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Trident is a Python package for creating synthetic absorption-line spectra from astrophysical hydrodynamics simulations. It utilizes the yt package to read in simulation datasets and extends it to provide realistic synthetic observations appropriate for studies of the interstellar, circumgalactic, and intergalactic media.

To avoid confusion, make sure you are viewing the correct documentation for the version of Trident you are using: stable vs. development. For more information, see *Versions of Trident*. 
Follow these steps to successfully install Trident and its dependencies.

1.1 Versions of Trident

There are currently two versions of Trident: a stable version and a development version. Make sure you are reading the correct docs for the version you are using!

The stable version is tried and tested and easy to install with pip. The development version is actively being updated with new features including superior support for particle-based datasets (previously known as the demeshening). Note that the stable version of trident requires the stable version of yt, and the development version of trident requires the development version of yt, due to some backwards-incompatible changes regarding particle-support in yt/trident.

Thus, the installation steps are slightly different for stable and development, so pay attention in the steps below. Don’t worry if you want to change later, you can always switch between the two versions easily enough by following the directions in Uninstallation or Switching Code Versions.

1.2 Trident’s Major Dependency: yt

yt is a python-based software package for the analysis and visualization of a different numerical datasets, including astrophysical hydrodynamical data. yt is the primary dependency of Trident, so you must install it before Trident will work. There are several methods for installing yt, which are all discussed in detail in the yt installation documentation. Use the one that is appropriate for you. We find that using conda is the most streamlined and reliable.

1.3 Installing the Stable Version of yt and Trident

Installation of the stable versions of yt and Trident is quite simple:

```
$ pip install yt
$ pip install trident
```

Now, you can try to run Trident for the first time, where it will download some additional files. See Step 3: Get Ionization Table and Verify Installation, for more information:

```
$ python
>>> import trident
```

Follow the instructions to download the ion_balance table and then verify that everything is working correctly. You should now be ready to do some Step 4: Science!
1.4 Installing the Development Version of yt and Trident

1.4.1 Step 0: Ensure Conda is Installed

Conda is a package manager providing a clean, stand-alone installation of python that is self-contained in its installation directory. yt & trident require a modern installation of python to work. conda provides that installation.

You can see if conda is already installed by running:

```bash
$ conda -h
```

If conda is installed, move to the next step. Otherwise install Mini-conda.

Use the appropriate conda install script for your architecture. We recommend getting the latest version of conda for Python3 for your architecture here: https://repo.continuum.io/miniconda/

For modern macs:

```bash
$ curl -O https://repo.anaconda.com/miniconda/Miniconda3-latest-MacOSX-x86_64.sh
$ bash Miniconda3-latest-MacOSX-x86_64.sh
```

For modern linux machines:

```bash
$ wget https://repo.continuum.io/miniconda/Miniconda3-latest-Linux-x86_64.sh
$ bash Miniconda3-latest-Linux-x86_64.sh
```

At the end of the installation step, allow conda to add its installation directory to the $PATH.

1.4.2 Step 1: Install yt

First you need yt’s major dependencies:

```bash
$ conda install numpy cython mpi4py git
```

Now you pull directly from the yt github repository to access the up-to-date version of the source code and build it:

```bash
$ git clone https://github.com/yt-project/yt.git yt
$ cd yt
$ pip install -e .
$ cd ..
```

Note, you’ll also need a separate library, `yt_astro_analysis`, to get some of the functionality necessary for Trident to work correctly:

```bash
$ git clone https://github.com/yt-project/yt_astro_analysis.git yt_astro_analysis
$ cd yt_astro_analysis
$ pip install -e .
$ cd ..
```
1.4.3 Step 2: Install Trident

Like yt, in order to get the development version of Trident, you must clone and build the up-to-date source code from its repository:

```
$ git clone https://github.com/trident-project/trident.git trident
$ cd trident
$ pip install -e .
$ cd ..
```

1.4.4 Step 3: Get Ionization Table and Verify Installation

In order to calculate the ionization fractions for various ions from density, temperature, metallicity fields, you will need an ionization table datafile and a configuration file. Because this datafile can be large, it is not packaged with the main source code. The first time you try to do anything that requires it, Trident will attempt to automatically set this all up for you with a series of interactive prompts. **This step requires an internet connection the first time you run it.**

In addition, Trident provides a simple test function to verify that your install is functioning correctly. This function not only tries to set up your configuration and download your ion table file, but it will create a simple one-zone dataset, generate a ray through it, and create a spectrum from that ray. This should execute very quickly, and if it succeeds it demonstrates that your installation has been totally successful:

```
$ python
>>> import trident
>>> trident.verify()
...Series of Interactive Prompts...
```

If you cannot directly access the internet on this computer, or you lack write access to your `$HOME` directory, or this step fails for any reason, please follow our documentation on **Manually Installing your Ionization Table.**

1.4.5 Step 4: Science!

Congratulations, you’re now ready to use Trident! Please refer to the documentation for how to use it with your data or with one of our sample datasets. A good place to start is the annotated example, and the example scripts found in the source code.

Please join our **mailing list** or **slack channel** for announcements and updates when new features are added to the code.

1.5 Manually Installing your Ionization Table

If for some reason you are unable to install the config file and ionization table data automatically, you must set it up manually. When Trident runs, it looks for a configuration file called `config.tri` in the `$HOME/.trident` directory or alternatively in the current working directory (for users lacking write access to their `$HOME` directories). This configuration file is simple in that it tells Trident a few things about your install including the location and filename of your desired ionization table. Manually create a text file called `config.tri` with contents following the form:

```
[Trident]
ion_table_dir = ~/.trident
ion_table_file = hm2012_hr.h5
```

1.5. Manually Installing your Ionization Table
To manually obtain an ion table datafile, download and gunzip one from: http://trident-project.org/data/ion_table. While the config.tri file needs to exist in your $HOME/.trident directory or in the working directory when you import trident, the ion_table datafile can exist anywhere on the file system. Just assure that the config file points to the proper location and filename of the ion table datafile.

Now, to confirm everything is working properly, verify your installation following Step 3: Get Ionization Table and Verify Installation. If this fails or you have additional problems, please contact our mailing list.

1.6 Uninstallation or Switching Code Versions

Uninstallation of the Trident source code is easy. If you installed the stable version of the code via pip, just run:

```
$ pip uninstall trident
```

If you installed the dev version of Trident, you’ll have to delete the source as well:

```
$ pip uninstall trident
$ rm -rf <YOUR_PATH_TO_TRIDENT_REPO>
```

If you want to switch between the two stable and development versions, just uninstall your version of the code as above, and then install the desired version as described in Step 2: Install Trident.

To fully remove the code from your system, remember to remove any ion table datafiles you may have downloaded in your $HOME/.trident directory, and follow the instructions for how to uninstall yt.

1.7 Updating to the Latest Version

If you want more recent features, you should periodically update your Trident codebase.

1.7.1 Updating to the Latest Stable Release

If you installed the “stable” version of the code using pip, then you can easily update your trident and yt installations:

```
$ pip install -U trident
$ yt update
```

1.7.2 Updating to the Latest Development Version

If you installed the “development” version of the code, it’s slightly more involved:

```
$ cd <YOUR_PATH_TO_TRIDENT_REPO>
$ git pull origin main
$ pip install -e .
$ yt update
```

For more information on updating your yt installation, see the yt update instructions.
The best way to get a feel for what Trident can do is to go through an annotated example of its use. This section will walk you through the steps necessary to produce a synthetic spectrum based on simulation data and to view its path through the parent dataset. The following example, available in the source code itself, can be applied to datasets from any of the different simulation codes that Trident and yt support, although it may require some tweaking of parameters for optimal performance. If you want to recreate the following analysis with the exact dataset used, it can be downloaded here.

The basic process for generating a spectrum and overplotting a sightline's trajectory through the dataset goes in three steps:

1. Generate a LightRay from the simulation data representing a sightline through the data.
2. Define the desired spectrum features and use the LightRay to create a corresponding synthetic spectrum.
3. Create a projected image and overplot the path of the LightRay.

### 2.1 Simple LightRay Generation

A LightRay is a 1D object representing the path a ray of light takes through a simulation volume on its way from some bright background object to the observer. It records all of the gas fields it intersects along the way for use in many tasks, including construction of a spectrum.

In order to generate a LightRay from your data, you need to first make sure that you’ve imported both the yt and Trident packages, and specify the filename of the dataset from which to extract the light ray:

```python
import yt
import trident
fn = 'enzo_cosmology_plus/RD0009/RD0009'
```

We need to decide the trajectory that the LightRay will take through our simulation volume. This arbitrary trajectory is specified with coordinates in code length units (e.g. \([x_{\text{start}}, y_{\text{start}}, z_{\text{start}}]\) to \([x_{\text{end}}, y_{\text{end}}, z_{\text{end}}]\)). Probably the simplest trajectory is cutting diagonally from the origin of the simulation volume to its outermost corner using the yt `domain_left_edge` and `domain_right_edge` attributes. Here we load the dataset into yt to get access to these attributes:

```python
ds = yt.load(fn)
ray_start = ds.domain_left_edge
ray_end = ds.domain_right_edge
```

Let’s define what lines or species we want to be added to our final spectrum. In this case, we want to deposit all hydrogen, carbon, nitrogen, oxygen, and magnesium lines to the resulting spectrum from the dataset:
```
line_list = ['H', 'C', 'N', 'O', 'Mg']
```

We can now generate the light ray using the `make_simple_ray()` function by passing the dataset and the trajectory endpoints to it as well as telling trident to save the resulting ray dataset to an HDF5 file. We explicitly instruct trident to pull all necessary fields from the dataset in order to be able to add the lines from our `line_list`:

```
ray = trident.make_simple_ray(ds,  
    start_position=ray_start,  
    end_position=ray_end,  
    data_filename="ray.h5",  
    lines=line_list)
```

The resulting `ray` is a `LightRay` object, consisting of a series of arrays representing the different fields it probes in the original dataset along its length. Each element in the arrays represents a different resolution element along the path of the ray. The ray also possesses some special fields not originally present in the original dataset:

- ('gas', 1') Location along the LightRay length from 0 to 1.
- ('gas', 'dl') Pathlength of resolution element (not a true pathlength for particle-based codes)
- ('gas', 'redshift') Cosmological redshift of resolution element
- ('gas', 'redshift_dopp') Doppler redshift of resolution element
- ('gas', 'redshift_eff') Effective redshift (combined cosmological and Doppler)

Like any dataset, you can see what fields are present on the ray by examining its `derived_field_list` (e.g., `print(ds.derived_field_list)`). If you want more ions present on this ray than are currently shown, you can add them with `add_ion_fields` (see: Adding Ion Fields).

This `ray` object is also saved to disk as an HDF5 file, which can later be loaded into yt as a stand-alone dataset (e.g., `ds = yt.load('ray.h5')`).

### 2.2 Overplotting a LightRay’s Trajectory on a Projection

Here we create a projection of the density field along the x axis of the dataset, and then overplot the path the `LightRay` takes through the simulation, before saving it to disk. The `annotate_ray()` operation should work for any volumetric plot, including slices, and off-axis plots:

```
p = yt.ProjectionPlot(ds, 'x', 'density')
p.annotate_ray(ray, arrow=True)
p.save('projection.png')
```
2.3 Calculating Column Densities

Perhaps we wish to know the total column density of a particular ion present along this LightRay. This can easily be done by multiplying the desired ion number density field by the pathlength field, \( d_l \), to yield an array of column densities for each resolution element, and then summing them together:

```python
column_density_HI = ray.r[('gas', 'H_p0_number_density')] * ray.r[('gas', 'dl')]
print('HI Column Density = %g' % column_density_HI.sum())
```


## 2.4 Spectrum Generation

Now that we have our LightRay we can use it to generate a spectrum. To create a spectrum, we need to make a `SpectrumGenerator` object defining our desired wavelength range and bin size. You can do this by manually setting these features, or just using one of the presets for an instrument. Currently, we have three pre-defined instruments, the G130M, G160M, and G140L observing modes for the Cosmic Origins Spectrograph aboard the Hubble Space Telescope: COS–G130M, COS–G160M, and COS–G140L. Notably, instrument COS aliases to COS–G130M.

We then use this `SpectrumGenerator` object to make a raw spectrum according to the intersecting fields it encountered in the corresponding LightRay. We save this spectrum to disk, and plot it:

```python
sg = trident.SpectrumGenerator('COS-G130M')
sg.make_spectrum(ray, lines=line_list)
sg.save_spectrum('spec_raw.txt')
sg.plot_spectrum('spec_raw.png')
```

![Raw Spectrum](image)

From here we can do some post-processing to the spectrum to include additional features that would be present in an actual observed spectrum. We add a background quasar spectrum, a Milky Way foreground, apply the COS line spread function, and add gaussian noise with SNR=30:

```python
sg.add_qso_spectrum()
sg.add_milky_way_foreground()
sg.apply_lsf()
sg.add_gaussian_noise(30)
```

Finally, we use plot and save the resulting spectrum to disk:

```python
sg.save_spectrum('spec_final.txt')
sg.plot_spectrum('spec_final.png')
```

which produces:
To create more complex or ion-specific spectra, refer to Advanced Spectrum Generation.

### 2.5 Compound LightRays

In some cases (e.g. studying redshift evolution of the IGM), it may be desirable to create a LightRay that covers a range in redshift that is larger than the domain width of a single simulation snapshot. Rather than simply sampling the same dataset repeatedly, which is inherently unphysical since large scale structure evolves with cosmic time, Trident allows the user to create a ray that samples multiple datasets from different redshifts to produce a much longer ray that is continuous in redshift space. This is done by using the make_compound_ray() function. This function is similar to the previously mentioned make_simple_ray() function, but instead of accepting an individual dataset, it takes a simulation parameter file, the associated simulation type, and the desired range in redshift to be probed by the ray, while still allowing the user to specify the same sort of line list as before::

```python
fn = 'enzo_cosmology_plus/AMRCosmology.enzo'
ray = trident.make_compound_ray(fn, simulation_type='Enzo',
                                 near_redshift=0.0, far_redshift=0.1,
                                 lines=line_list)
```

In this example, we’ve created a ray from an Enzo simulation (the same one used above) that goes from $z = 0$ to $z = 0.1$. This ray can now be used to generate spectra in the exact same ways as before.

Obviously, there need to be sufficient simulation outputs over the desired redshift range of the compound ray in order to have continuous sampling. To assure adequate simulation output frequency for this, one can use yt's plan_cosmology_splice() function. See an example of its usage in the yt_astro_analysis documentation.

We encourage you to look at the detailed documentation for make_compound_ray() in the API Reference section to understand how to control how the ray itself is constructed from the available data.

**Note:** The compound ray functionality has only been implemented for the Enzo and Gadget simulation codes (and Gadget’s derivatives including Gizmo and AREPO). If you would like to help us implement this functionality for your simulation code, please contact us about this on the mailing list.
In addition to being able to create absorption spectra, Trident can be used to postprocess datasets to add fields for ions not explicitly tracked in the simulation. These can later be analyzed using the standard yt analysis packages. This page provides some examples as to how these fields can be generated and analyzed.

3.1 How does it work?

When you installed Trident, you were forced to download an ion table, a data table consisting of dimensions in density, temperature, and redshift. This ion table was constructed by running many independent Cloudy instances to approximate the ionization states of all ionic species of the first 30 elements. The ionic species were calculated assuming collisional ionization equilibrium based on different density and temperature values and photoionization from a metagalactic ultraviolet background unique to each ion table. The currently preferred ion table uses the Haardt Madau 2012 model. You can change your default ionization model by changing your config file (see: Manually Installing your Ionization Table), or by specifying it directly in the ionization_table keywords of the following functions.

By following the process below, you will add different ion fields to your dataset based on the above assumptions using the dataset’s redshift, and the values of density, temperature, and metallicity found for each gas parcel in your dataset.

3.2 Generating species fields

As always, we first need to import yt and Trident and then we load up a dataset:

```python
import yt
import trident
fn = 'enzo_cosmology_plus/RD0009/RD0009'
ds = yt.load(fn)
```

To add ion fields we use the `add_ion_fields` function. This will add fields for whatever ions we specify in the form of:

- Ion fraction field. e.g. `Mg_p1_ion_fraction`
- Number density field. e.g. `Mg_p1_number_density`
- Density field. e.g. `Mg_p1_density`
- Mass field. e.g. `Mg_p1_mass`

Note: Trident follows yt’s naming convention for atomic, molecular, and ionic species fields. In short, the ionic prefix consists of the element and the number of times ionized it is: e.g. H I = H_p0, Mg II = Mg_p1, O VI = O_p5 (p is for
Let’s add fields for O VI (five-times-ionized oxygen):

```
trident.add_ion_fields(ds, ions=['O VI'])
```

To show how one can use this newly generated field, we’ll make a projection of the O VI number density field to show its column density map:

```
proj = yt.ProjectionPlot(ds, "z", "O_p5_number_density")
proj.save()
```

which produces:

![Projected O VI Number Density](image)

We can similarly create a phase plot to show where the O VI mass lives as a function of density and temperature:

```
# we need to create a data object from the dataset to make a phase plot
ad = ds.all_data()
phase = yt.PhasePlot(ad, "density", "temperature", ["O_p5_mass"],
```

(continues on next page)
weight_field="O_p5_mass", fractional=True)

phase.save()

resulting in:
CHAPTER
FOUR

LIGHT RAY GENERATOR

The LightRay is the one-dimensional object representing the pencil beam of light traveling from the source to the observer. Light rays can stack multiple datasets together to span a redshift interval larger than the simulation box.

4.1 Simple Rays

For a simple ray, you specify the dataset to use, the start and end coordinates of your 1D line, and then optionally any additional fields you want stored on the LightRay or optionally any ionic species you will want to use with this ray:

```python
import yt
import trident
ds = yt.load('FIRE_M12i_ref11/snapshot_600.hdf5')
ray = trident.make_simple_ray(ds,
   start_position=[0, 0, 0],
   end_position=[60000, 60000, 60000],
   lines=['H', 'Mg', 'O'],
   fields=[('gas', 'temperature'), ('gas', 'metallicity')])
```
4.2 Compound Rays

For a compound ray, you specify the simulation parameter filename, the simulation code, the start and end redshifts of the LightRay, and optionally any additional fields you want stored or any ionic species you will want to use with this ray:

```python
import trident
fn = 'enzo_cosmology_plus/AMRCosmology.enzo'
ray = trident.make_compound_ray(fn,
    simulation_type='Enzo',
    near_redshift=0.0,
    far_redshift=0.1,
    lines=['H', 'Mg', 'O'],
    fields=[('gas', 'temperature'), ('gas', 'metallicity')])
```

4.3 Ray Fields

The resulting ray is a LightRay object, consisting of a series of arrays representing the different fields it probes in the original dataset along its length. Each element in the arrays represents a different resolution element along the path of the ray. The ray also possesses some special fields not originally present in the original dataset:

- (`'gas', 'l'`) Location along the LightRay length from 0 to 1.
- (`'gas', 'dl'`) Pathlength of resolution element (not a true pathlength for particle-based codes)
- (`'gas', 'redshift'`) Cosmological redshift of resolution element
- (`'gas', 'redshift_dopp'`) Doppler redshift of resolution element
- (`'gas', 'redshift_eff'`) Effective redshift (combined cosmological and Doppler)

Like any dataset, you can see what fields are present on the ray by examining its derived_field_list (e.g., print(ds.derived_field_list). If you want more ions present on this ray than are currently available, you can add them with add_ion_fields (see: Adding Ion Fields).

This ray object is also saved to disk as an HDF5 file, which can later be loaded into yt as a stand-alone dataset. By default it is saved as ray.h5, but you can specify other filenames when you create it. To later access this file and load it into yt, load it like any other dataset: ds = yt.load('ray.h5').

4.4 Calculating Column Densities

Perhaps we wish to know the total column density of a particular ion present along this LightRay. This can easily be done by multiplying the desired ion number density field by the pathlength field, dl, to yield an array of column densities for each resolution element, and then summing them together:

```python
column_density_HI = ray.r['gas', 'H_p0_number_density'] * ray.r['gas', 'dl']
print('HI Column Density = %g' % column_density_HI.sum())
```
4.5 Examining LightRay Solution Data

When a LightRay is created, it saves the source information from the dataset that produced it in a dictionary, including its filename, its start and end points in the original dataset, etc. This is all accessible when you load up the LightRay again through the `light_ray_solution`:

```python
import yt
ds = yt.load('ray.h5')
print(ds.light_ray_solution)

[{
'end': unyt_array([1., 1., 1.], 'unitary'),
'filename': 'snapshot_600.hdf5',
'redshift': 0.05,
'start': unyt_array([0.48810148, 0.51748806, 0.54316002], 'unitary'),
'traversal_box_fraction': unyt_quantity(0.83878521, 'unitary'),
'unique_identifier': '1436307563512020127'}]
```

4.6 Useful Tips for Making Compound LightRays

Below are some tips that may come in handy for creating proper LightRays. For full use of these, you may have to create the LightRay by hand instead of using the `make_compound_ray()` helper function.

4.6.1 How many snapshots do I need for a compound ray?

The number of snapshots required to traverse some redshift interval depends on the simulation box size and cosmological parameters. Before running an expensive simulation only to find out that you don't have enough outputs to span the redshift interval you want, have a look at the guide Planning Simulations for LightCones or LightRays. The functionality described there will allow you to calculate the precise number of snapshots and specific redshifts at which they should be written.

4.6.2 My snapshots are too far apart!

The `max_box_fraction` keyword, provided when creating the LightRay, allows the user to control how long a ray segment can be for an individual dataset. By default, the LightRay generator will try to make segments no longer than the size of the box to avoid sampling the same structures more than once. However, this can be increased in the case that the redshift interval between datasets is longer than the box size. Increasing this value should be done with caution as longer ray segments run a greater risk of coming back to somewhere near their original position.

4.6.3 What if I have a zoom-in simulation?

A zoom-in simulation has a high resolution region embedded within a larger, low resolution volume. In this type of simulation, it is likely that you will want the ray segments to stay within the high resolution region. To do this, you must first specify the size of the high resolution region when creating the LightRay using the `max_box_fraction` keyword. This will make sure that the calculation of the spacing of the segment datasets only takes into account the high resolution region and not the full box size. If your high resolution region is not a perfect cube, specify the smallest side. Then, in the call to `make_light_ray()`, use the `left_edge` and `right_edge` keyword arguments to specify the precise location of the high resolution region.
Technically speaking, the ray segments should no longer be periodic since the high resolution region is only a sub-volume within the larger domain. To make the ray segments non-periodic, set the periodic keyword to False. The LightRay generator will continue to generate randomly oriented segments until it finds one that fits entirely within the high resolution region. If you have a high resolution region that can move and change shape slightly as structure forms, use the min_level keyword to mandate that the ray segment only pass through cells that are refined to at least some minimum level.

If the size of the high resolution region is not large enough to span the required redshift interval, the LightRay generator can be configured to treat the high resolution region as if it were periodic simply by setting the periodic keyword to True. This option should be used with caution as it will lead to the creation of disconnected ray segments within a single dataset.

### 4.6.4 I want a continuous trajectory over the entire ray.

Set the minimum_coherent_box_fraction keyword argument to a very large number, like infinity (numpy.inf).
In addition to generating a basic spectrum as demonstrated in the annotated example, the user can also customize the generated spectrum in a variety of ways. One can choose which spectral lines to deposit or choose different settings for the characteristics of the spectrograph, and more. The following code goes through the process of setting these properties and shows what impact it has on resulting spectra.

For this demonstration, we’ll be using a light ray passing through a very dense disk of gas, taken from the initial output from the AGORA isolated box simulation using ART-II in Kim et al. (2016). If you’d like to try to reproduce the spectra included below you can get the LightRay file from the Trident sample data using the command:

```
$ wget http://trident-project.org/data/sample_data/ART-II_ray.h5
```

Now, we’ll load up the ray using yt:

```
import yt
import trident
ray = yt.load('ART-II_ray.h5')
```

### 5.1 Setting the spectrograph

Let’s set the characteristics of the spectrograph we will use to create this spectrum. We can either choose the wavelength range and resolution and line spread function explicitly, or we can choose one of the preset instruments that come with Trident. To list the presets and their respective values, use this command:

```
print(trident.valid_instruments)
```

Currently, we have three settings for the Cosmic Origins Spectrograph available: COS-G130M, COS-G140L, and COS-G160M, but we plan to add more instruments soon. To use one of them, we just use the name string in the SpectrumGenerator class:

```
sg = trident.SpectrumGenerator('COS-G130M')
```

But instead, let’s just set our wavelength range manually from 1150 angstroms to 1250 angstroms with a resolution of 0.01 angstroms:

```
sg = trident.SpectrumGenerator(lambda_min=1150, lambda_max=1250, dlambda=0.01)
```

From here, we can pass the ray to the SpectrumGenerator object to use in the construction of a spectrum.
5.2 Choosing what absorption features to include

There is a LineDatabase class that controls which spectral lines you can add to your spectrum. Trident provides you with a default LineDatabase with 213 spectral lines commonly used in CGM and IGM studies, but you can create your own LineDatabase with different lines. To see a list of all the lines included in the default line list:

```python
ldb = trident.LineDatabase('lines.txt')
print(ldb)
```

which is reading lines from the ‘lines.txt’ file present in the data directory (see where is Trident installed?) We can specify any subset of these spectral lines to use when creating the spectrum from our master line list. So if you’re interested in just looking at neutral hydrogen lines in your spectrum, you can see what lines will be included with the command:

```python
print(ldb.parse_subset('H I'))
```

As a first pass, we’ll create a spectrum that just include lines produced by hydrogen:

```python
sg.make_spectrum(ray, lines=['H'])
sg.plot_spectrum('spec_H.png')
```

The resulting spectrum contains a nice, big Lyman-alpha feature.

If, instead, we want to shows the lines that would be in our spectral range due to carbon, nitrogen, and oxygen, we can do the following:

```python
sg.make_spectrum(ray, lines=['C', 'N', 'O'])
sg.plot_spectrum('spec_CNO.png')
```

And now we have:
We can see how these two spectra combined when we include all of the same lines:

```
sg.make_spectrum(ray, lines=['H', 'C', 'N', 'O'])
sg.plot_spectrum('spec_HCNO.png')
```

which gives:

![Spectrum with all lines](spec_HCNO.png)

We can get even more specific, by generating a spectrum that only contains lines due to a single ion species. For example, we might just want the lines from four-times-ionized nitrogen, N V:

```
sg.make_spectrum(ray, lines=['N V'])
sg.plot_spectrum('spec_NV.png')
```

This spectrum only shows a couple of small lines on the right hand side.

![Spectrum with N V lines](spec_NV.png)
But if that level of specificity isn’t enough, we can request individual lines:

```python
sg.make_spectrum(ray, lines=['C I 1193', 'C I 1194'])
sg.plot_spectrum('spec_CI_1193_1194.png')
```

And we end up with:

![Graph showing two distinct absorption features](image)

Or we can just include all of the available lines in our `LineDatabase` with:

```python
sg.make_spectrum(ray, lines='all')
sg.plot_spectrum('spec_all.png')
```

Giving us:

![Graph showing a wide range of absorption features](image)

To understand how to further customize your spectra, look at the documentation for the `SpectrumGenerator` and `LineDatabase` classes and other API documentation.

### 5.3 Setting Wavelength Bounds Automatically

If you are interested in creating a spectrum that contains all possible absorption features for a given set of lines, the `SpectrumGenerator` can be configured to automatically enlarge the wavelength window until all absorption is captured. This is done by setting the `lambda_min` and `lambda_max` keywords to ‘auto’ and specifying a bin size with the `dlambda` keyword:
sg = trident.SpectrumGenerator(lambda_min='auto', lambda_max='auto',
dlambda=0.01)
sg.make_spectrum("ray.h5", lines=['H I 1216'])
sg.plot_spectrum('spec_auto.png')

Note, the above example is for a different ray than is used in the previous examples. The resulting spectrum will minimally contain all absorption present in the ray. This should be used with care when depositing multiple lines as this can lead to an extremely large spectrum.

5.4 Making Spectra in Velocity Space

Trident can be configured to create spectra in velocity space instead of wavelength space where velocity corresponds to the velocity offset from the rest wavelength of a given line. This can be done by providing the keyword `bin_space='velocity'` to the `SpectrumGenerator`:

sg = trident.SpectrumGenerator(lambda_min='auto', lambda_max='auto',
dlambda=1., bin_space='velocity')
sg.make_spectrum("ray.h5", lines=['H I 1216'])
sg.plot_spectrum('spec_velocity.png')

When working in velocity space, limits and bin sizes should be provided in km/s. If more than one transition is added to the spectrum (e.g., Ly-a and Ly-b), the zero point will correspond to the rest wavelength of the first transition added.
5.5 Making Spectra from a Subset of a Ray

The situation may arise where you want to see the spectrum that is generated by only a portion of the gas along a line of sight. For example, you may want to see the spectrum of only the cold gas. This can be done by creating a YTCutRegion from a loaded ray dataset:

```python
import trident
import yt
ds = yt.load('ray.h5')
all_data = ds.all_data()
cold_gas = ds.cut_region(all_data, 'obj["gas", "temperature"] < 10000')

sg = trident.SpectrumGenerator(lambda_min=1200, lambda_max=1225, dlambda=0.01)

# spectrum of entire ray
sg.make_spectrum(all_data, lines=['H I 1216'])
all_spectrum = sg.flux_field[:]

# spectrum of cold gas
sg.make_spectrum(cold_gas, lines=['H I 1216'])
cold_spectrum = sg.flux_field[:]

trident.plot_spectrum(sg.lambda_field, [all_spectrum, cold_spectrum], label=['all gas', 'cold gas'], stagger=None)
```

![Graph showing relative flux against wavelength for 'all gas' and 'cold gas' spectra.](image)
FITTING ABSORPTION SPECTRA

This tool can be used to fit absorption spectra, particularly those generated using Trident. For more details on its uses and implementation please see (Egan et al. (2013)). If you find this tool useful we encourage you to cite accordingly.

6.1 Loading an Absorption Spectrum

To load an absorption spectrum created by SpectrumGenerator, specify the output file name. It is advisable to use either an .h5 or .fits file, rather than an ascii file to save the spectrum as rounding errors produced in saving to a ascii file will negatively impact fit quality.

```python
f = h5py.File('spectrum.h5')
wavelength = f['wavelength'][:]
flux = f['flux'][:]
f.close()
```

6.2 Specifying Species Properties

Before fitting a spectrum, you must specify the properties of all the species included when generating the spectrum.

The physical properties needed for each species are the rest wavelength, f-value, gamma value, and atomic mass. These will be the same values as used to generate the initial absorption spectrum. These values are given in list form as some species generate multiple lines (as in the OVI doublet). The number of lines is also specified on its own.

To fine tune the fitting procedure and give results in a minimal number of optimizing steps, we specify expected maximum and minimum values for the column density, doppler parameter, and redshift. These values can be well outside the range of expected values for a typical line and are mostly to prevent the algorithm from fitting to negative values or becoming numerically unstable.

Common initial guesses for doppler parameter and column density should also be given. These values will not affect the specific values generated by the fitting algorithm, provided they are in a reasonably appropriate range (ie: within the range given by the max and min values for the parameter).

For a spectrum containing both the H Lyman-alpha line and the OVI doublet, we set up a fit as shown below.

```python
HIParameters = {'name':'HI',
    'f': [.4164],
    'Gamma':[6.265E8],
    'wavelength':[1215.67],
    'numLines':1,
    'maxN': 1E22, 'minN':1E11,
}
```
6.3 Generating Fit of Spectrum

After loading a spectrum and specifying the properties of the species used to generate the spectrum, an appropriate fit can be generated.

```python
from trident.absorption_spectrum.absorption_spectrum_fit import generate_total_fit

orderFits = ['OVI', 'HI']

fitted_lines, fitted_flux = generate_total_fit(wavelength,
                                           flux, orderFits, speciesDicts)
```

The `orderFits` variable is used to determine in what order the species should be fitted. This may affect the results of the resulting fit, as lines may be fit as an incorrect species. For best results, it is recommended to fit species the generate multiple lines first, as a fit will only be accepted if all of the lines are fit appropriately using a single set of parameters. At the moment no cross correlation between lines of different species is performed.

The parameters of the lines that are needed to fit the spectrum are contained in the `fitted_lines` variable. Each species given in `orderFits` will be a key in the `fitted_lines` dictionary. The entry for each species key will be another dictionary containing entries for ‘N’, ‘b’, ‘z’, and ‘group#’ which are the column density, doppler parameter, redshift, and associate line complex respectively. The i\textsuperscript{th} line of a given species is then given by the parameters `N[i]`, `b[i]`, and `z[i]` and is part of the same complex (and was fitted at the same time) as all lines with the same group number as `group#[i]`.

The `fitted_flux` is an ndarray of the same size as `flux` and `wavelength` that contains the cumulative absorption spectrum generated by the lines contained in `fitted_lines`. 

```python
OVI_parameters = {
    'name': 'OVI',
    'f': [.1325, .06580],
    'Gamma': [4.148E8, 4.076E8],
    'wavelength': [1031.9261, 1037.6167],
    'numLines': 2,
    'maxN': 1E17, 'minN': 1E11,
    'maxb': 300, 'minb': 1,
    'maxz': 6, 'minz': 0,
    'init_b': 20,
    'init_N': 1E12
}
```

```python
speciesDicts = {'HI': HI_parameters, 'OVI': OVI_parameters}
```
6.4 Saving a Spectrum Fit

Saving the results of a fitted spectrum for further analysis is accomplished automatically using the h5 file format. A group is made for each species that is fit, and each species group has a group for the corresponding N, b, z, and group# values.

6.5 Procedure for Generating Fits

To generate a fit for a spectrum `generate_total_fit()` is called. This function controls the identification of line complexes, the fit of a series of absorption lines for each appropriate species, checks of those fits, and returns the results of the fits.

6.6 Finding Line Complexes

Line complexes are found using the `_find_complexes` function. The process by which line complexes are found involves walking through the array of flux in order from minimum to maximum wavelength, and finding series of spatially contiguous cells whose flux is less than some limit. These regions are then checked in terms of an additional flux limit and size. The bounds of all the passing regions are then listed and returned. Those bounds that cover an exceptionally large region of wavelength space will be broken up if a suitable cut point is found. This method is only appropriate for noiseless spectra.

The optional parameter `complexLim` (default = 0.999), controls the limit that triggers the identification of a spatially contiguous region of flux that could be a line complex. This number should be very close to 1 but not exactly equal. It should also be at least an order of magnitude closer to 1 than the later discussed `fitLim` parameter, because a line complex where the flux of the trough is very close to the flux of the edge can be incredibly unstable when optimizing.

The `fitLim` parameter controls what is the maximum flux that the trough of the region can have and still be considered a line complex. This effectively controls the sensitivity to very low column absorbers. Default value is `fitLim = 0.99`. If a region is identified where the flux of the trough is greater than this value, the region is simply ignored.

The `minLength` parameter controls the minimum number of array elements that an identified region must have. This value must be greater than or equal to 3 as there are a minimum of 3 free parameters that must be fit. Default is `minLength = 3`.

The `maxLength` parameter controls the maximum number of array elements that an identified region can have before it is split into separate regions. Default is `maxLength = 1000`. This should be adjusted based on the resolution of the spectrum to remain appropriate. The value correspond to a wavelength of roughly 50 angstroms.

The `splitLim` parameter controls how exceptionally large regions are split. When such a region is identified by having more array elements than `maxLength`, the point of maximum flux (or minimum absorption) in the middle two quartiles is identified. If that point has a flux greater than or equal to `splitLim`, then two separate complexes are created: one from the lower wavelength edge to the minimum absorption point and the other from the minimum absorption point to the higher wavelength edge. The default value is `splitLim = .99`, but it should not drastically affect results, so long as the value is reasonably close to 1.
6.7 Fitting a Line Complex

After a complex is identified, it is fitted by iteratively adding and optimizing a set of Voigt Profiles for a particular species until the region is considered successfully fit. The optimizing is accomplished using scipy’s least squares optimizer. This requires an initial estimate of the parameters to be fit (column density, b-value, redshift) for each line.

Each time a line is added, the guess of the parameters is based on the difference between the line complex and the fit so far. For the first line this just means the initial guess is based solely on the flux of the line complex. The column density is given by the initial column density given in the species parameters dictionary. If the line is saturated (some portion of the flux with a value less than .1) than the larger initial column density guess is chosen. If the flux is relatively high (all values >.9) than the smaller initial guess is given. These values are chosen to make optimization faster and more stable by being closer to the actual value, but the final results of fitting should not depend on them as they merely provide a starting point.

After the parameters for a line are optimized for the first time, the optimized parameters are then used for the initial guess on subsequent iterations with more lines.

The complex is considered successfully fit when the sum of the squares of the difference between the flux generated from the fit and the desired flux profile is less than \( \text{errBound} \). \( \text{errBound} \) is related to the optional parameter to \textit{generate_total_fit()} \( \text{maxAvgError} \) by the number of array elements in the region such that \( \text{errBound} = \text{number of elements} \times \text{maxAvgError} \).

There are several other conditions under which the cycle of adding and optimizing lines will halt. If the error of the optimized fit from adding a line is an order of magnitude worse than the error of the fit without that line, then it is assumed that the fitting has become unstable and the latest line is removed. Lines are also prevented from being added if the total number of lines is greater than the number of elements in the flux array being fit divided by 3. This is because there must not be more free parameters in a fit than the number of points to constrain them.

6.8 Checking Fit Results

After an acceptable fit for a region is determined, there are several steps the algorithm must go through to validate the fits.

First, the parameters must be in a reasonable range. This is a check to make sure that the optimization did not become unstable and generate a fit that diverges wildly outside the region where the fit was performed. This way, even if particular complex cannot be fit, the rest of the spectrum fitting still behaves as expected. The range of acceptability for each parameter is given in the species parameter dictionary. These are merely broad limits that will prevent numerical instability rather than physical limits.

In cases where a single species generates multiple lines (as in the OVI doublet), the fits are then checked for higher wavelength lines. Originally the fits are generated only considering the lowest wavelength fit to a region. This is because we perform the fitting of complexes in order from the lowest wavelength to the highest, so any contribution to a complex being fit must come from the lower wavelength as the higher wavelength contributions would already have been subtracted out after fitting the lower wavelength.
6.9 Saturated Lyman Alpha Fitting Tools

In cases where a large or saturated line (there exists a point in the complex where the flux is less than .1) fails to be fit properly at first pass, a more robust set of fitting tools is used to try and remedy the situation. The basic approach is to simply try a much wider range of initial parameter guesses in order to find the true optimization minimum, rather than getting stuck in a local minimum. A set of hard coded initial parameter guesses for Lyman alpha lines is given by the \_get_test_lines function Also included in these parameter guesses is an an initial guess of a high column cool line overlapping a lower column warm line, indicative of a broad Lyman alpha (BLA) absorber.
These internal classes and related extensions used to be part of yt but are now contained within Trident. The internal classes are documented below and can be used independently, but the primary Trident interfaces outlined in the main documentation are recommended.

### 7.1 Internal Classes

#### 7.1.1 AbsorptionSpectrum

For documentation on the main interface to spectrum creation in Trident, see *Spectrum Generation*.

The *AbsorptionSpectrum* is the internal class for creating absorption spectra in Trident from *LightRay* objects. The *AbsorptionSpectrum* and its workhorse method *make_spectrum()* return two arrays, one with wavelengths, the other with the normalized flux values at each of the wavelength values. It can also output a text file listing all important lines.

**Method for Creating Absorption Spectra**

Once a *LightRay* has been created traversing a dataset using the *Light Ray Generator*, a series of arrays store the various fields of the gas parcels (represented as cells) intersected along the ray. *AbsorptionSpectrum* steps through each element of the *LightRay*’s arrays and calculates the column density for desired ion by multiplying its number density with the path length through the cell. Using these column densities along with temperatures to calculate thermal broadening, voigt profiles are deposited on to a featureless background spectrum. By default, the peculiar velocity of the gas is included as a doppler redshift in addition to any cosmological redshift of the data dump itself.

**Subgrid Deposition**

For features not resolved (i.e. possessing narrower width than the spectral resolution), *AbsorptionSpectrum* performs subgrid deposition. The subgrid deposition algorithm creates a number of smaller virtual bins, by default the width of the virtual bins is 1/10th the width of the spectral feature. The Voigt profile is then deposited into these virtual bins where it is resolved, and then these virtual bins are numerically integrated back to the resolution of the original spectral bin size, yielding accurate equivalent widths values. *AbsorptionSpectrum* informs the user how many spectral features are deposited in this fashion.
Creating an Absorption Spectrum

Initialization

To instantiate an `AbsorptionSpectrum` object, the arguments required are the minimum and maximum wavelengths (assumed to be in Angstroms), and the number of wavelength bins to span this range (including the endpoints):

```python
from trident.absorption_spectrum.absorption_spectrum import AbsorptionSpectrum
sp = AbsorptionSpectrum(900.0, 1800.0, 10001)
```

Adding Features to the Spectrum

Absorption lines and continuum features can then be added to the spectrum. To add a line, you must know some properties of the line: the rest wavelength, f-value, gamma value, and the atomic mass in amu of the atom. That line must be tied in some way to a field in the dataset you are loading, and this field must be added to the LightRay object when it is created. Below, we will add the H Lyman-alpha line, which is tied to the neutral hydrogen field (`'H_p0_number_density'`).

```python
my_label = 'HI Lya'
field = 'H_p0_number_density'
wavelength = 1215.6700  # Angstroms
f_value = 4.164E-01
gamma = 6.265e+08
mass = 1.00794
sp.add_line(my_label, field, wavelength, f_value, gamma, mass, label_threshold=1.e10)
```

In the the call to `add_line()` the `field` argument tells the spectrum generator which field from the ray data to use to calculate the column density. The `label_threshold` keyword tells the spectrum generator to add all lines above a column density of $10^{10}$ cm$^{-2}$ to the text line list output at the end. If None is provided, as is the default, no lines of this type will be added to the text list.

Continuum features with optical depths that follow a power law can be added with the `add_continuum()` function. Like adding lines, you must specify details like the wavelength and the field in the dataset and LightRay that is tied to this feature. The wavelength refers to the location at which the continuum begins to be applied to the dataset, and as it moves to lower wavelength values, the optical depth value decreases according to the defined power law. The normalization value is the column density of the linked field which results in an optical depth of 1 at the defined wavelength. Below, we add the hydrogen Lyman continuum.

```python
my_label = 'HI Lya'
field = 'H_p0_number_density'
wavelength = 912.323660  # Angstroms
normalization = 1.6e17
index = 3.0
sp.add_continuum(my_label, field, wavelength, normalization, index)
```
## Making the Spectrum

Once all the lines and continua are added, the spectrum is made with the `make_spectrum()` function.

```python
code{python}
wavelength, flux = sp.make_spectrum('lightray.h5',
                                   output_file='spectrum.fits',
                                   line_list_file='lines.txt')
```

A spectrum will be made using the specified ray data and the wavelength and flux arrays will also be returned. If you set the optional `use_peculiar_velocity` keyword to False, the lines will not incorporate doppler redshifts to shift the deposition of the line features.

Three output file formats are supported for writing out the spectrum: fits, hdf5, and ascii. The file format used is based on the extension provided in the `output_file` keyword: `.fits` for a fits file, `.h5` for an hdf5 file, and anything else for an ascii file.

**Note:** To write out a fits file, you must install the `astropy` python library in order to access the `astropy.io.fits` module. You can usually do this by simply running `pip install astropy` at the command line.

## Generating Spectra in Parallel

Spectrum generation is parallelized using a multi-level strategy where each absorption line is deposited by a different processor. If the number of available processors is greater than the number of lines, then the deposition of individual lines will be divided over multiple processors.

Absorption spectrum creation can be run in parallel simply by adding the following to the top of the script and running with `mpirun`.

```python
code{python}
import yt
yt.enable_parallelism()
```

For more information on parallelism in yt, see [Parallel Computation With yt](#).

## 7.2 Extensions
We maintain a series of tests in Trident to make sure the code gives consistent results and to catch accidental breakages in our source code and dependencies. These tests are run by Travis automatically and regularly to assure consistency in functionality, but you can run them locally too (see below). The tests consist of a mix of unit tests (tests to assure Trident functions don’t actively fail) and answer tests (tests comparing newly generated results against some old established results to assure consistency).

### 8.1 Running the Test Suite

Running the test suite requires a version of Trident installed from source (see *Step 2: Install Trident*).

The tests are run using the *pytest* Python module. This can be installed with *conda* or *pip*.

```bash
$ conda install pytest
```

The test suite requires a number of datasets for testing functionality. Trident comes with a helper script that will download all the datasets and untar them. Before running this, make sure you have the `answer_test_data_dir` variable set in your config file (see *Step 3: Get Ionization Table and Verify Installation*). This variable should point to a directory where these datasets will be stored. The helper script is located in the `tests` directory of the Trident source.

```bash
$ cd tests
$ python download_test_data.py
```

If this is your first time running the tests, then you need to generate a “gold standard” for the answer tests. Follow *Generating Gold Standard Answer Test Results for Comparison* before continuing with running the tests, otherwise your answer tests will fail.

Make sure you’re on the desired version of yt and trident that you want to test and use (usually the tip of the development branch i.e., main).

```bash
$ export TRIDENT_GENERATE_TEST_RESULTS=0
$ cd /path/to/yt/
$ git checkout main
$ pip install -e .
$ cd /path/to/trident
$ git checkout main
$ pip install -e .
```

The test suite is run by calling `py.test` from within the `tests` directory.
If a test fails for some reason, you will be given a detailed traceback and reason for it failing. You can use this to identify what is wrong with your source or perhaps a change in the code of your dependencies. The tests should take around ten minutes to run.

### 8.2 Generating Gold Standard Answer Test Results for Comparison

In order to assure the Trident codebase gives consistent results over time, we compare the outputs of tests of new versions of Trident against an older, vetted version of the code we think gives accurate results. To create this “gold standard” result from the older version of the code, you must roll back the Trident and yt source back to the older “trusted” versions of the code. You can find the tags for the most recent trusted versions of the code by running `gold_standard_versions.py` and then rebuilding yt and Trident with these versions of the code. Lastly, set the `TRIDENT_GENERATE_TEST_RESULTS` environment variable to 1 and run the tests:

```bash
$ cd tests
$ py.test

Collecting test data for test_absorption_spectrum.py 
Collecting test_download.py .
Collecting test_generate.py .
Collecting test_instrument.py .
Collecting test_ion_balance.py ............
Collecting test_light_ray.py ..... 
Collecting test_line_database.py ....
Collecting test_lsf.py ....
Collecting test_pipelines.py ...
Collecting test_plotting.py .
Collecting test_ray_generator.py .
Collecting test_spectrum_generator.py ......

52 test sessions run.
52 tests ran.
52 passed in 117.32 seconds
```
8.3 The Tests Failed – What Do I Do?

If the tests have failed (either locally, or through the automatically generated test from Travis), you want to figure out what caused the breakage. It was either a change in trident or a change in one of Trident’s dependencies (e.g., yt). So first examine the output from `py.test` to see if you can deduce what went wrong.

Sometimes it isn’t obvious what caused the break, in which case you may need to use `git bisect` to track down the change, either in Trident or in yt. First, start with the tip of yt, and bisect the changes in Trident since its gold standard version (see below). If that doesn’t ID the bad changeset, then do the same with yt back to its gold standard version. Once you have identified the specific commit that caused the tests to break, you have to identify if it was a good or bad change. If the unit tests failed and some functionality no longer works, then it was a bad, and you’ll want to change the code that caused the break. On the other hand, if the answer tests changed, and they did so because of an improvement to the code, then you’ll simply want to go about Updating the Testing Gold Standard.

8.4 Updating the Testing Gold Standard

Periodically, the gold standard for our answer tests must be updated as bugs are caught or new more accurate behavior is enabled that causes the answer tests to fail. The first thing to do is to identify the most accurate version of the code (e.g., changesets for yt and trident that give the desired behavior). Tag the Trident changeset with the next gold standard iteration. You can see the current iteration by looking in the `.travis.yml` file at the TRIDENT_GOLD entry—increment this and tag the changeset. Update the `.travis.yml` file so that the YT_GOLD and TRIDENT_GOLD entries point to your desired changeset and tag. You have to explicitly push the new tag (hereafter `test-standard-v3`) to your repository (here: origin). Issue a pull request.

```
$ git tag test-standard-v3 <trident-changeset>
$ ... edit .travis.yml files to update YT_GOLD=<yt changeset>
$ ... and TRIDENT_GOLD=test-standard-v3
$ git add .travis.yml
$ git commit
$ git push origin test-standard-v3
$ <MAKE PULL REQUEST>
```

Once the pull request has been accepted, someone with admin access to the main trident repository (here upstream) will have to push the gold standard tag.

```
$ git push upstream test-standard-v3
```

Lastly, that person will have to also clear Travis’ cache, so that it regenerates new answer test results. This can be done manually here: https://travis-ci.org/trident-project/trident/caches.
CHAPTER NINE

FREQUENTLY ASKED QUESTIONS

9.1 Why don’t I have any absorption features in my spectrum?

There are many reasons you might not have any absorption features in your spectrum, but we’ll cover a few of the basic explanations here.

1. Your absorbers are in a different part of the spectrum than you’re plotting. Make sure you are plotting the wavelength range where you expect to see the absorption by taking into account the wavelength of your absorption features coupled with the redshift of your dataset: \( \lambda_{\text{obs}} = (1 + z) \lambda_{\text{rest}} \). To see the wavelength of specific ionic transitions, see the line list in: /trident/trident/data/line_lists/lines.txt.

2. Your sightlines do not have sufficient column densities of the desired ions to actually make an absorption feature. Look at the total column density of your desired ions in your sightline by multiplying the density times the path length and summing it all up. Here is an example for showing the total O VI column density in a ray:

```python
import trident
<generate/load your ray object>
trident.add_ion_fields(ray, ['O VI'])
ad = ray.all_data()
print((ad[('gas', 'O_p5_number_density')] * ad[('gas', 'dl')]).sum())
```

Depending on the ion, you usually need to see at least \( 10^{12}\text{cm}^{-2} \) to have any appreciable absorption. Try sending a sightline through a denser region in your simulation that might have more of that ion.

9.2 I don’t have a metallicity field in my dataset—What can I do?

In order to estimate the density of ions throughout your dataset, Trident needs a metallicity field. But some datasets may not have one generated by default. I highly recommend re-running the dataset with metals present, as this will lead to the best estimate of ions from Trident, but if you just want to create a “dummy” metallicity field, include the following code at the top of your script to automatically add a uniform metallicity field to any datasets loaded lacking one (in this case it’s 0.3 solar metallicity). For more information on creating derived fields like this one, see the yt documentation on derived fields:

```python
import yt
import numpy as np

def _metallicity(field, data):
    factor = 0.3 # 0.3 solar metallicity
    return (data.ds.arr(np.ones_like(data['gas', 'density']), 'Zsun') * factor
```
9.3 What functions are available and what is their syntax?

Go see the full documentation for all of our available classes and functions in the *API Documentation*.

9.4 What version of Trident am I running?

To learn what version of Trident you’re running, type:

```bash
$ python
>>> import trident
>>> print(trident.__version__)
```

If you have a version ending in dev, it means you’re on the development branch and you should also figure out which particular changeset you’re running. You can do this by:

```bash
$ cd <path/to/trident>
$ git log --pretty=format:%h -n 1
```

To figure out what version of yt you’re running, type:

```bash
$ yt version
```

If you’re writing to the mailing list with a problem, be sure to include all of the above with your bug report or question.

9.5 Where is Trident installed? Where are its data files?

One can easily identify where Trident is installed:

```bash
$ python
>>> import trident
>>> print(trident.path)
```

The data files are located in that path with an appended /data.
9.6 How do I join the mailing list?

You can join our mailing list for announcements, bugs reports, and changes at:
https://groups.google.com/forum/#!forum/trident-project-users

9.7 How do I learn more about the algorithms used in Trident?

We have a full description of all the methods used in Trident including citations to previous related works in our Trident method paper.

9.8 How do I cite Trident in my research?

Check out our citation page.

9.9 How do I get an invite to the Trident slack channel?

Click on this link.
10.1 Generating Rays

---

10.2 Generating Spectra

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10.2.1 trident.spectrum_generator.SpectrumGenerator

class trident.spectrum_generator.SpectrumGenerator(instrument=None, lambda_min=None, lambda_max=None, n_lambda=None, dlambda=None, lsf_kernel=None, line_database='lines.txt', ionization_table=None, bin_space='wavelength')

Preferred class for generating, storing, and plotting absorption-line spectra. SpectrumGenerator is a subclass of yt’s AbsorptionSpectrum class with additional functionality like line lists, post-processing to include Milky Way foreground, quasar backgrounds, applying line-spread functions, and plotting.

User first specifies the telescope/instrument used for generating spectra (e.g. ‘COS’ for the Cosmic Origins Spectrograph aboard the Hubble Space Telescope). This can be done by naming the Instrument, or manually setting all of the spectral characteristics including lambda_min, lambda_max, lsf_kernel, and n_lambda or dlambda. If none of these arguments are set, defaults to ‘COS’ as the default instrument covering 1150-1450 Angstroms with a binsize (dlambda) of 0.1 Angstroms.

Once a SpectrumGenerator has been initialized, pass it LightRay objects using make_spectrum to actually generate the spectra themselves. Then one can post-process, plot, or save them using add_milky_way_foreground, add_qso_spectrum, apply_lsf, save_spectrum, and plot_spectrum.
Parameters

**Instrument** string, optional

The spectrograph to use. Currently, the only named options are different observing modes of the Cosmic Origins Spectrograph ‘COS’: ‘COS-G130M’, ‘COS-G160M’, and ‘COS-G140L’ as well as ‘COS’ which aliases to ‘COS-G130M’. These automatically set the \(\lambda_{\text{min}}\), \(\lambda_{\text{max}}\), \(\Delta\lambda\) and \(\text{lsf\_kernel}\)’s appropriately. If you’re going to set \(\lambda_{\text{min}}, \lambda_{\text{max}}, \Delta\lambda\) and \(\text{lsf\_kernel}\) manually, leave this set to None. Default: None

**Lambda\_min** float, YTQuantity, or ‘auto’

lower wavelength bound in angstroms or velocity bound in km/s (if bin_space set to ‘velocity’). If set to ‘auto’, the lower bound will be automatically adjusted to encompass all absorption lines. The window will not be expanded for continuum features, only absorption lines.

**Lambda\_max** float, YTQuantity, or ‘auto’

upper wavelength bound in angstroms or velocity bound in km/s (if bin_space set to ‘velocity’). If set to ‘auto’, the upper bound will be automatically adjusted to encompass all absorption lines. The window will not be expanded for continuum features, only absorption lines.

**N\_lambda** int

The number of bins in the spectrum (inclusive), so if extrema = 10 and 20, and dlambda (binsize) = 1, then n_lambda = 11. Default: None

**Dlambda** float

size of the wavelength bins in angstroms or velocity bins in km/s. Default: None

**Bin\_space** ‘wavelength’ or ‘velocity’

Sets the dimension in which spectra are created. If set to wavelength, the resulting spectra are flux (or tau) vs. observed wavelength. If set to velocity, the spectra are flux vs. velocity offset from the rest wavelength of the absorption line. Default: wavelength

**Lsf\_kernel** string, optional

The filename for the LSF kernel. Files are found in trident.__path__/data/lsf_kernels or current working directory. Only necessary if you are applying an LSF to the spectrum in postprocessing. Default: None

**Line\_database** string or LineDatabase, optional

A text file listing the various lines to insert into the line database, or a LineDatabase object in memory. The line database provides a list of all possible lines that could be added to the spectrum. For a text file, it should have 4 tab-delimited columns of name (e.g. MgII), wavelength in angstroms, gamma of transition, and f-value of transition. See example datasets in trident.path/data/line_lists for examples. Default: lines.txt

**Ionization\_table** hdf5 file, optional

An HDF5 file used for computing the ionization fraction of the gas based on its density, temperature, metallicity, and redshift. If set to None, will use the ion table defined in your Trident config file. Default: None

Example

Create a one-zone ray, and generate a COS spectrum from that ray.

```python
>>> import trident
>>> ray = trident.make_onezone_ray()
```
Create a one-zone ray at redshift 0.5, and generate a spectrum with 1 angstrom spectral bins from 2000-4000 angstroms, then post-process by adding a MW foreground a QSO background at z=0.5 and add a boxcar line spread function of 100 angstroms width. Plot it and save the figure to 'spec_final.png'.

```python
>>> import trident
>>> ray = trident.make_onezone_ray(redshift=0.5)
>>> sg = trident.SpectrumGenerator(lambda_min=2000, lambda_max=4000, ...
    dlambda=1)
>>> sg.make_spectrum(ray)
>>> sg.add_qso_spectrum(emitting_redshift=.5)
>>> sg.add_milky_way_foreground()
>>> sg.apply_lsf(function='boxcar', width=100)
>>> sg.plot_spectrum('spec_final.png')
```

Methods

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<td><code>save_spectrum</code></td>
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</tbody>
</table>
trident.spectrum_generator.SpectrumGenerator.__init__

SpectrumGenerator.__init__(instrument=None, lambda_min=None, lambda_max=None, n_lambda=None, dlambda=None, lsf_kernel=None, line_database='/ts1/lens_lines.txt', ionization_table=None, bin_space='wavelength')

trident.spectrum_generator.SpectrumGenerator.add_continuum

SpectrumGenerator.add_continuum(label, field_name, wavelength, normalization, index)

Add a continuum feature that follows a power-law.

Parameters

Label  string
     label for the feature.

Field_name  string
     field name from ray data for column densities.

Wavelength  float
     line rest wavelength in angstroms.

Normalization  float
     the column density normalization.

Index  float
     the power-law index for the wavelength dependence.

trident.spectrum_generator.SpectrumGenerator.add_gaussian_noise

SpectrumGenerator.add_gaussian_noise(snr, seed=None)

Postprocess a spectrum to add gaussian random noise of a given SNR.

Parameters

Snr  float
     The desired signal-to-noise ratio for determining the amount of gaussian noise

Seed  optional, int
     Seed for the random number generator. This should be used to ensure than the same noise is added each time the spectrum is regenerated, if desired. Default: None

Example

Make a one zone ray and generate a COS spectrum for it. Add noise to the spectrum as though it were observed with a signal to noise ratio of 30.

```python
>>> import trident
>>> ray = trident.make_onezone_ray(redshift=0.5)
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.make_spectrum(ray)
>>> sg.add_gaussian_noise(30)
>>> sg.plot_spectrum('spec_noise_corrected.png')
```
Plot a DLA with SNR of 10.

```python
>>> import trident
>>> ray = trident.make_onezone_ray(column_densities={'H_p0_number_density':1e21})
>>> sg = trident.SpectrumGenerator(lambda_min=1200, lambda_max=1300, dlambda=0.1)
>>> sg.make_spectrum(ray, lines=['Ly a'])
>>> sg.add_gaussian_noise(10)
>>> sg.plot_spectrum('spec_noise.png')
```

**trident.spectrum_generator.SpectrumGenerator.add_line**

SpectrumGenerator.add_line(label, field_name, wavelength, f_value, gamma, atomic_mass, label_threshold=None)

Add an absorption line to the list of lines included in the spectrum.

**Parameters**

- **Label** string
  
  label for the line.

- **Field_name** string
  
  field name from ray data for column densities.

- **Wavelength** float
  
  line rest wavelength in angstroms.

- **F_value** float
  
  line f-value.

- **Gamma** float
  
  line gamma value.

- **Atomic_mass** float
  
  mass of atom in amu.

**trident.spectrum_generator.SpectrumGenerator.add_line_to_database**

SpectrumGenerator.add_line_to_database(element, ion_state, wavelength, gamma, f_value, field=None, identifier=None)

Adds desired line to the current LineDatabase object.

**Parameters**

- **Element** string
  
  The element of the transition using element’s symbol on periodic table

- **Ion_state** string
  
  The roman numeral representing the ionic state of the transition

- **Wavelength** float
  
  The wavelength of the transition in angstroms

10.2. Generating Spectra
**Gamma** float

The gamma of the transition in Hertz

**F_value** float

The oscillator strength of the transition

**Field** string, optional

The default yt field name associated with the ion responsible for this line Default: None

**Identifier** string, optional

An optional identifier for the transition Default: None

---

```
trident.spectrum_generator.SpectrumGenerator.add_milky_way_foreground
```

SpectrumGenerator.add_milky_way_foreground(flux_field=None, filename=None)

Postprocess a spectrum to add a Milky Way foreground. Data from Charles Danforth. Median-filter of 92 normalized COS/G130M+G160M AGN spectra spanning the wavelength range of 1130 to 1800 Angstroms in 0.07 Angstrom bin size.

**Parameters**

- **Flux_field** optional, array

  Array of flux values to which the Milky Way foreground is applied. Default: None

- **Filename** string

  Filename where the Milky Way foreground values used to modify the flux are stored. Default: None

**Example**

Make a one zone ray and generate a COS spectrum for it. Add MW foreground to it, and save it.

```python
>>> import trident

>>> ray = trident.make_onezone_ray()

>>> sg = trident.SpectrumGenerator('COS')

>>> sg.make_spectrum(ray)

>>> sg.add_milky_way_foreground()

>>> sg.plot_spectrum('spec_mw_corrected.png')
```

Plot a naked MW spectrum.

```python
>>> import trident

>>> sg = trident.SpectrumGenerator('COS')

>>> sg.add_milky_way_foreground()

>>> sg.plot_spectrum('spec_mw.png')
```
trident.spectrum_generator.SpectrumGenerator.add_noise_vector

SpectrumGenerator.add_noise_vector(noise)

Add an array of noise to the spectrum.

Parameters

- **Noise** array of floats

  The array of noise values to be added to the spectrum. This array must be of the same size as the flux array.

Example

```python
>>> import numpy as np
>>> import trident
>>> ray = trident.make_onezone_ray(column_densities={'H_p0_number_density':1e21})
>>> sg = trident.SpectrumGenerator(lambda_min=1200, lambda_max=1300, dlambda=0.1)
>>> sg.make_spectrum(ray, lines=['Ly a'])
>>> my_noise = np.random.normal(loc=0.0, scale=0.1, size=sg.flux_field.size)
>>> sg.add_noise_vector(my_noise)
>>> sg.plot_spectrum('spec_noise.png')
```

trident.spectrum_generator.SpectrumGenerator.add_qso_spectrum

SpectrumGenerator.add_qso_spectrum(flux_field=None, emitting_redshift=None, observing_redshift=None, filename=None)


Parameters

- **Flux_field** array, optional

  Array of flux values to which the quasar background is applied. Default: None

- **Emitting_redshift** float, optional

  Redshift value at which the QSO emitted its light. If specified as None, use 0. Default: None

- **Observing_redshift** float, optional

  Redshift value at which the quasar is observed. If specified as None, use the observing_redshift value specified in make_spectrum() which defaults to 0. Default: None

- **Filename** string

  Filename where the Milky Way foreground values used to modify the flux are stored. Default: None

Example

Make a one zone ray at redshift of .5 and generate a COS spectrum for it. Add z=0.5 quasar background to it, and save it.

```python
>>> import trident
>>> ray = trident.make_onezone_ray(redshift=0.5)
>>> sg = trident.SpectrumGenerator('COS')
```
>>> sg.make_spectrum(ray)
>>> sg.add_qso_spectrum(emitting_redshift=0.5)
>>> sg.plot_spectrum('spec_qso_corrected.png')

Plot a naked QSO spectrum at z=.1

>>> import trident
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.add_qso_spectrum(emitting_redshift=.1)
>>> sg.plot_spectrum('spec_qso.png')

trident.spectrum_generator.SpectrumGenerator.apply_lsf

SpectrumGenerator._apply_lsf(func=None, width=None, filename=None)
SpectrumGenerator.apply_lsf(func=fun: None, width=None, filename=None)

Postprocess a spectrum to apply a line spread function. If the SpectrumGenerator already has an LSF kernel set, it will be used when no keywords are supplied. Otherwise, the user can specify a filename of a user-defined kernel or a function+width for a kernel. Valid functions are: “boxcar” and “gaussian”.

For more information, see LSF and Instrument.

Parameters

Function  string, optional
- Desired functional form for the applied LSF kernel. Valid options are currently “boxcar” or “gaussian” Default: None

Width  int, optional
- Width of the desired LSF kernel in bin elements Default: None

Filename  string, optional
- The filename of the user-supplied kernel for applying the LSF Default: None

Example

Make a one zone ray and generate a COS spectrum for it. Apply the COS line spread function to it.

>>> import trident
>>> ray = trident.make_onezone_ray()
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.make_spectrum(ray)
>>> sg.apply_lsf()
>>> sg.plot_spectrum('spec_lsf_corrected.png')

Make a one zone ray and generate a spectrum with bin width = 1 angstrom. Apply a boxcar LSF to it with width 50 angstroms.

>>> import trident
>>> ray = trident.make_onezone_ray()
>>> sg = trident.SpectrumGenerator(lambda_min=1100, lambda_max=1200, dlambda=1)
>>> sg.make_spectrum(ray)
>>> sg.apply_lsf(function='boxcar', width=50)
>>> sg.plot_spectrum('spec_lsf_corrected.png')
**trident.spectrum_generator.SpectrumGenerator.clear_spectrum**

```python
SpectrumGenerator.clear_spectrum()
```

Clear the current spectrum in the SpectrumGenerator. Clears the existing spectrum’s flux and tau fields and replaces them with ones and zeros respectively. Clear the line list kept in the AbsorptionSpectrum object as well. Also clear the line_subset stored by the LineDatabase.

**trident.spectrum_generator.SpectrumGenerator.error_func**

```python
SpectrumGenerator.error_func(flux)
```

Approximate the flux error for a spectrum. Many observational analysis programs require a flux error channel in addition to a flux channel. So we create a zeroth order approximation of the flux error, simply by taking the square root of the flux. Unfortunately, with flux normalized to be $< 1$, this would result in errors larger than the flux values themselves, so we normalize by an arbitrary signal-to-noise ratio, which by default is set to 100. This yields a typical error for a normalized spectrum of $\sqrt{1.0*100}/100 = 0.1$. This assures our flux errors are smaller than our fluxes for most flux reasonable flux values. Note that when a signal to noise ratio is specified for adding gaussian noise, it uses this updated value for estimating the errors. SNR is set as an attribute of AbsorptionSpectrum directly (e.g., as.snr = N).

**Parameters**

- **Flux** array of floats
  - The array of flux values

**trident.spectrum_generator.SpectrumGenerator.load_spectrum**

```python
SpectrumGenerator.load_spectrum(lambda_field=None, tau_field=None, flux_field=None)
```

Load data arrays into an existing spectrum object.

**Parameters**

- **Lambda_field** array
  - The array of valid wavelengths Default: None
- **Tau_field** array
  - The array of optical depths for the corresponding wavelengths Default: None
- **Flux_field** array
  - The array of flux values for the corresponding wavelengths Default: None

**Example**

Loading a custom set of data into an existing SpectrumGenerator object:

```python
>>> import trident
>>> import numpy as np
>>> lambda_field = np.arange(1200,1400)
>>> flux_field = np.ones(len(lambda_field))
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.load_spectrum(lambda_field=lambda_field, flux_field=flux_field)
>>> sg.plot_spectrum('temp.png')
```
trident.spectrum_generator.SpectrumGenerator.make_spectrum

SpectrumGenerator.make_spectrum(ray, lines='all', output_file=None, output_absorbers_file=None,
use_peculiar_velocity=True, observing_redshift=0.0, ly_continuum=True,
store_observables=False, min_tau=0.001, njobs='auto')

Make a spectrum from ray data depositing the desired lines. Make sure to pass this function a LightRay object and potentially also a list of strings representing what lines you’d like to actually have be deposited in your final spectrum.

Parameters

Ray  string, dataset, or data container
   If a string, the path to the ray dataset. As a dataset, this is the ray dataset loaded by yt. As a data container, this is a data object created from a ray dataset, such as a cut region.

Lines  list of strings
   List of strings that determine which lines will be added to the spectrum. List can include things like “C”, “O VI”, or “Mg II ####”, where #### would be the integer wavelength value of the desired line. If set to ‘all’, includes all lines in LineDatabase set in SpectrumGenerator. Default: ‘all’

Output_file  optional, string
   Filename of output if you wish to save the spectrum immediately without any further processing. File formats are chosen based on the filename extension. ‘.h5’ for HDF5, ‘.fits’ for FITS, and everything else is ASCII. Equivalent of calling save_spectrum. Default: None

Output_absorbers_file  optional, string
   Option to save a text file containing all of the absorbers and corresponding wavelength and redshift information. For parallel jobs, combining the lines lists can be slow so it is recommended to set to None in such circumstances. Default: None

Use_peculiar_velocity  optional, bool
   If True, include the effects of doppler redshift of the gas in shifting lines in the final spectrum. Default: True

Observing_redshift  optional, float
   This is the value of the redshift at which the observer of this spectrum exists. In most cases, this will be a redshift of 0. Default: 0.

Ly_continuum  optional, boolean
   If any H I lines are used in the line list, this assures a Lyman continuum will be included in the spectral generation. Lyman continuum begins at final Lyman line deposited (Ly 39 = 912.32 Å) not at formal Lyman Limit (911.76 Å) so as to not have a gap between final Lyman lines and continuum. Uses power law of index 3 and normalization to match opacity of final Lyman lines. Default: True

Store_observables  optional, boolean
   If set to true, observable properties for each cell in the light ray will be saved for each line in the line list. Properties include the column density, tau, thermal b, and the wavelength where tau was deposited. Best applicable for a reasonable number of lines. These quantities will be saved to the SpectrumGenerator attribute: ‘line_observables_dict’. Default: False

Min_tau  optional, float
   This value determines size of the wavelength window used to deposit lines or continua. The wavelength window is expanded until the optical depth at the edge is below this value. If too high, this will result in features appearing cut off at the edges. Decreasing this will
make features smoother but will also increase run time. An increase by a factor of ten will result in roughly a 2x slow down. Default: 1e-3.

Njobs  optional, int or “auto”

The number of process groups into which the loop over absorption lines will be divided. If set to -1, each absorption line will be deposited by exactly one processor. If njobs is set to a value less than the total number of available processors (N), then the deposition of an individual line will be parallelized over (N / njobs) processors. If set to “auto”, it will first try to parallelize over the list of lines and only parallelize the line deposition if there are more processors than lines. This is the optimal strategy for parallelizing spectrum generation. Default: “auto”

Example

Make a one zone ray and generate a COS spectrum for it including only Oxygen VI, Mg II, and all Carbon lines, and plot to disk.

```python
>>> import trident

>>> ray = trident.make_onezone_ray()

>>> sg = trident.SpectrumGenerator('COS')

>>> sg.make_spectrum(ray, lines=['O VI', 'Mg II', 'C'])

>>> sg.plot_spectrum('spec_raw.png')
```

```
trident.spectrum_generator.SpectrumGenerator.plot_spectrum

SpectrumGenerator.plot_spectrum(filename='spectrum.png', lambda_limits=None, flux_limits=None, step=False, title=None, label=None, figsize=None, features=None, axis_labels=None)

Plot the current spectrum and save to disk.

This is a convenience method that wraps the plot_spectrum standalone function for use with the data from the SpectrumGenerator itself.

Parameters

Filename  string, optional

Output filename of the plotted spectrum. Will be a png file. Default: ‘spectrum.png’

Lambda_limits  tuple or list of floats, optional

The minimum and maximum of the lambda range (x-axis) for the plot in angstroms. If specified as None, will use whole lambda range of spectrum. Example: (1200, 1400) for 1200-1400 Angstroms. Default: None

Flux_limits  tuple or list of floats, optional

The minimum and maximum of the flux range (y-axis) for the plot. If specified as None, limits are automatically from [0, 1.1*max(flux)]. Example: (0, 1) for normal flux range before post-processing. Default: None

Step  boolean, optional

Plot the spectrum as a series of step functions. Appropriate for plotting processed and noisy data.

Title  string, optional

Optional title for plot Default: None

Label  string, optional
```
Label for spectrum to be plotted. Will automatically trigger a legend to be generated. Default: None

**Features** dict, optional

Include vertical lines with labels to represent certain spectral features. Each entry in the dictionary consists of a key string to be overplot and the value float as to where in wavelength space it will be plot as a vertical line with the corresponding label.

Example: features={‘Ly a’: 1216, ‘Ly b’: 1026}

Default: None

**Axis_labels** tuple of strings, optional

Optionally set the axis labels directly. If set to None, defaults to ‘Wavelength [$\text{\AA}$]’, ‘Relative Flux’). Default: None

**Example**

Create a one-zone ray, and generate a COS spectrum from that ray. Plot the resulting spectrum highlighting the Lyman alpha feature.

```python
>>> import trident
>>> ray = trident.make_onezone_ray()
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.make_spectrum(ray)
>>> sg.plot_spectrum('spec_raw.png', features={'Ly a': 1216})
```

**trident.spectrum_generator.SpectrumGenerator.save_spectrum**

SpectrumGenerator.save_spectrum(filename='spectrum.h5', format=None)

Save the current spectrum data to an output file. Unless specified, the output data format will be determined by the suffix of the filename provided (‘h5’:HDF5, ‘fits’:FITS, all other:ASCII).

ASCII data is stored as a tab-delimited text file.

**Parameters**

- **Filename** string, optional
  
  Output filename for storing the data. Default: ‘spectrum.h5’

- **Format** string, optional
  
  Data format of the output file. Valid examples are “HDF5”, “FITS”, and “ASCII”. If None is set, selects based on suffix of filename. Default: None

**Example**

Save a spectrum to disk, load it from disk, and plot it.

```python
>>> import trident
>>> ray = trident.make_onezone_ray()
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.make_spectrum(ray)
>>> sg.save_spectrum('temp.h5')
>>> sg.clear_spectrum()
>>> sg.load_spectrum('temp.h5')
>>> sg.plot_spectrum('temp.png')
```
Attributes

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>current_tau_field</td>
<td>This is the optical depth array for the current absorption line being deposited.</td>
</tr>
<tr>
<td>lambda_field</td>
<td>The lambda field.</td>
</tr>
<tr>
<td>tau_field</td>
<td>This is the total optical depth of all lines and continua.</td>
</tr>
</tbody>
</table>

**trident.spectrum_generator.SpectrumGenerator.current_tau_field**

**property SpectrumGenerator.current_tau_field**

This is the optical depth array for the current absorption line being deposited. We will do the deposition of lines into this array, and then add it to self.tau_field at the end.

**trident.spectrum_generator.SpectrumGenerator.lambda_field**

**property SpectrumGenerator.lambda_field**

The lambda field.

**trident.spectrum_generator.SpectrumGenerator.tau_field**

**property SpectrumGenerator.tau_field**

This is the total optical depth of all lines and continua.

### 10.2.2 trident.absorption_spectrum.absorption_spectrum.AbsorptionSpectrum

**class trident.absorption_spectrum.absorption_spectrum.AbsorptionSpectrum**

Base class for generating absorption spectra. This code was originally based in yt and more restrictive in terms of what development was allowed, so the SpectrumGenerator subclass has more advanced functionality built on top of this. The base algorithm and functionality for spectral generation occurs here though.

**Parameters**

- **Lambda_min**  float, YTQuantity, or ‘auto’
  
  lower wavelength bound in angstroms or velocity bound in km/s (if bin_space set to ‘velocity’).
  
  If set to ‘auto’, the lower bound will be automatically adjusted to encompass all absorption lines.
  
  The window will not be expanded for continuum features, only absorption lines.

- **Lambda_max**  float, YTQuantity, or ‘auto’
  
  upper wavelength bound in angstroms or velocity bound in km/s (if bin_space set to ‘velocity’).
  
  If set to ‘auto’, the upper bound will be automatically adjusted to encompass all absorption lines.
  
  The window will not be expanded for continuum features, only absorption lines.
trident Documentation, Release 1.3.dev1

N\_lambda  optional, int
number of bins. This cannot be set when setting either lambda\_min or lambda\_max to auto.

D\_lambda  optional, float or YTQuantity
size of the wavelength bins in angstroms or velocity bins in km/s.

Bin\_space  ‘wavelength’ or ‘velocity’
Sets the dimension in which spectra are created. If set to wavelength, the resulting spectra are
flux (or tau) vs. observed wavelength. If set to velocity, the spectra are flux vs. velocity offset
from the rest wavelength of the absorption line. Default: wavelength

Methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
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<tbody>
<tr>
<td><strong>init</strong></td>
<td>Add a continuum feature that follows a power-law.</td>
</tr>
<tr>
<td>add_continuum</td>
<td>Add an absorption line to the list of lines included in the spectrum.</td>
</tr>
<tr>
<td>error_func</td>
<td>Approximate the flux error for a spectrum.</td>
</tr>
<tr>
<td>make_spectrum</td>
<td>Make spectrum from ray data using the line list.</td>
</tr>
</tbody>
</table>

trident.absorption\_spectrum.absorption\_spectrum.AbsorptionSpectrum.__init__

AbsorptionSpectrum.__init__(\(lambda\_min, lambda\_max, n\_lambda=None, d\_lambda=None, bin\_space='wavelength'\))

trident.absorption\_spectrum.absorption\_spectrum.AbsorptionSpectrum.add\_continuum

AbsorptionSpectrum.add\_continuum(label, field\_name, wavelength, normalization, index)
Add a continuum feature that follows a power-law.

Parameters

- **Label**  string
  label for the feature.

- **Field\_name**  string
  field name from ray data for column densities.

- **Wavelength**  float
  line rest wavelength in angstroms.

- **Normalization**  float
  the column density normalization.

- **Index**  float
  the power-law index for the wavelength dependence.
AbsorptionSpectrum.add_line(label, field_name, wavelength, f_value, gamma, atomic_mass, label_threshold=None)

Add an absorption line to the list of lines included in the spectrum.

Parameters

Label string
label for the line.

Field_name string
field name from ray data for column densities.

Wavelength float
line rest wavelength in angstroms.

F_value float
line f-value.

Gamma float
line gamme value.

Atomic_mass float
mass of atom in amu.

AbsorptionSpectrum.error_func(flux)

Approximate the flux error for a spectrum. Many observational analysis programs require a flux error channel in addition to a flux channel. So we create a zeroth order approximation of the flux error, simply by taking the square root of the flux. Unfortunately, with flux normalized to be < 1, this would result in errors larger than the flux values themselves, so we normalize by an arbitrary signal-to-noise ratio, which by default is set to 100. This yields a typical error for a normalized spectrum of sqrt(1.0*100)/100 = 0.1. This assures our flux errors are smaller than our fluxes for most flux reasonable flux values. Note that when a signal to noise ratio is specified for adding gaussian noise, it uses this updated value for estimating the errors. SNR is set as an attribute of AbsorptionSpectrum directly (e.g., as.snr = N).

Parameters

Flux array of floats
The array of flux values
trident.absorption_spectrum.absorption_spectrum.AbsorptionSpectrum.make_spectrum

AbsorptionSpectrum.make_spectrum(input_object, output_file=None, line_list_file=None, output_absorbers_file=None, use_peculiar_velocity=True, store_observables=False, subgrid_resolution=10, observing_redshift=0.0, min_tau=0.001, njobs='auto')

Make spectrum from ray data using the line list.

Parameters

Input_object string, dataset, or data container

If a string, the path to the ray dataset. As a dataset, this is the ray dataset loaded by yt. As a data container, this is a data object created from a ray dataset, such as a cut region.

Output_file optional, string

Option to save a file containing the wavelength, flux, and optical depth fields. File formats are chosen based on the filename extension. .h5 for hdf5, .fits for fits, and everything else is ASCII. Default: None

Output_absorbers_file optional, string

Option to save a text file containing all of the absorbers and corresponding wavelength and redshift information. For parallel jobs, combining the lines lists can be slow so it is recommended to set to None in such circumstances. Default: None

Use_peculiar_velocity optional, bool

if True, include peculiar velocity for calculating doppler redshift to shift lines. Requires similar flag to be set in LightRay generation. Default: True

Store_observables optional, bool

if True, stores observable properties of each cell along the line of sight for each line, such as tau, column density, and thermal b. These quantities will be saved to the AbsorptionSpectrum attribute: ‘line_observables_dict’. Default: False

Subgrid_resolution optional, int

When a line is being added that is unresolved (ie its thermal width is less than the spectral bin width), the voigt profile of the line is deposited into an array of virtual wavelength bins at higher resolution. The optical depth from these virtual bins is integrated and then added to the coarser spectral wavelength bin. The subgrid_resolution value determines the ratio between the thermal width and the bin width of the virtual bins. Increasing this value yields smaller virtual bins, which increases accuracy, but is more expensive. A value of 10 yields accuracy to the 4th significant digit in tau. Default: 10

Observing_redshift optional, float

This is the redshift at which the observer is observing the absorption spectrum. Default: 0

Min_tau optional, float

This value determines size of the wavelength window used to deposit lines or continua. The wavelength window is expanded until the optical depth at the edge is below this value. If too high, this will result in features appearing cut off at the edges. Decreasing this will make features smoother but will also increase run time. An increase by a factor of ten will result in roughly a 2x slow down. Default: 1e-3.

Njobs optional, int or “auto”
the number of process groups into which the loop over absorption lines will be divided. If set to -1, each absorption line will be deposited by exactly one processor. If njobs is set to a value less than the total number of available processors (N), then the deposition of an individual line will be parallelized over \((N / njobs)\) processors. If set to “auto”, it will first try to parallelize over the list of lines and only parallelize the line deposition if there are more processors than lines. This is the optimal strategy for parallelizing spectrum generation. Default: “auto”

### Attributes

<table>
<thead>
<tr>
<th>Property</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>current_tau_field</code></td>
<td>This is the optical depth array for the current absorption line being deposited.</td>
</tr>
<tr>
<td><code>lambda_field</code></td>
<td>The lambda field.</td>
</tr>
<tr>
<td><code>tau_field</code></td>
<td>This is the total optical depth of all lines and continua.</td>
</tr>
</tbody>
</table>

### 10.2.3 trident.instrument.Instrument

#### class `trident.instrument.Instrument`(

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>lambda_min</code></td>
<td>float or YTQuantity</td>
</tr>
<tr>
<td><code>lambda_max</code></td>
<td>float or YTQuantity</td>
</tr>
<tr>
<td><code>n_lambda</code></td>
<td>int</td>
</tr>
</tbody>
</table>

An instrument class for specifying a spectrograph/telescope pair

### 10.2. Generating Spectra
**Dlambda**  float or YTQuantity

Desired bin width for the spectrum in angstroms Setting dlambda overrides n_lambda value Default: None

**Lsf_kernel**  string

The filename for the LSF kernel Default: None

<table>
<thead>
<tr>
<th>Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>string</td>
</tr>
<tr>
<td>Name assigned to the Instrument object Default: None</td>
</tr>
</tbody>
</table>

**Methods**

__init__

**trident.instrument.Instrument.__init__**

Instrument.__init__(lambda_min, lambda_max, n_lambda=None, dlambda=None, lsf_kernel=None, bin_space='wavelength', name=None)

**10.2.4 trident.lsf.LSF**

**class trident.lsf.LSF(function=None, width=None, filename=None)**

A class representing a spectrograph’s line spread function.

A line spread function can be defined either by a function and width or by a filename containing a custom kernel.

<table>
<thead>
<tr>
<th>Parameters</th>
</tr>
</thead>
<tbody>
<tr>
<td>Function string, optional</td>
</tr>
<tr>
<td>The function defining the LSF kernel. valid functions are “boxcar” or “gaussian”</td>
</tr>
<tr>
<td>Width int, optional</td>
</tr>
<tr>
<td>The width of the LSF kernel in bins.</td>
</tr>
<tr>
<td>Filename string, optional</td>
</tr>
<tr>
<td>The filename of a textfile for a user-specified kernel. Each line in the textfile contains a normalized flux value of the kernel. For examples, see contents of trident.<strong>path</strong>/data/lsf_kernels Trident searches for these files either in the aforementioned directory or in the execution directory.</td>
</tr>
</tbody>
</table>

**Examples**

Generate an LSF based on a text file:

```python
>>> LSF(filename='avg_COS.txt')
```

Generate a boxcar-based LSF:

```python
>>> LSF(function='boxcar', width=30)
```

Generate a gaussian-based LSF:
trident Documentation, Release 1.3.dev1

```python
>>> LSF(function='guassian', width=7)
```

Methods

```python
trident.lsf.LSF.__init__
```

```text
LSF.__init__(function=None, width=None, filename=None)
```

### 10.2.5 trident.line_database.Line

class trident.line_database.Line(element, ion_state, wavelength, gamma, f_value, field=None, identifier=None)

A class representing an individual atomic transition. Each Line object is uniquely identified by element, ionic state, wavelength, gamma, oscillator strength, and identifier.

**Parameters**

- **Element** string
  The element of the transition using element's symbol on periodic table Example: ‘H’, ‘C’, ‘Mg’

- **Ion_state** string
  The roman numeral representing the ionic state of the transition Example: ‘I’ for neutral species, ‘II’ for singly ionized, etc.

- **Wavelength** float
  The wavelength of the transition in angstroms Example: 1216 for Lyman alpha

- **Gamma** float
  The gamma of the transition in Hertz

- **F_value** float
  The oscillator strength of the transition

- **Field** string, optional
  The default yt field name associated with the ion responsible for this line Example: ‘H_p1_number_density’ for HII

- **Identifier** string, optional
  An optional identifier for the transition Example: ‘Ly a’ for Lyman alpha

**Example**

Create a Line object for the neutral hydrogen 1215 Angstroms transition.

```python
>>> HI = Line('H', 'I', 1215.67, 469860000, 0.41641, 'Ly a')
```
Methods

__init__

trident.line_database.Line.__init__

Line.__init__\((\text{element}, \text{ion\_state}, \text{wavelength}, \text{gamma}, \text{f\_value}, \text{field=None}, \text{identifier=None})\)

10.2.6 trident.line_database.LineDatabase

class trident.line_database.LineDatabase\((\text{input\_file=None})\)

Class for storing and selecting collections of spectral lines. These lines will be used in the SpectrumGenerator and add\_ion\_fields() functionality.

Without arguments, the LineDatabase will be empty, and you must manually add individual lines to it using the add\_line function. If LineDatabase is provided with an optional :input\_file:, it will automatically add spectral lines for each corresponding line in the list.

Once created, you can select a subset of the total lines present in the database for further use. Use the parse\_subset function to accomplish this.

Parameters

\begin{itemize}
\item \textbf{Input\_file} string, optional
\end{itemize}

An optional input\_file can be provided to pre-store a list of Line objects. input\_file should be a tab delimited text file of the format:

\begin{itemize}
\item element, ion\_state, wavelength, gamma, f\_value, (name)
\end{itemize}

H, I, 1215.67, 4.69e8, 4.16e-1, Ly a

Example

\begin{verbatim}
>>> # Create a LineDatabase using the lines present in lines.txt
>>> ldb = LineDatabase('lines.txt')

>>> # Parse ldb and only select Lyman alpha, Mg II and Fe lines
>>> lines = ldb.parse_subset(lines=['H I 1216', 'Mg II', 'Fe'])
>>> print(lines)
\end{verbatim}

Methods

__init__

add\_line Manually add a line to the LineDatabase.

load\_line\_list\_from\_file Load a line list from a file into the LineDatabase.

parse\_subset Select multiple lines based on atom, ion state, identifier, and/or wavelength.

parse\_subset\_to\_ions Select ions based on those needed to create specific lines.

continues on next page
Table 10 – continued from previous page

| select_lines | Select lines based on atom, ion state, identifier, and/or wavelength. |

**trident.line_database.LineDatabase.__init__**

`LineDatabase.__init__(input_file=None)`

**trident.line_database.LineDatabase.add_line**

`LineDatabase.add_line(element, ion_state, wavelength, gamma, f_value, field=None, identifier=None)`
Manually add a line to the LineDatabase.

**Parameters**
- **Element** string
  The element of the transition using element’s symbol on periodic table Example: ‘H’, ‘C’, ‘Mg’
- **Ion_state** string
  The roman numeral representing the ionic state of the transition Example: ‘I’ for neutral species, ‘II’ for singly ionized, etc.
- **Wavelength** float
  The wavelength of the transition in angstroms Example: 1216 for Lyman alpha
- **Gamma** float
  The gamma of the transition in Hertz
- **F_value** float
  The oscillator strength of the transition
- **Field** string, optional
  The default yt field name associated with the ion responsible for this line Example: ‘H_p1_number_density’ for HII
- **Identifier** string, optional
  An optional identifier for the transition Example: ‘Ly a’ for Lyman alpha

**Example**

```python
>>> # Create a LineDatabase using the lines present in lines.txt
>>> ldb = LineDatabase('lines.txt')

>>> # Manually add the neutral hydrogen line to ldb
>>> ldb.add_line('H', 'I', 1215.67, 469860000, 0.41641, 'Ly a')

>>> print(ldb.lines_all)
```

10.2. Generating Spectra
trident.line_database.LineDatabase.load_line_list_from_file

LineDatabase.load_line_list_from_file(filename)
Load a line list from a file into the LineDatabase. Line list file is a tab-delimited text file in the format:
  element, ion_state, wavelength, gamma, f_value, (name)
  H, I, 1215.67, 4.69e8, 4.16e-1, Ly a

Parameters
  filename : string
    The filename of the list to add. First looks in trident.__path__/data/line_lists directory, then in cwd.

trident.line_database.LineDatabase.parse_subset

LineDatabase.parse_subset(subsets='all')
Select multiple lines based on atom, ion state, identifier, and/or wavelength. Once you've created a Line-
Database, you can subselect certain lines from it based on line characteristics. Preferred to use this method
over select_lines.
Will return the unique union of all lines matching the specified subsets from the LineDatabase.

Parameters
  Subsets  list of strings, optional
    List strings matching possible lines. Strings can be of the form: * Atom - Examples: “H”, “C”,
    1336”, “Mg II 1240” * Identifier - Examples: “Ly a”, “Ly b”
    If set to None, selects all lines in LineDatabase. Default: None

Returns
  Line subset  list of trident.Line objects
    A list of the Lines that were selected

Example

>>> # Get a list of all lines of Carbon, Mg II and Lyman alpha
>>> ldb = LineDatabase('lines.txt')
>>> lines = ldb.parse_subset(['C', 'Mg II', 'H I 1216'])
>>> print(lines)

trident.line_database.LineDatabase.parse_subset_to_ions

LineDatabase.parse_subset_to_ions(subsets=None)
Select ions based on those needed to create specific lines. Once you've created a LineDatabase, you can subselect
certain ions from it based on the line characteristics of atom, ion state, identifier, and/or wavelength. Similar to
parse_subset but outputs a list of ion tuples (e.g. (‘H’, 1), (‘Fe’, 2)), instead of a list of Line objects.
Will return the unique union of all ions matching the specified subsets from the LineDatabase.

Parameters
**Subsets** list of strings, optional


If set to None, selects ions necessary to produce all lines in LineDatabase. Default: None

**Returns**

**Ion subset** list of ion tuples

A list of the ions necessary to produce the desired lines Each ion tuple is of the form (‘H’, 1) = neutral hydrogen

**Example**

Get a list of all ions necessary to generate lines for Carbon, Mg II and Lyman alpha

```python
>>> ldb = LineDatabase('lines.txt')
>>> ions = ldb.parse_subset_to_ions(['C', 'Mg II', 'H I 1216'])
>>> print(ions)
```

---

**trident.line_database.LineDatabase.select_lines**

`LineDatabase.select_lines(element=None, ion_state=None, wavelength=None, identifier=None, source_list=None)`

Select lines based on atom, ion state, identifier, and/or wavelength. Once you've created a LineDatabase, you can subselect certain lines from it based on line characteristics. Recommended to use `parse_subset` instead which allows selecting of multiple sets of lines simultaneously.

**Parameters**

- **Element** string, optional
  
  The element of the transition using element's symbol on periodic table Example: ‘H’, ‘C’, ‘Mg’
  
  Default: None

- **Ion_state** string, optional
  
  The roman numeral representing the ionic state of the transition Example: ‘I’ for neutral species, ‘II’ for singly ionized, etc. Default: None

- **Wavelength** float, optional
  
  The wavelength of the transition in angstroms Example: 1216 for Lyman alpha Default: None

- **Identifier** string, optional
  
  An optional identifier for the transition Example: ‘Ly a’ for Lyman alpha Default: None

- **Source_list** list of `Line` objects, optional
  
  The source list from which to select lines. If set to None, use the LineDatabase’s list ‘lines_all’. Default: None

**Returns**

**Selected_lines** list

A list of which lines were selected.

**Example**
>>> ldb = LineDatabase('lines.txt')
>>> selected_lines = ldb.select_lines(element='Mg', ion_state='II')

10.3 Plotting Spectra

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>load_spectrum</td>
<td>Load a previously saved spectrum from disk.</td>
</tr>
<tr>
<td>plot_spectrum</td>
<td>Plot a spectrum or a collection of spectra and save to disk.</td>
</tr>
</tbody>
</table>

10.3.1 trident.spectrum_generator.load_spectrum

trident.spectrum_generator.load_spectrum(filename, format='auto', instrument=None, lsf_kernel=None, line_database=None, ionization_table=None)

Load a previously saved spectrum from disk.

Parameters

**Filename** string

Filename of the saved spectrum.

**Format** string

File format of the saved spectrum file. Valid values are: “auto”, “hdf5”, “fits”, and “ascii”. If you select “auto”, the code will attempt to auto-detect the file format from the extension of the data file: “.h5” or “.hdf5” -> hdf5, “.fits” or “.FITS” -> fits, all other -> ascii. Default: “auto”

**Instrument** string, optional

The telescope+instrument combination to use for the loaded spectrum. Default: None

**Lsf_kernel** string, optional

The filename for the LSF kernel to use for the loaded spectrum. Default: None

**Line_database** string, optional

A text file listing the various lines to insert into the line database to use for the loaded spectrum. Default: None

**Ionization_table** hdf5 file, optional

An HDF5 file used for computing the ionization fraction of the gas based on its density, temperature, metallicity, and redshift. Default: None

Example

Create a simple spectrum, save it to disk, and load it back as a new SpectrumGenerator object.

```python
>>> import trident
>>> ray = trident.make_onezone_ray()
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.make_spectrum(ray)
>>> sg.save_spectrum('spec.h5')
>>> sg_copy = trident.load_spectrum('spec.h5')
```
10.3.2 trident.spectrum_generator.plot_spectrum

```python
trident.spectrum_generator.plot_spectrum(wavelength, flux, filename='spectrum.png',
   lambda_limits=None, flux_limits=None, title=None, label=None, figsize=None, step=False, stagger=0.2,
   features=None, axis_labels=None)
```

Plot a spectrum or a collection of spectra and save to disk.

This function wraps some Matplotlib plotting functionality for plotting spectra generated with the `SpectrumGenerator`. In its simplest form, it accepts a wavelength array consisting of wavelength values and a corresponding flux array consisting of relative flux values, and it plots them and saves to disk.

In addition, it can plot several spectra on the same axes simultaneously by passing a list of arrays to the `wavelength`, `flux` arguments (and optionally to the `label` and `step` keywords).

Returns the Matplotlib Figure object for further processing.

**Parameters**

- **Wavelength** array of floats or list of arrays of floats
  
  Wavelength values in angstroms. Either as an array of floats in the case of plotting a single spectrum, or as a list of arrays of floats in the case of plotting several spectra on the same axes.

- **Flux** array of floats or list of arrays of floats
  
  Relative flux values (from 0 to 1) corresponding to wavelength array. Either as an array of floats in the case of plotting a single spectrum, or as a list of arrays of floats in the case of plotting several spectra on the same axes.

- **Filename** string, optional
  
  Output filename of the plotted spectrum. Will be a png file. Default: ‘spectrum.png’

- **Lambda_limits** tuple or list of floats, optional
  
  The minimum and maximum of the wavelength range (x-axis) for the plot in angstroms. If specified as None, will use whole lambda range of spectrum. Example: (1200, 1400) for 1200-1400 Angstroms Default: None

- **Flux_limits** tuple or list of floats, optional
  
  The minimum and maximum of the flux range (y-axis) for the plot. If specified as None, limits are automatically from [0, 1.1*max(flux)]. Example: (0, 1) for normal flux range before post-processing. Default: None

- **Step** boolean or list of booleans, optional
  
  Plot the spectrum as a series of step functions. Appropriate for plotting processed and noisy data. Use a list of booleans when plotting multiple spectra, where each boolean corresponds to the entry in the `wavelength` and `flux` lists.

- **Title** string, optional
  
  Optional title for plot Default: None

- **Label** string or list of strings, optional
  
  Label for each spectrum to be plotted. Useful if plotting multiple spectra simultaneously. Will automatically trigger a legend to be generated. Default: None

- **Stagger** float, optional
  
  If plotting multiple spectra on the same axes, do we offset them in the y direction? If set to None, no. If set to a float, stagger them by the flux value specified by this parameter.
Features
dict, optional

Include vertical lines with labels to represent certain spectral features. Each entry in the dictionary consists of a key string to be overplot and the value float as to where in wavelength space it will be plot as a vertical line with the corresponding label.

Example: features={'Ly a' : 1216, 'Ly b' : 1026}
Default: None

Axis_labels
tuple of strings, optional

Optionally set the axis labels directly. If set to None, defaults to (‘Wavelength [$\text{\AA}$]’, ‘Relative Flux’). Default: None

Returns
Matplotlib Figure object for further processing

Example
Plot a flat spectrum

```python
>>> import numpy as np
>>> import trident
>>> wavelength = np.arange(1200, 1400)
>>> flux = np.ones(len(wavelength))
>>> trident.plot_spectrum(wavelength, flux)
```

Generate a one-zone ray, create a Lyman alpha spectrum from it, and add gaussian noise to it. Plot both the raw spectrum and the noisy spectrum on top of each other.

```python
>>> import trident
>>> ray = trident.make_onezone_ray(column_densities={'H_p0_number_density':1e21})
>>> sg_final = trident.SpectrumGenerator(lambda_min=1200, lambda_max=1300, dlambda=0.5)
>>> sg_final.make_spectrum(ray, lines=['Ly a'])
>>> sg_final.save_spectrum('spec_raw.h5')
>>> sg_final.add_gaussian_noise(10)
>>> sg_raw = trident.load_spectrum('spec_raw.h5')
>>> trident.plot_spectrum([sg_raw.lambda_field, sg_final.lambda_field], ...
  [sg_raw.flux_field, sg_final.flux_field], stagger=0, step=[False, True], ...
  label=['Raw', 'Noisy'], filename='raw_and_noise.png')
```

10.4 Adding Ion Fields

<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>add_ion_fields</code></td>
<td>Preferred method for adding ion fields to a yt dataset.</td>
</tr>
<tr>
<td><code>add_ion_fraction_field</code></td>
<td>Add ion fraction field to a yt dataset for the desired ion.</td>
</tr>
<tr>
<td><code>add_ion_number_density_field</code></td>
<td>Add ion number density field to a yt dataset for the desired ion.</td>
</tr>
<tr>
<td><code>add_ion_density_field</code></td>
<td>Add ion mass density field to a yt dataset for the desired ion.</td>
</tr>
<tr>
<td><code>add_ion_mass_field</code></td>
<td>Add ion mass field to a yt dataset for the desired ion.</td>
</tr>
</tbody>
</table>
10.4.1 trident.ion_balance.add_ion_fields

trident.ion_balance.add_ion_fields(ds, ions, ftype='gas', ionization_table=None, field_suffix=False, line_database=None, sampling_type='local', particle_type=None)

Preferred method for adding ion fields to a yt dataset.

Select ions based on the selection indexing set up in parse_subset_to_ions function, that is, by specifying a list of strings where each string represents an ion or line. Strings are of one of three forms:

- <element>
- <element> <ion state>
- <element> <ion state> <line_wavelength>

If a line_database is selected, then the ions chosen will be a subset of the ions present in the equivalent LineDatabase, nominally located in trident.__path__/data/line_lists.

For each ion species selected, four fields will be added (example for Mg II):

- Ion fraction field. e.g. (“gas”, ‘Mg_p1_ion_fraction’)
- Number density field. e.g. (“gas”, ‘Mg_p1_number_density’)
- Density field. e.g. (“gas”, ‘Mg_p1_density’)
- Mass field. e.g. (“gas”, ‘Mg_p1_mass’)

This function is the preferred method for adding ion fields to one’s dataset, but for more fine-grained control, one can also employ the add_ion_fraction_field, add_ion_number_density_field, add_ion_density_field, add_ion_mass_field functions individually.

Fields are added assuming collisional ionization equilibrium and photoionization in the optically thin limit from a redshift-dependent metagalactic ionizing background using the ionization_table specified.

Parameters

- **Ds**: yt dataset object
  This is the dataset to which the ion fraction field will be added.
- **Ions**: list of strings
  If set to ‘all’, creates all ions for the first 30 elements: (ie hydrogen to zinc). If set to ‘all’ with line_database keyword set, then creates all ions associated with the lines specified in the equivalent LineDatabase.
- **Ionization_table**: string, optional
  Path to an appropriately formatted HDF5 table that can be used to compute the ion fraction as a function of density, temperature, metallicity, and redshift. When set to None, it uses the table specified in ~/.trident/config Default: None
- **Field_suffix**: boolean, optional
  Determines whether or not to append a suffix to the field name that indicates what ionization table was used. Useful when using generating ion_fields that already exist in a dataset.
- **Line_database**: string, optional
  Ions are selected out of the set of ions present in the line_database constructed from the line list filename specified here. See LineDatabase for more information.
**Ftype** string, optional

This is deprecated and no longer necessary since all relevant fields are aliased to the ‘gas’ ftype. Default: ‘gas’

**Sampling_type** string, optional

This is deprecated and no longer necessary. Default: ‘local’

**Particle_type** boolean, optional

This is deprecated and no longer necessary. Default: ‘auto’

**Example**

To add ionized hydrogen, doubly-ionized Carbon, and all of the Magnesium species fields to a dataset, you would run:

```python
>>> import yt
>>> import trident

>>> ds = yt.load('path/to/file')
>>> trident.add_ion_fields(ds, ions= ['H II', 'C III', 'Mg'])
```

### 10.4.2 trident.ion_balance.add_ion_fraction_field

`trident.ion_balance.add_ion_fraction_field(atom, ion, ds, ftype='gas', ionization_table=None, field_suffix=False, sampling_type='local', particle_type=None)`

Add ion fraction field to a yt dataset for the desired ion.

**Note:** The preferred method for adding ion fields to a dataset is using `add_ion_fields`,

For example, `add_ion_fraction_field('O', 6, ds)` creates a field called `O_p5_ion_fraction` for dataset `ds`, which represents 5-ionized oxygen (O plus 5 = O VI = ‘O’, 6).

Fields are added assuming collisional ionization equilibrium and photoionization in the optically thin limit from a redshift-dependent metagalactic ionizing background using the `ionization_table` specified.

**Parameters**

- **Atom** string: Atomic species for desired ion fraction (e.g. ‘H’, ‘C’, ‘Mg’)
- **Ion** integer: Ion number for desired species (e.g. 1 = neutral, 2 = singly ionized, 3 = doubly ionized, etc.)
- **Ds** yt dataset object: This is the dataset to which the ion fraction field will be added.
- **Ftype** string, optional
  
  This is deprecated and no longer necessary since all relevant fields are aliased to the ‘gas’ ftype. Default: ‘gas’
- **Ionization_table** string, optional: Path to an appropriately formatted HDF5 table that can be used to compute the ion fraction as a function of density, temperature, metallicity, and redshift. By default, it uses the table specified in `~/.trident/config`
- **Field_suffix** boolean, optional: Determines whether or not to append a suffix to the field name that indicates what ionization table was used
Sampling_type string, optional
This is deprecated and no longer necessary. Default: ‘local’

Particle_type boolean, optional
This is deprecated and no longer necessary. Default: ‘auto’

Example
Add C IV (triply-ionized carbon) ion fraction field to dataset

```python
>>> import yt
>>> import trident
>>> ds = yt.load('path/to/file')
>>> trident.add_ion_fraction_field('C', 4, ds)
>>> yt.ProjectionPlot(ds, 'x', 'C_p3_ion_fraction').save()
```

10.4.3 trident.ion_balance.add_ion_number_density_field

drident.ion_balance.add_ion_number_density_field(atom, ion, ds, ftype='gas', ionization_table=None, field_suffix=False, sampling_type='local', particle_type=None)

Add ion number density field to a yt dataset for the desired ion.

**Note:** The preferred method for adding ion fields to a dataset is using add_ion_fields.

For example, `add_ion_number_density_field('O', 6, ds)` creates a field called `O_p5_number_density` for dataset `ds`, which represents 5-ionized oxygen (O plus 5 = O VI).

Fields are added assuming collisional ionization equilibrium and photoionization in the optically thin limit from a redshift-dependent metagalactic ionizing background using the ionization_table specified.

**Parameters**

- **Atom** string
  Atomic species for desired ion fraction (e.g. ‘H’, ‘C’, ‘Mg’)

- **Ion** integer
  Ion number for desired species (e.g. 1 = neutral, 2 = singly ionized, 3 = doubly ionized, etc.)

- **Ds** yt dataset object
  This is the dataset to which the ion fraction field will be added.

- **Ftype** string, optional
  This is deprecated and no longer necessary since all relevant fields are aliased to the ‘gas’ ftype. Default: ‘gas’

- **Ionization_table** string, optional
  Path to an appropriately formatted HDF5 table that can be used to compute the ion fraction as a function of density, temperature, metallicity, and redshift. By default, it uses the table specified in ~/.trident/config

- **Field_suffix** boolean, optional
  Add a suffix to the field name.
Determines whether or not to append a suffix to the field name that indicates what ionization table was used

**Sampling_type** string, optional
This is deprecated and no longer necessary. Default: ‘local’

**Particle_type** boolean, optional
This is deprecated and no longer necessary. Default: ‘auto’

**Example**
Add C IV (triply-ionized carbon) number density field to dataset

```python
>>> import yt
>>> import trident

>>> ds = yt.load('path/to/file')
>>> trident.add_ion_number_density('C', 4, ds)

>>> yt.ProjectionPlot(ds, 'x', 'C_p3_number_density').save()
```

### 10.4.4 trident.ion_balance.add_ion_density_field

Add ion mass density field to a yt dataset for the desired ion.

**Parameters**
- **Atom** string
  Atomic species for desired ion fraction (e.g. ‘H’, ‘C’, ‘Mg’)
- **Ion** integer
  Ion number for desired species (e.g. 1 = neutral, 2 = singly ionized, 3 = doubly ionized, etc.)
- **Ds** yt dataset object
  This is the dataset to which the ion fraction field will be added.
- **Ftype** string, optional
  This is deprecated and no longer necessary since all relevant fields are aliased to the ‘gas’ ftype. Default: ‘gas’
- **Ionization_table** string, optional
  Path to an appropriately formatted HDF5 table that can be used to compute the ion fraction as a function of density, temperature, metallicity, and redshift. By default, it uses the table specified in ~/.trident/config
Field_suffix  boolean, optional
  Determines whether or not to append a suffix to the field name that indicates what ionization
table was used

Sampling_type  string, optional
  This is deprecated and no longer necessary. Default: 'local'

Particle_type  boolean, optional
  This is deprecated and no longer necessary. Default: 'auto'

Example
Add C IV (triply-ionized carbon) mass density field to dataset

```python
>>> import yt
>>> import trident

>>> ds = yt.load('path/to/file')

>>> trident.add_ion_density_field('C', 4, ds)

>>> yt.ProjectionPlot(ds, 'x', 'C_p3_density').save()
```

10.4.5 trident.ion_balance.add_ion_mass_field

trident.ion_balance.add_ion_mass_field(atom, ion, ds, ftype='gas', ionization_table=None,
  field_suffix=False, sampling_type='local', particle_type=None)

Add ion mass field to a yt dataset for the desired ion.

Note: The preferred method for adding ion fields to a dataset is using add_ion_fields,

For example, add_ion_mass_field('O', 6, ds) creates a field called O_p5_mass for dataset ds, which represents
5-ionized oxygen (O plus 5 = O VI).

Fields are added assuming collisional ionization equilibrium and photoionization in the optically thin limit from
a redshift-dependent metagalactic ionizing background using the ionization_table specified.

Parameters
Atom  string
  Atomic species for desired ion fraction (e.g. 'H', 'C', 'Mg')

Ion  integer
  Ion number for desired species (e.g. 1 = neutral, 2 = singly ionized, 3 = doubly ionized, etc.)

Ds  yt dataset object
  This is the dataset to which the ion fraction field will be added.

Ftype  string, optional
  This is deprecated and no longer necessary since all relevant fields are aliased to the 'gas' ftype.
  Default: 'gas'

Ionization_table  string, optional
  Path to an appropriately formatted HDF5 table that can be used to compute the ion fraction as a
  function of density, temperature, metallicity, and redshift. By default, it uses the table specified
  in ~/.trident/config
Field_suffix  boolean, optional
Determines whether or not to append a suffix to the field name that indicates what ionization
table was used

Sampling_type  string, optional
This is deprecated and no longer necessary. Default: 'local'

Particle_type  boolean, optional
This is deprecated and no longer necessary. Default: 'auto'

Example
Add C IV (triply-ionized carbon) mass field to dataset

```python
>>> import yt
>>> import trident

>>> ds = yt.load('path/to/file')
>>> trident.add_ion_mass_field('C', 4, ds)

>>> yt.ProjectionPlot(ds, 'x', 'C_p3_mass').save()
```

10.5 Miscellaneous Utilities

- **make_onezone_dataset**
  Create a one-zone hydro dataset for use as test data.

- **make_onezone_ray**
  Create a one-zone ray object for use as test data.

- **to_roman**
  Convert an integer to a Roman numeral.

- **from_roman**
  Convert a Roman numeral to an integer.

- **trident_path**
  Return the path where the trident source is installed.

- **trident**
  Print a Trident ASCII logo to the screen.

- **verify**
  Verify that the bulk of Trident’s functionality is working.

- **generate_total_fit**
  Fit an absorption-line spectrum into line profiles.

10.5.1 trident.utilities.make_onezone_dataset

*trident.utilities.make_onezone_dataset*(density=1e-26, temperature=1000, metallicity=0.3, domain_width=10.0)

Create a one-zone hydro dataset for use as test data. The dataset consists of a single cubicle cell of gas with hydro
quantities specified in the function kwargs. It makes an excellent test dataset through which to send a sightline
and test Trident’s capabilities for making absorption spectra.

Using the defaults and passing a ray through the full domain should result in a spectrum with a good number of
absorption features.

**Parameters**

- **Density**  float, optional
  The gas density value of the dataset in g/cm**3** Default: 1e-26

- **Temperature**  float, optional
  The gas temperature value of the dataset in K Default: 10**3

- **Metallicity**  float, optional
The gas metallicity value of the dataset in Zsun Default: 0.3

**Domain_width** float, optional

The width of the dataset in kpc Default: 10.

**Returns**

**Example**

Create a simple one-zone dataset, pass a ray through it, and generate a COS spectrum for that ray.

```python
>>> import trident
>>> ds = trident.make_onezone_dataset()
>>> ray = trident.make_simple_ray(ds,
...     start_position=ds.domain_left_edge,
...     end_position=ds.domain_right_edge,
...     fields=['density', 'temperature', 'metallicity'])
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.make_spectrum(ray)
>>> sg.plot_spectrum('spec_raw.png')
```

### 10.5.2 trident.utilities.make_onezone_ray

**trident.utilities.make_onezone_ray**

Create a one-zone ray object for use as test data. The ray consists of a single absorber of hydrodynamic characteristics specified in the function kwargs. It makes an excellent test dataset to test Trident’s capabilities for making absorption spectra.

You can specify the column densities of different ions explicitly using the column_densities keyword, or you can let Trident calculate the different ion columns internally from the density, temperature, and metallicity fields.

Using the defaults will produce a ray that should result in a spectrum with a good number of absorption features.

**Parameters**

- **Density** float, optional
  The gas density value of the ray in g/cm**3** Default: 1e-26

- **Temperature** float, optional
  The gas temperature value of the ray in K Default: 10**3

- **Metallicity** float, optional
  The gas metallicity value of the ray in Zsun Default: 0.3

- **Length** float, optional
  The length of the ray in kpc Default: 10.

- **Redshift** float, optional
  The redshift of the ray Default: 0

- **Filename** string, optional
  The filename to which to save the ray to disk. Due to the mechanism for passing rays, the ray data must be saved to disk. Default: ‘ray.h5’
**Column_densities**  dict, optional

The user can create a dictionary which adds more number density ion fields to the ray. Each key in the dictionary should be the desired ion field name according to the field name format: i.e. `<ELEMENT>_p<IONSTATE>_number_density` e.g. neutral hydrogen = "H_p0_number_density".

The corresponding value for each key should be the desired column density of that ion in cm⁻².

See example below. Default: None

**Returns**

A YT LightRay object

**Example**

Create a one-zone ray, and generate a COS spectrum from that ray.

```python
>>> import trident
>>> ray = trident.make_onezone_ray()
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.make_spectrum(ray)
>>> sg.plot_spectrum('spec_raw.png')
```

Create a one-zone ray with an HI column density of 1e21 (DLA) and generate a COS spectrum from that ray for just the Lyman alpha line.

```python
>>> import trident
>>> ds = trident.make_onezone_ray(column_densities={'H_p0_number_density': 1e21})
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.make_spectrum(ray, lines=['Ly a'])
>>> sg.plot_spectrum('spec_raw.png')
```

### 10.5.3 trident.roman.to_roman

**trident.roman.to_roman(n)**

Convert an integer to a Roman numeral. Only works for integers > 0.

**Parameters**

- `n` int

  Integer to convert to Roman numeral

**Returns**

String representing the roman numeral equivalent of argument `n`.

**Example**

```python
>>> num = to_roman(5)
```
10.5.4 trident.roman.from_roman

trident.roman.from_roman(s)
Convert a Roman numeral to an integer.

Parameters
S string

Returns
Integer value equivalent to s Roman numeral argument.

Example

```
>>> num = from_roman('V')
```

10.5.5 trident.config.trident_path

trident.config.trident_path()
Return the path where the trident source is installed. Useful for identifying where data files are (e.g. path/data). Note that ion table datafiles are downloaded separate and placed in another location according to the ~/.trident/config.tri file.

Example

```
>>> print(trident_path())
```

10.5.6 trident.config.trident

trident.config.trident()
Print a Trident ASCII logo to the screen.

10.5.7 trident.config.verify

trident.config.verify(save=False)
Verify that the bulk of Trident’s functionality is working. First, it ensures that the user has a configuration file and ion table datafile, and creates/downloads these files if they do not exist. Next, it creates a single-cell grid-based dataset in memory, generates a ray by sending a sightline through that dataset, then makes a spectrum from the ray object. It saves all data to a tempdir before deleting it.

Parameters
Save boolean, optional
By default, verify saves all of its outputs to a temporary directory and then removes it upon completion. If you would like to see the resulting data from verify(), set this to be True and it will save a light ray, and raw and processed spectra in the current working directory. Default: False

Example
Verify Trident works.
>>> import trident
>>> trident.verify()

10.5.8 trident.absorption_spectrum.absorption_spectrum_fit.generate_total_fit

trident.absorption_spectrum.absorption_spectrum_fit.generate_total_fit(x, fluxData, orderFits, speciesDicts, minError=0.0001, complexLim=0.995, fitLim=0.97, minLength=3, maxLength=1000, splitLim=0.99, output_file=None)

Fit an absorption-line spectrum into line profiles.

Fits the spectrum into absorption complexes and iteratively adds and optimizes voigt profiles for each complex.

Parameters

**X**

(N) ndarray

1d array of wavelengths

**FluxData**

(N) ndarray

array of flux corresponding to the wavelengths given in x. (needs to be the same size as x)

**OrderFits** list

list of the names of the species in the order that they should be fit. Names should correspond to the names of the species given in speciesDicts. (ex: ['lya', 'OVI'])

**SpeciesDicts** dictionary

Dictionary of dictionaries (I’m addicted to dictionaries, I confess). Top level keys should be the names of all the species given in orderFits. The entries should be dictionaries containing all relevant parameters needed to create an absorption line of a given species (f,Gamma,lambda0) as well as max and min values for parameters to be fit

**ComplexLim** float, optional

Maximum flux to start the edge of an absorption complex. Different from fitLim because it decides extent of a complex rather than whether or not a complex is accepted.

**FitLim** float, optional

Maximum flux where the level of absorption will trigger identification of the region as an absorption complex. Default = .98. (ex: for a minSize=.98, a region where all the flux is between 1.0 and .99 will not be separated out to be fit as an absorbing complex, but a region that contains a point where the flux is .97 will be fit as an absorbing complex.)

**MinLength** int, optional

number of cells required for a complex to be included. default is 3 cells.
**MaxLength**  int, optional  
number of cells required for a complex to be split up. Default is 1000 cells.

**SplitLim**  float, optional  
if attempting to split a region for being larger than maxlength the point of the split must have a 
flux greater than splitLim (ie: absorption greater than splitLim). Default=.99.

**Output_file**  string, optional  
location to save the results of the fit.

**Returns**

**AllSpeciesLines**  dictionary  
Dictionary of dictionaries representing the fit lines. Top level keys are the species given in order- 
Fits and the corresponding entries are dictionaries with the keys ‘N’, ‘b’, ‘z’, and ‘group#’. Each 
of these corresponds to a list of the parameters for every accepted fitted line. (ie: N[0],b[0],z[0] 
will create a line that fits some part of the absorption spectrum). ‘group#’ is a similar list but 
identifies which absorbing complex each line belongs to. Lines with the same group# were fit at 
the same time. group#’s do not correlate between species (ie: an lya line with group number 1 
and an OVI line with group number 1 were not fit together and do not necessarily correspond to 
the same region)

**YFit**

(\(N\)) ndarray  
array of flux corresponding to the combination of all fitted absorption profiles. Same size as x.
If you use Trident for a research application, please cite the Trident method paper in your work with the bibtex entry below:

```latex
@ARTICLE{2017ApJ...847...59H,
  author = {{Hummels}, C.-B. and {Smith}, B.-D. and {Silvia}, D.-W.},
  title = "{Trident: A Universal Tool for Generating Synthetic Absorption Spectra from Astrophysical Simulations}",
  journal = \apj,
  archivePrefix = "arXiv",
  eprint = {1612.03935},
  primaryClass = "astro-ph.IM",
  keywords = {cosmology: theory, methods: data analysis, methods: numerical, radiative transfer},
  year = 2017,
  month = sep,
  volume = 847,
  eid = {59},
  pages = {59},
  doi = {10.3847/1538-4357/aa7e2d},
  adsurl = {http://adsabs.harvard.edu/abs/2017ApJ...847...59H},
  adsnote = {Provided by the SAO/NASA Astrophysics Data System}
}
```
This document summarizes changes to the codebase with time for Trident.

12.1 Contributors

The CREDITS file has an updated list of contributors to the codebase.

12.2 Version 1.2.3 (March 18, 2020)

This is a bug fix release.

12.2.1 Enhancements

• Move testing to circleci. (PR 109)

12.2.2 Bug Fixes

• Allow access to find_outputs kwarg from make_compound_ray. (PR 126)
• Fix periodic rays. (PR 125)
• Be more careful about limiting size of line deposition array. (PR 106)

12.3 Version 1.2.2 (November 14, 2019)

This is a bug fix release.
12.3.1 Bug Fixes

- Shift wavelength of velocity center to redshift from light ray solution (PR 102)

12.4 Version 1.2.1 (October 1, 2019)

This is a bug fix release.

12.4.1 Bug Fixes

- Logging info doesn’t use correct units (PR 99)

12.5 Version 1.2 (September 19, 2019)

12.5.1 New Features

- Add support for creating spectra in velocity space (PR 90)
- Add ability to set wavelength limits to ‘auto’ (PR 87)
- Add ability to make spectrum from data container (PR 91)

12.5.2 Bug Fixes

- off by one error in subgrid index calculation (PR 85)
- fixing error in _ion_mass (PR 81)
- H_p0_number_density to default, H_number_density to alias (PR 78)
- Implements a better way of calculating the redshift on the light ray (PR 71)
- Assures that ion_fraction field reflects on-disk fields (PR 64)
- Fix atomic data for Si II 1260 according to Morton 2003 (PR 43)
- A check to avoid failure when no continuum absorbers were found in the ray (PR 39)
- Auto-addition of H_nuclei_density to a LightRay when present in the base dataset (PR 39)
- Adding max_box_fraction as a kwarg to make_compound_ray (PR 37)
- Updated trident_path() to be OS Independent (PR 36)
- simplify setting up ion fields using the “local” field type (PR 30)
- split and join filenames using os.sep instead of assuming unix (PR 29)
- updated oscillator strengths and gamma’s for Si II 1206 and Si III 1260 (PR 25)
12.5.3 Minor Enhancements

- Calculating LOS velocity with relative velocities to account for bulk motion (PR 93)
- Enabling use of `output_absorbers_file` kwarg in SpectrumGenerator (PR 58)
- Switching imports from `yt.analysis_modules` to `yt_astro_analysis` (PR 55)
- Enable passing in-memory LineDatabase to SpectrumGenerator (PR 42)
- Added equivalent width calculation to `line_observables_dict` (PR 40)
- Numerous documentation updates
- Updates and fixes to testing

12.6 Version 1.1 (November 18, 2017)

- Trident development has changed from mercurial to git, and the source has moved from bitbucket to github. This was done in recognition that more people interact with git/github than do with hg/bitbucket, as well as to follow our major dependency yt in making the same transition. All previous repository history (e.g., commits, versions, tags, etc.) is retained under this transition. For users operating on the development branch of Trident, you must re-install Trident in order to continue to get updates. The installation instructions were updated accordingly.
- We totally rebuilt the testing interface to Trident, which includes more coverage in unit tests and answer tests over both grid-based and particle-based datasets. We now have continuous integration through Travis that tests the code daily and with each new pull request to assure consistent code results and to minimize bugs. For more information, see Testing.
- Much of the original Trident codebase was developed in yt as the base classes `AbsorptionSpectrum` and `LightRay`. We have now stripped these classes out of yt and moved them entirely into Trident for more flexibility, stability, and autonomy moving forward. This should not affect the user as these changes were behind the scenes.
- Added `store_observables` keyword to `make_spectrum()` to store a dictionary of observable properties (e.g., tau, column density, and thermal_b) for each cell along a line of sight for use in post-processing. See source of SpectrumGenerator for more information.
- Added an approximate `flux_error` field to output spectra, since many observational tools require its presence. See `error_func()` for more details.
- Made `min_tau` a keyword to `make_spectrum()` to enable higher precision (although more time intensive) absorption line deposition.
- Added ability to specify an arbitrary noise vector with `add_noise_vector()`.
- A bugfix was made in yt to the temperature field for Gadget-based code outputs. The internal energy field was mistakenly being read in co-moving instead of physical units, which led to gas temperatures being low by a factor of \((1+z)\). This is now resolved in yt dev and thus we recommend Trident users use yt dev until yt 3.5 stable is released.
- Another bugfix was made in Trident dependency astropy to the convolve function, which is used in `apply_lsf()`.
- Replaced internal instances of `particle_type` with `sampling_type` to match similar yt conversion.
12.7 Version 1.0 (November 16, 2017)

Initial release. See our *method paper* for details.

- Create absorption-line spectra for any trajectory through a simulated data set mimicking both background quasar and down-the-barrel configurations.
- Reproduce the spectral characteristics of common instruments like the Cosmic Origins Spectrograph.
- Operate across the ultraviolet, optical, and infrared using customizable absorption-line lists.
- Trace simulated physical structures directly to spectral features.
- Approximate the presence of ion species absent from the simulation outputs.
- Generate column density maps for any ion.
- Provide support for all major astrophysical hydrodynamical codes.
If you run into problems with any aspect of Trident, please follow the steps below. Don’t worry, we’ll help you get it sorted out.

13.1 Update the Code

The documentation is built for the latest version of Trident. Try Updating to the Latest Version to assure your code matches what the documentation describes. Remember to update to the latest version of yt too.

13.2 Search Documentation and Mailing List Archives

Most use cases for Trident can be found in our documentation and method paper. Try searching through the documentation using the search window in the upper left part of the screen.

If that doesn’t work, try looking at specific problems we might have addressed in our Frequently Asked Questions.

Lastly, try searching the archives of our mailing list. Chances are that someone else may have encountered the problem that you have and already wrote to the list. You can search the list here.

13.3 Contact our Mailing List

Compose a message to our low-volume mailing list. Remember to include details like the operating system you’re using, the type of dataset you’re trying to reduce, the version of Trident and yt you’re using (find it out here), and of course, a description of the problem you’re having with any relevant traceback errors. Our mailing list is located here: https://groups.google.com/forum/#!forum/trident-project-users

13.4 Join our Slack Channel

We have a slack channel for help and discussions amongst the users and developers of Trident. You can generate an invite for yourself by clicking on this link and following the instructions.
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