instance.

Parameters

- **name** (*str, optional*) – The name of the Step instance. Used in logging messages and in cache filenames. If not provided, one will be generated based on the class name.
- **parent** (*Step instance, optional*) – The parent step of this step. Used to determine a fully-qualified name for this step, and to determine the mode in which to run this step.
- **config_file** (*str path, optional*) – The path to the config file that this step was initialized with. Use to determine relative path names of other config files.
- ****kws** (*dict*) – Additional parameters to set. These will be set as member variables on the new Step instance.

Attributes Summary

reference_file_types	

Methods Summary

process(input)	This is where real work happens.

Attributes Documentation

reference_file_types = ['saturation']

Methods Documentation

process(*input*)

This is where real work happens. Every Step subclass has to override this method. The default behaviour is to raise a NotImplementedError exception.

Class Inheritance Diagram

7.1.13 Reference Pixel Correction

Description

Overview

The `refpix` step corrects for additional signal from the electronics using the reference pixels.

Reference Pixels in Data

The WFI has two sets of reference pixels: a 4-pixel border of reference pixels around the science pixels, and the Amp33 reference pixels which are a 4096 x 128 section of the detector adjacent to the border pixels.

In the data files, the storage location of the reference pixels depends on level of processing.

A Level 1, uncalibrated image has one array that contains both the science pixels and the border reference pixel, and a separate array for the Amp33 pixels.

A RampModel, which is created during the `dq_init` step, represents a dataset at any intermediate step between Level 1 and the final Level 2 image. Like the Level 1 file, RampModels also contain an array with both the science and border reference pixels, and another with the Amp 33 reference pixels. In addition to these arrays, there are four more arrays that contain the original border reference pixels (top, bottom, left, and right), and an additional four for their DQ arrays. The border pixels are copied during the `dq_init`, so they reflect the original state of the border pixels before any calibration. The border pixels that are still attached to the science data in the RampModel will later be discarded when the Level 2 image is created. Note that the border reference pixel arrays each include the overlap regions in the corners, so that each slice contains the full span of border pixels at the top, bottom, left, or right.

In the Level 2, calibrated image, the data array only contains the science pixels. The border reference pixels are trimmed from this image duing ramp_fit. The additional arrays for the original border reference pixels (which are 3D) and their DQ arrays, and the Amp 33 reference pixels, remain in the Level 2 file.

7.2 Error Propagation

7.2.1 Description

Steps in the various pipeline modules calculate variances due to different sources of noise or modify variances that were computed by previous steps. For some cases these arrays are being propagated to subsequent steps in the pipeline. Anytime a step creates or updates variances, the total error (ERR) array values are recomputed as the square root of the quadratic sum of all variances available to the step. Note that the ERR array values are always expressed as a standard deviation (the square root of the variance).

The table below is a summary of which steps create or update variance and error arrays, as well as which steps make use of these data. Details of how each step computes or uses these data are given in the subsequent sections below.

Step	Stage	Creates arrays	Updates arrays	Step uses
ramp_fitting	ELPP	VAR_POISSON, VAR_RNOISE	ERR	None
flat_field	ELPP	VAR_FLAT	ERR, VAR_POISSON, VAR_RNOISE	None

7.2.2 ELPP Processing

ELPP processing pipelines perform detector-level corrections and ramp fitting for individual exposures, for nearly all imaging and spectroscopic modes. Details of the pipelines can be found at *roman_elp*.

The ELPP pipeline steps that alter the ERR, VAR_POISSON, or VAR_RNOISE arrays the science countrate data are discussed below. Any step not listed here does not alter or use the variance or error arrays in any way and simply propagates the information to the next step.

ramp_fitting

This step calculates and populates the VAR_POISSON and VAR_RNOISE arrays to pass to the next step or saved in the optional output 'rate' files. The ERR array is updated as the square root of the quadratic sum of the variances. VAR_POISSON and VAR_RNOISE represent the uncertainty in the computed slopes (per pixel) due to Poisson and read noise, respectively. The details of the calculations can be found at *ramp_fitting*.

flat_field

The SCI array of the exposure being processed is divided by the flat-field reference image, and the VAR_POISSON and VAR_RNOISE arrays are divided by the square of the flat. A VAR_FLAT array is created, computed from the science data and the flat-field reference file ERR array. The science data ERR array is then updated to be the square root of the quadratic sum of the three variance arrays. For more details see *flat_field*.

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