trident Documentation

Release 1.2-dev

Team Trident

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Contents

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*.

CHAPTER 1

Installation

Follow these steps to successfully install Trident and its dependencies.

1.1 Versions of Trident

Currently, there are three versions of Trident: the stable version, the developent version, and the demeshening version. The stable version is tried and tested, and it normally operates on a stable version of yt. The development version is actively being updated with new features, and it is also tied to the development version of yt, so occasionally unforseen bugs can crop up as these new features are added. The demeshening version is currently in beta and active development and is used for better results on particle-based datasets. The installation steps are slightly different between the three versions, 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*.

Note: The demeshening version is a variant of Trident for treating particle-based datasets more natively. The demeshening version will give faster and more accurate results with less memory overhead for particle-based datasets. For more information about the demeshening and full installation instructions, please see our demeshening notebook.

1.2 Step 1: Install yt

yt is a python-based software package for the analysis and visualization of a variety of different datasets, including astrophysical hydrodynamical data. yt is a 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.

We find that the easiest way to install yt is with the all-in-one install script, which installs yt and its dependencies via a new conda installation:

```
$ wget https://raw.githubusercontent.com/yt-project/yt/master/doc/install_script.sh
$ ... edit the install_script.sh to mark INST_SCIPY=1, INST_ASTROPY=1,
```

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```
$ ... and INST_YT_SOURCE=1
$ bash install_script.sh
$ ... update your path flag as described by the install_script.sh
```

Alternatively, if you already have conda installed, you can skip the commands above and just run the following command to get yt and its dependencies. To get the nightly build of the development version of yt, type:

```
$ conda install -c http://use.yt/with_conda/ -c conda-forge yt
```

1.3 Step 2: Install Trident

1.3.1 Installing the Stable Release

You can install the most recent stable release of Trident using pip:

```
$ pip install trident
```

1.3.2 Installing the Development Version

To get the development version, you'll pull the source code from its repository using git, which should be installed as part of your yt installation. If it isn't try: `conda install git`. After that, you'll use pip to install the source directly. Go to your desired source code installation directory and run:

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

1.4 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*.

1.5 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. Please join our *mailing list* for announcements and when new features are added to the code.

1.6 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
```

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.

1.7 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 </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.

1.8 Updating to the Latest Version

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

1.8.1 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
```

1.8.2 Updating to the Latest Development Version

If you installed the "development" version of the code, it's slightly more involved:

```
$ cd <path/to/trident/repo>
$ git pull origin master
$ pip install -e .
$ yt update
```

For more information on updating your yt installation, see the yt update instructions.

CHAPTER 2

Annotated Example

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 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:

```
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_start, y_start, z_start] to [x_end, y_end, z_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:

```
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`. Lastly, we set the `ftype` keyword as the field type of the fields where Trident will look to find density, temperature, and metallicity for building the required ion fields:

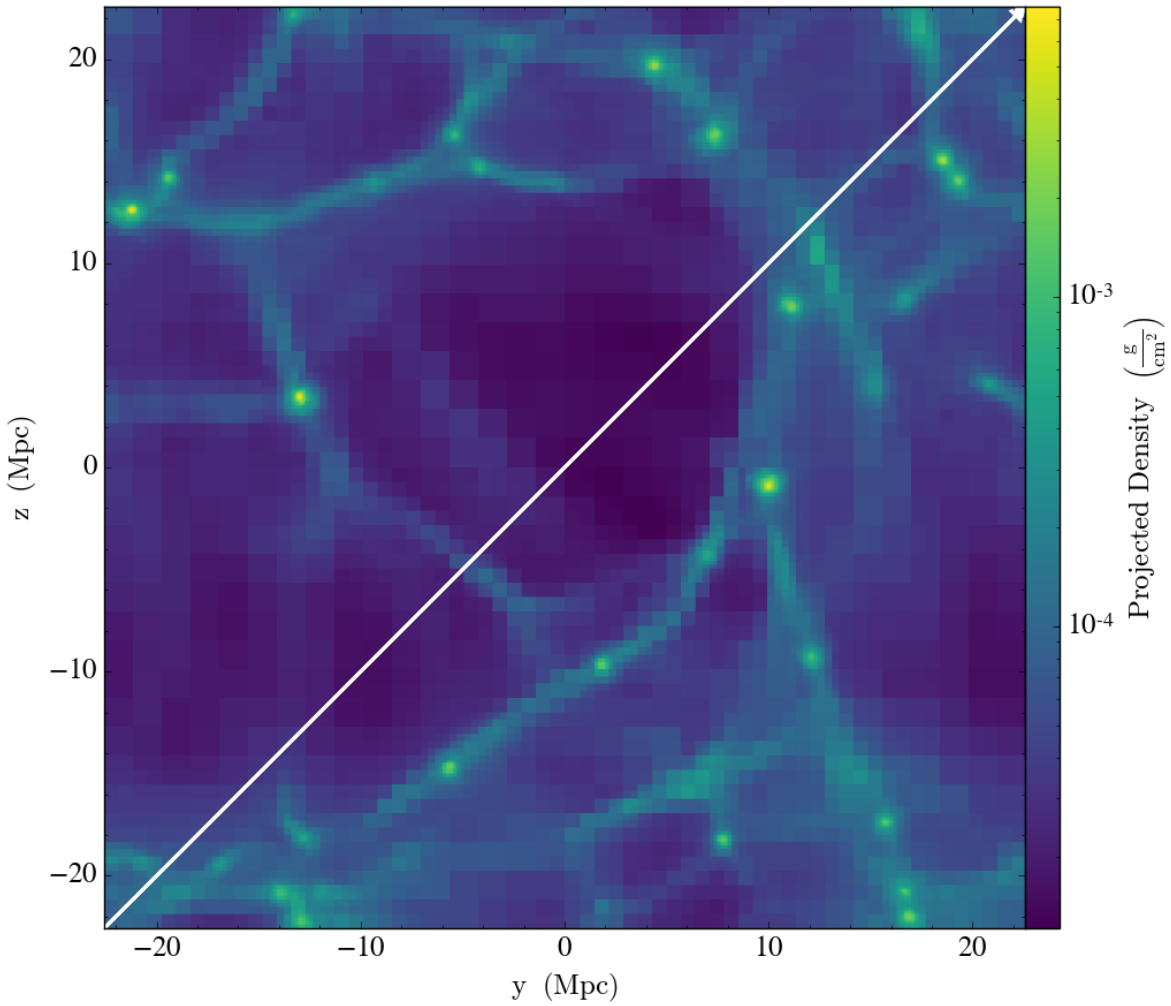
```
ray = trident.make_simple_ray(ds,
                              start_position=ray_start,
                              end_position=ray_end,
                              data_filename="ray.h5",
                              lines=line_list,
                              ftype='gas')
```

Warning: It is imperative that you set the `ftype` keyword properly for your dataset. An `ftype` of 'gas' is adequate for grid-based codes, but not particle. Particle-based datasets must set `ftype` to the field type of their gas particles (e.g. 'PartType0') to assure that Trident builds the ion fields on the particles themselves before smoothing these fields to the grid. By not setting this correctly, you risk bad ion values by building from smoothed gas fields.

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 volumentric plot, including slices, and off-axis plots:

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

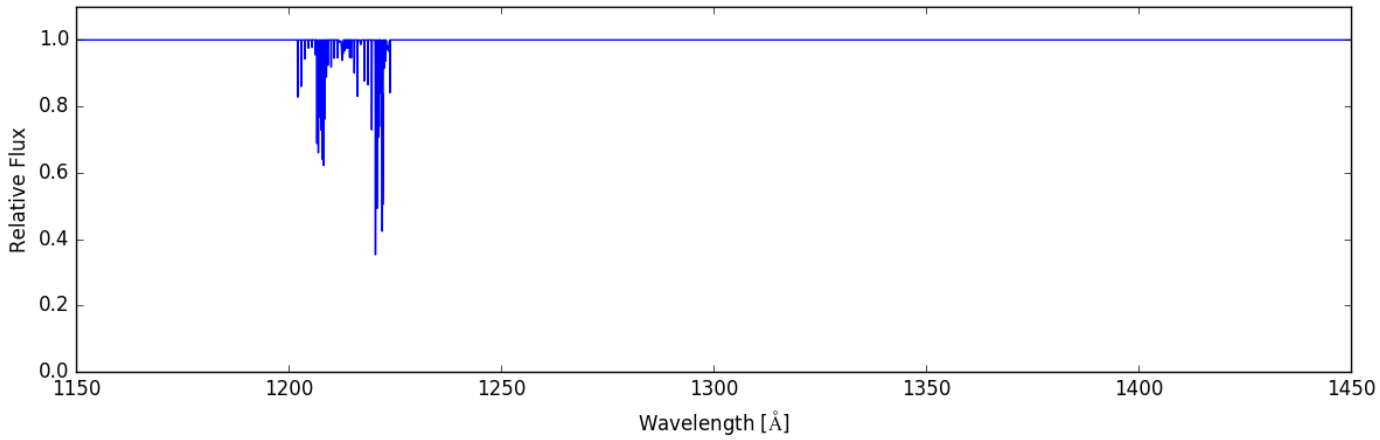


2.3 Spectrum Generation

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:

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



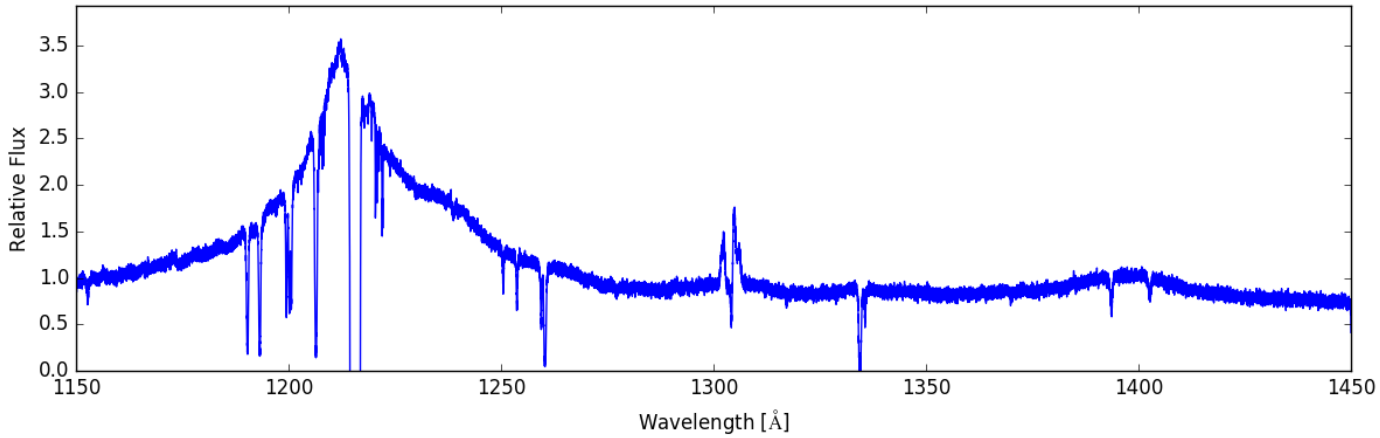
From here we can do some post-processing to the spectrum to include additional features that would be present in an actual observed spectrum. We add a background quasar spectrum, a Milky Way foreground, apply the COS line spread function, and add gaussian noise with SNR=30:

```
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:

```
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*.

2.4 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 snaptshot. 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::

```
fn = 'enzo_cosmology_plus/AMRCosmology.enzo'
ray = trident.make_compound_ray(fn, simulation_type='Enzo',
                                near_redshift=0.0, far_redshift=0.1,
                                ftype='gas',
                                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. If you would like to help us implement this functionality for your simulation code, please contact us about this on the mailing list.

CHAPTER 3

Advanced Spectrum Generation

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 demonstation, 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')
```

3.1 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.

3.2 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:

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

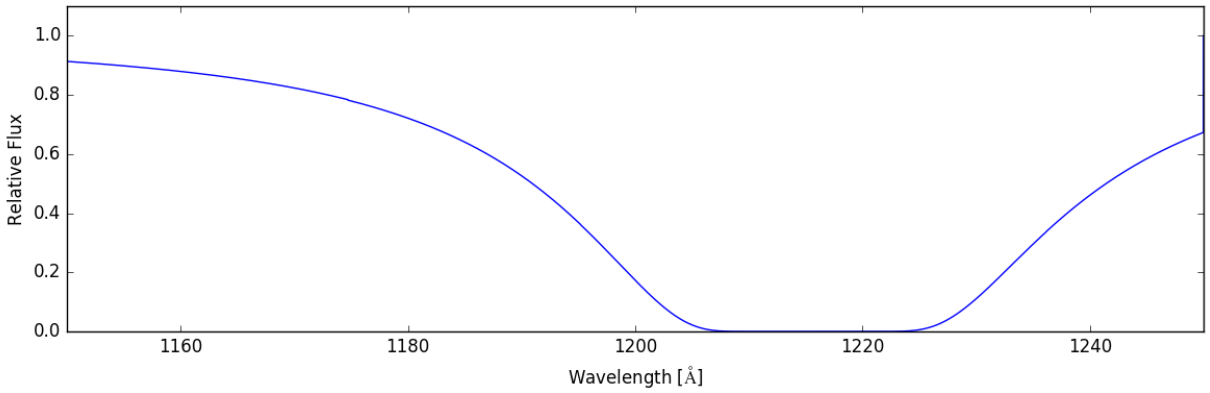
which is reading lines from the 'lines.txt' file present in the data directory (see *where is Trident installed?*) We can specify any subset of these spectral lines to use when creating the spectrum from our master line list. So if you're interested in just looking at neutral hydrogen lines in your spectrum,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

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

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

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

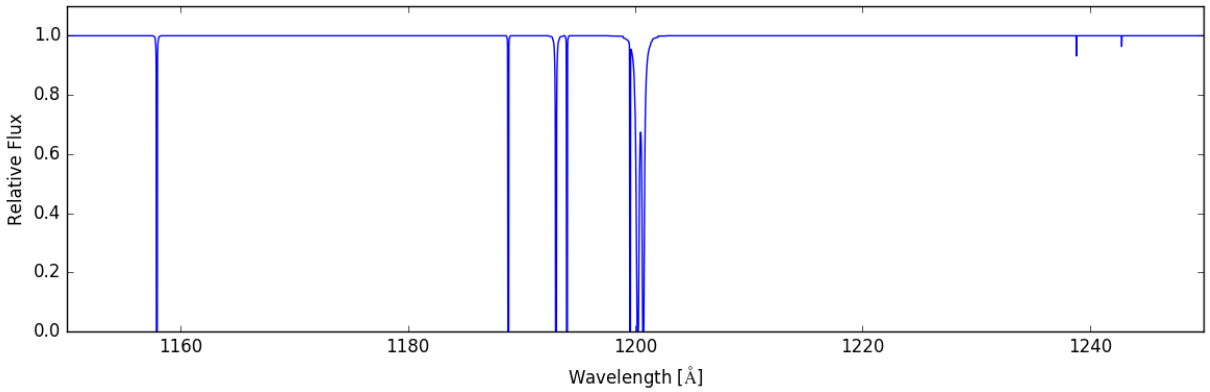
The resulting spectrum contains a nice, big Lyman-alpha feature.



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:

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

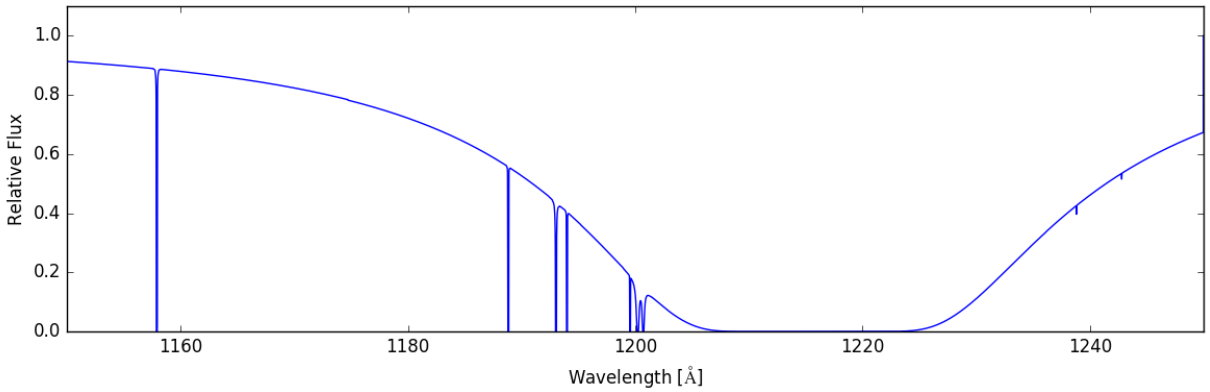
And now we have:



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')
```

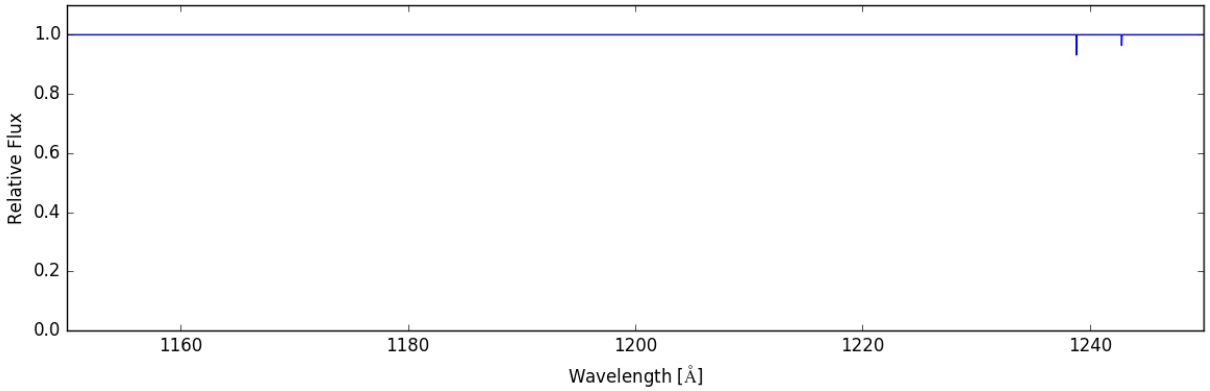
which gives:



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')
```

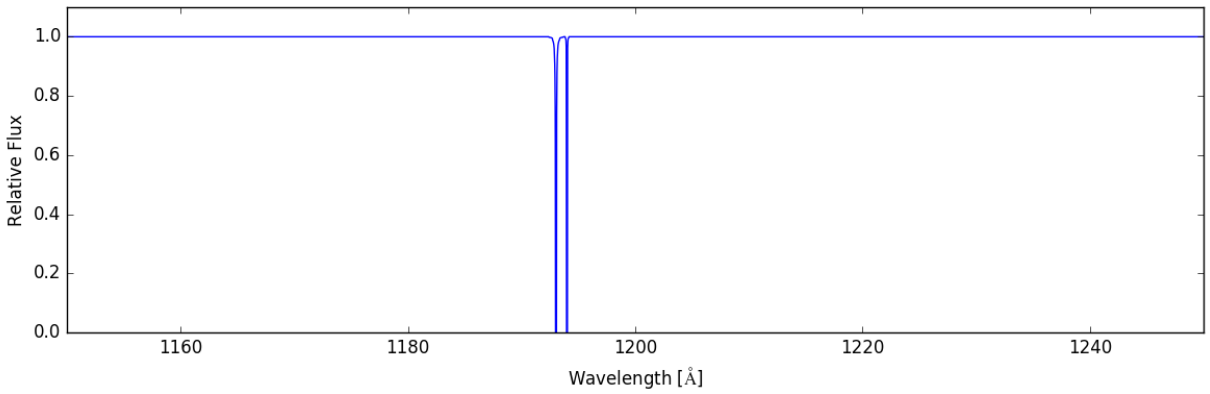
This spectrum only shows a couple of small lines on the right hand side.



But if that level of specificity isn't enough, we can request individual lines:

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

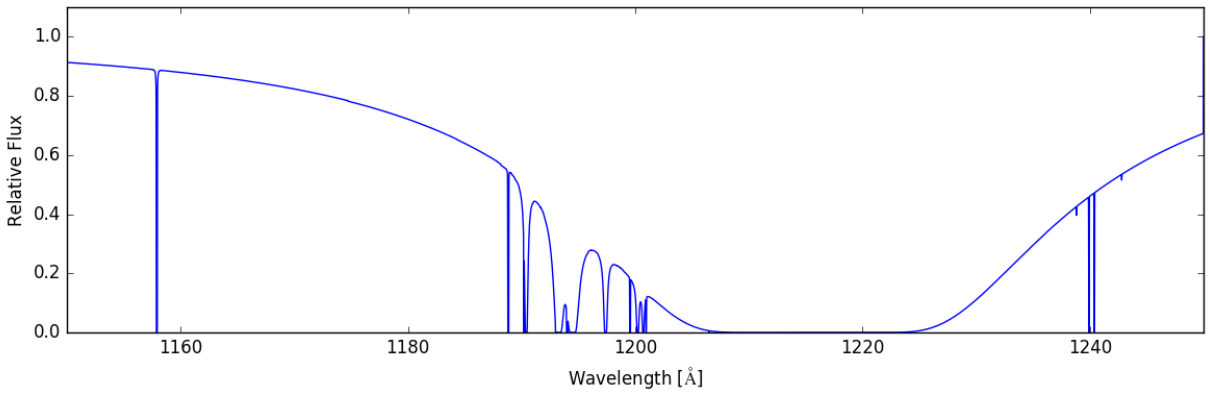
And we end up with:



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

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

Giving us:



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

CHAPTER 4

Adding Ion Fields

In addition to being able to create absorption spectra, Trident 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.

4.1 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.

4.2 Generating species fields

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

```
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 plus).

Let's add fields for O VI (five-times-ionized oxygen):

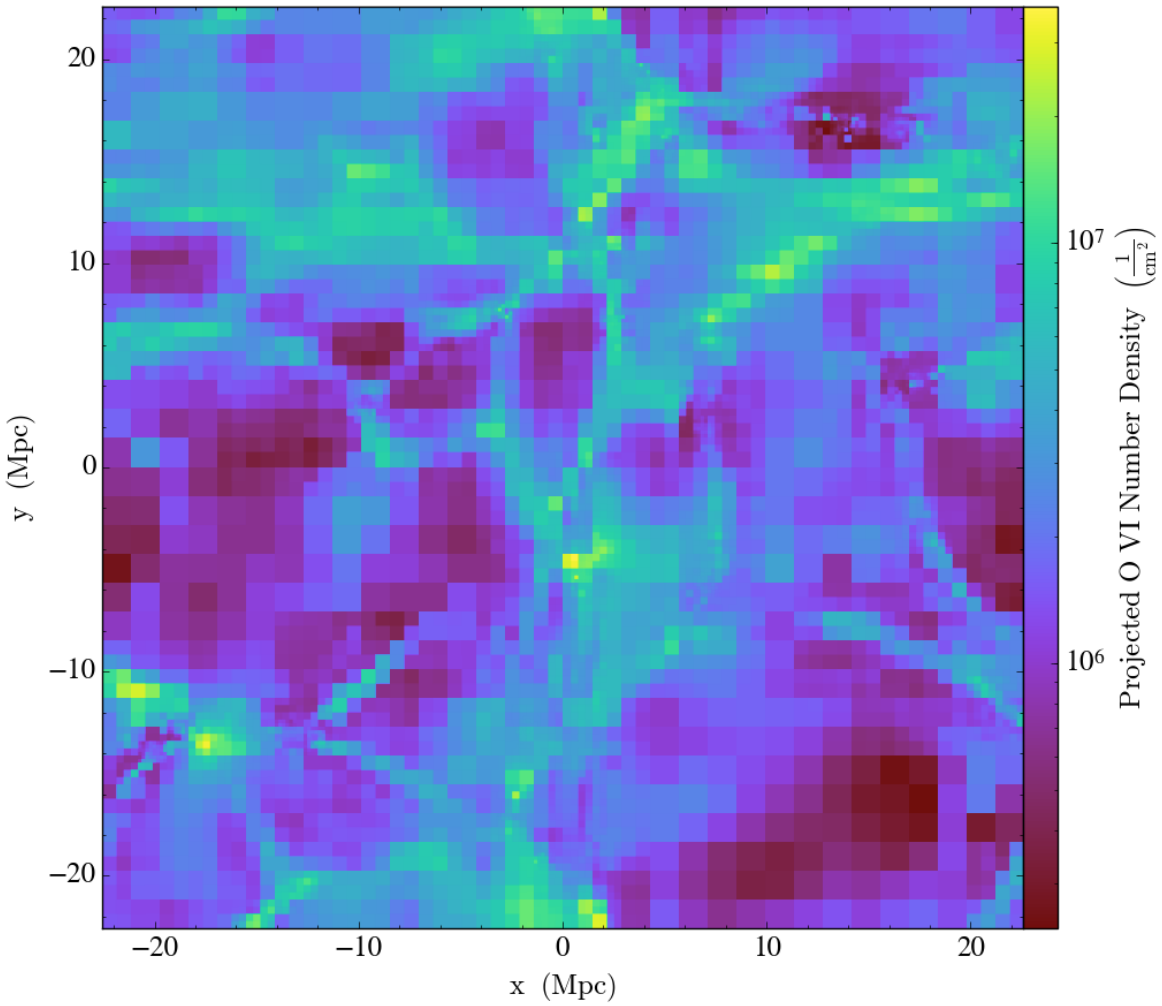
```
trident.add_ion_fields(ds, ions=['O VI'], ftype="gas")
```

Warning: Make sure you are using the appropriate value for *ftype* in adding your ion fields to a dataset. To get best results, the ion interpolation must take place on the gas fields provided by your simulation output. For grid-based codes, these fields are typically aliased to the *gas* fields (e.g., *("gas", "density")*), so using the default *ftype="gas"* is fine. But for particle-based codes, this is not usually the case, and the particle-based gas fields differ based on the code (e.g. *PartType0*, *Gas*, etc.). Inspection of your dataset may be necessary (`print(ds.field_list)`). Set *ftype* correctly to make sure ion generation takes place on the particle first, before being deposited to the grid-based fields, or you may get incorrect results.

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()
```

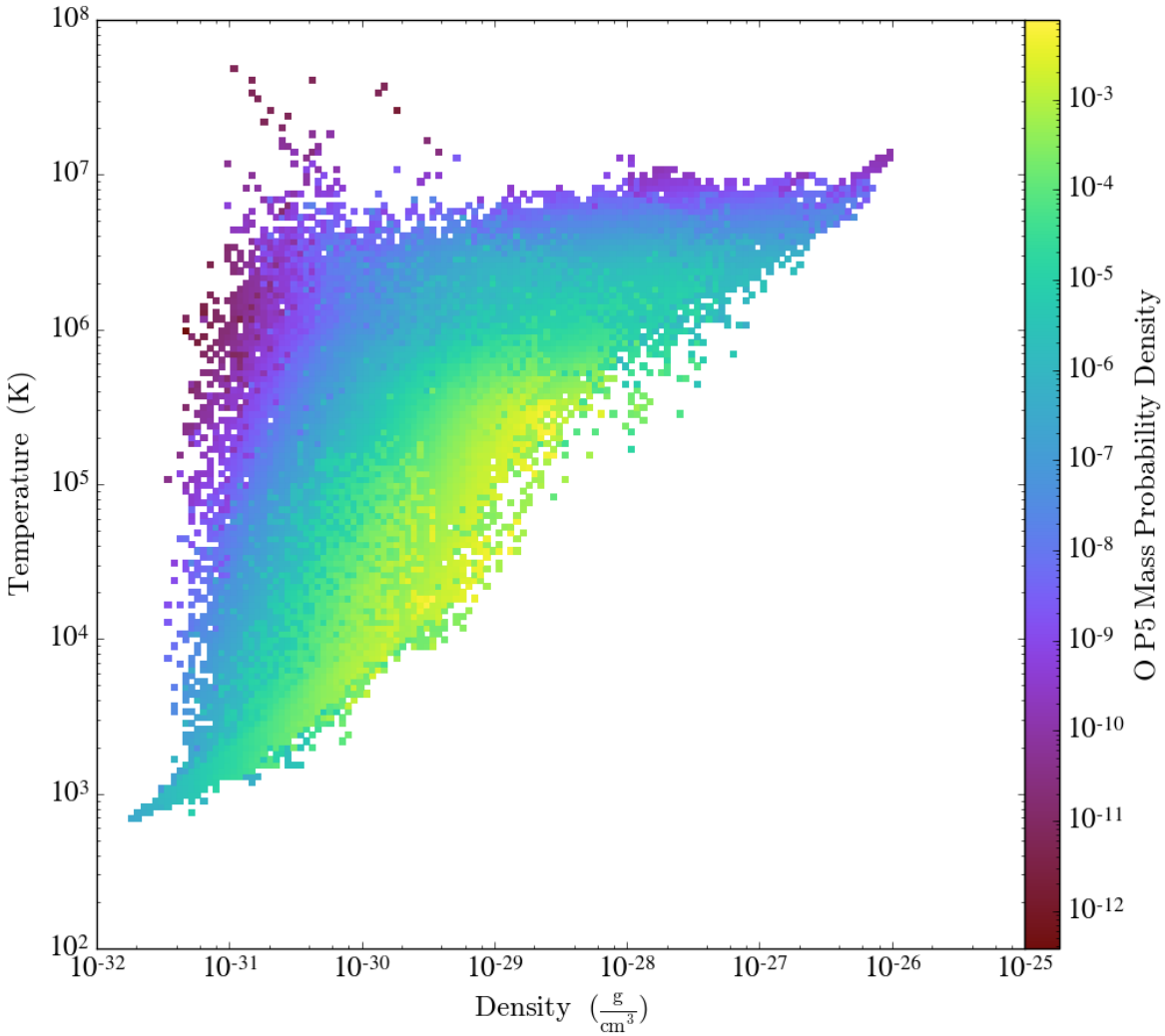
which produces:



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"],
                     weight_field="O_p5_mass", fractional=True)
phase.save()
```

resulting in:


Temperature (K)
Density ($\frac{g}{cm^3}$)
O P5 Mass Probability Density

CHAPTER 5

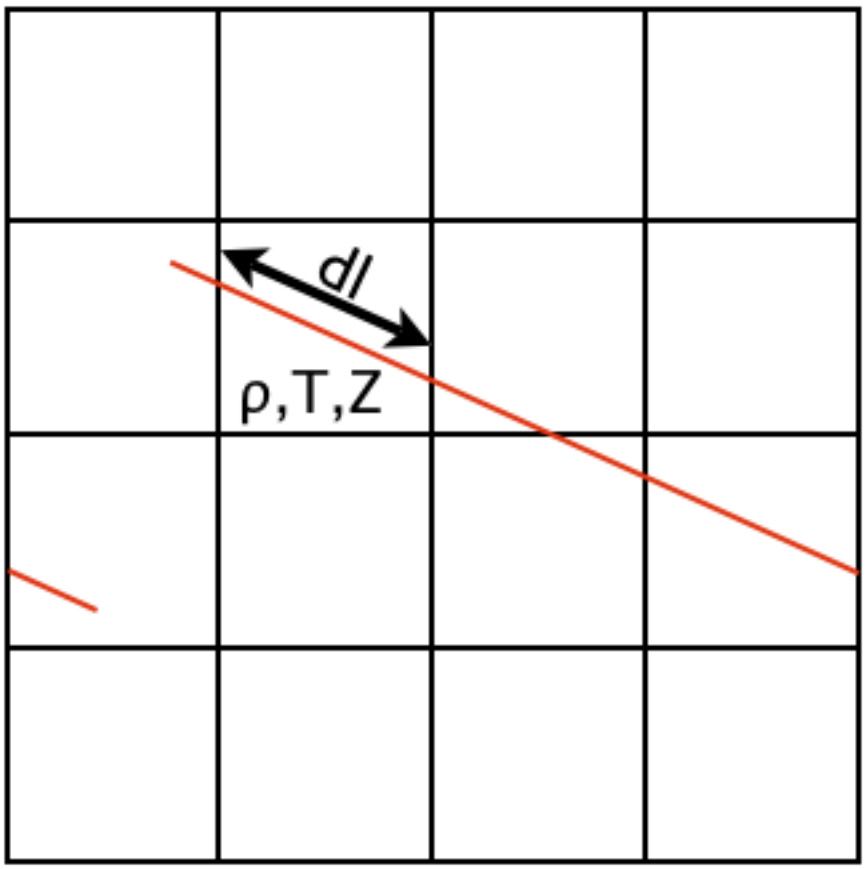
Internals and Extensions

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.

5.1 Internal Classes

5.1.1 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.



A ray segment records the information of all grid cells intersected by the ray as well as the path length, `dl`, of the ray through the cell. Column densities can be calculated by multiplying physical densities by the path length.

Configuring the Light Ray Generator

Below follows the creation of a light ray from multiple datasets stacked together. The primary Trident interface to this is covered in *Compound LightRays*. A light ray can also be made from a single dataset. For information on this, see *Light Rays Through Single Datasets*.

The arguments required to instantiate a *LightRay* are the simulation parameter file, the simulation type, the nearest redshift, and the furthest redshift.

```
from trident import LightRay
lr = LightRay("enzo_tiny_cosmology/32Mpc_32.enzo",
              simulation_type="Enzo",
              near_redshift=0.0, far_redshift=0.1)
```

Making Light Ray Data

Once the LightRay object has been instantiated, the `make_light_ray()` function will trace out the rays in each dataset and collect information for all the fields requested. The output file will be an yt-loadable dataset containing all the cell field values for all the cells that were intersected by the ray. A single LightRay object can be used over and over to make multiple randomizations, simply by changing the value of the random seed with the `seed` keyword.

```
lr.make_light_ray(seed=8675309,
                  fields=['temperature', 'density'],
                  use_peculiar_velocity=True)

# Optionally, we can now overplot the part of this ray that intersects
# one output from the source dataset in a ProjectionPlot
ds = yt.load('enzo_tiny_cosmology/RD0004/RD0004')
p = yt.ProjectionPlot(ds, 'z', 'density')
p.annotate_ray(lr)
p.save()
```

Light Rays Through Single Datasets

LightRays can also be configured for use with single datasets. In this case, one must specify the ray's trajectory explicitly. The main Trident interface to this functionality is covered in *Simple LightRay Generation*.

```
from trident import LightRay
import yt

ds = yt.load("IsolatedGalaxy/galaxy0030/galaxy0030")
lr = LightRay(ds)

lr.make_light_ray(start_position=ds.domain_left_edge,
                  end_position=ds.domain_right_edge,
                  solution_filename='lightraysolution.txt',
                  data_filename='lightray.h5',
                  fields=['temperature', 'density'])

# Overplot the ray on a projection.
p = yt.ProjectionPlot(ds, 'z', 'density')
p.annotate_ray(lr)
p.save()
```

Alternately, the `trajectory` keyword can be used in place of *end_position* to specify the (r, theta, phi) direction of the ray.

Useful Tips for Making LightRays

Below are some tips that may come in handy for creating proper LightRays.

How many snapshots do I need?

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.

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. Be 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.

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.

I want a continous trajectory over the entire ray.

Set the `minimum_coherent_box_fraction` keyword argument to a very large number, like infinity (`numpy.inf`).

5.1.2 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)

```
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_number_density').

```
my_label = 'HI Lya'
field = 'H_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.

```
my_label = 'HI Lya'
field = 'H_number_density'
wavelength = 912.323660 # Angstroms
normalization = 1.6e17
```

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```
index = 3.0

sp.add_continuum(my_label, field, wavelength, normalization, index)
```

Making the Spectrum

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

```
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`.

```
import yt
yt.enable_parallelism()
```

For more information on parallelism in yt, see Parallel Computation With yt.

5.2 Extensions

5.2.1 Fitting Absorption Spectra

This tool can be used to fit absorption spectra, particularly those generated using the *AbsorptionSpectrum*. 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.

Loading an Absorption Spectrum

To load an absorption spectrum created by *AbsorptionSpectrum*, 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.

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

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.

```
HI_parameters = {'name':'HI',
         'f': [.4164],
         'Gamma':[6.265E8],
         'wavelength':[1215.67],
         'numLines':1,
         'maxN': 1E22, 'minN':1E11,
         'maxb': 300, 'minb':1,
         'maxz': 6, 'minz':0,
         'init_b':30,
         'init_N':1E14}

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}

speciesDicts = {'HI':HI_parameters,'OVI':OVI_parameters}
```

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.

```
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 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`.

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.

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.

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.

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 `errBound`. `errBound` is related to the optional parameter to *`generate_total_fit()`* `maxAvgError` by the number of array elements in the region such that `errBound` = number of elements * `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.

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.

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, indictive of a broad Lyman alpha (BLA) absorber.

CHAPTER 6

Testing

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).

6.1 Running the Test Suite

Running the test suite requires a version of Trident installed from source (see *Installing the Development Version*).

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

```
$ 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.

```
$ 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., `master`).

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

The test suite is run by calling `py.test` from within the `tests` directory.

```
$ cd tests
$ py.test
============================= test session starts ==============================
platform darwin -- Python 3.6.0, pytest-3.0.7, py-1.4.32, pluggy-0.4.0
rootdir: /Users/britton/Documents/work/yt/extensions/trident/trident, inifile:
collected 52 items

test_absorption_spectrum.py ..........
test_download.py .
test_generate.py .
test_instrument.py .
test_ion_balance.py ............
test_light_ray.py .....
test_line_database.py .......
test_lsf.py ....
test_pipelines.py ...
test_plotting.py .
test_ray_generator.py .
test_spectrum_generator.py ......

========================== 52 passed in 117.32 seconds ==========================
```

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.

6.2 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:

```
$ cd tests
$ python gold_standard_versions.py

Latest Gold Standard Commit Tags
yt = 953248239966
Trident = test-standard-v2

To update to them, `git checkout <tag>` in appropriate repository
```

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```
$ cd /path/to/yt
$ git checkout 953248239966
$ pip install -e .
$ cd /path/to/trident
$ git checkout test-standard-v2
$ pip install -e .
$ export TRIDENT_GENERATE_TEST_RESULTS=1
$ cd tests
$ py.test
```

The test results should now be stored in the `answer_test_data_dir` that you specified in your Trident configuration file. You may now run the actual tests (see *Running the Test Suite*) with your current version of yt and Trident comparing against these gold standard results.

6.3 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*.

6.4 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 7

Frequently Asked Questions

7.1 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: $\lambda_{obs} = (1 + z)\lambda_{rest}$ 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:

```
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 $10^{12} cm^{-2}$ to have any appreciable absorption. Try sending a sightline through a denser region in your simulation that might have more of that ion.

7.2 What version of Trident am I running?

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

```
$ 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:

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

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

```
$ 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.

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

One can easily identify where Trident is installed:

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

The data files are located in that path with an appended `/data`.

7.4 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

7.5 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.

7.6 How do I cite Trident in my research?

Check out our *citation* page.

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

Click on this link.

CHAPTER 8

API Reference

8.1 Generating Rays

make_simple_ray	Create a yt LightRay object for a single dataset (eg CGM).
make_compound_ray	Create a yt LightRay object for multiple consecutive datasets (eg IGM).
LightRay	A 1D object representing the path of a light ray passing through a simulation.

8.1.1 trident.make_simple_ray

trident.**make_simple_ray**(*dataset_file*, *start_position*, *end_position*, *lines=None*, *ftype='gas'*, *fields=None*, *solution_filename=None*, *data_filename=None*, *trajectory=None*, *redshift=None*, *setup_function=None*, *load_kwargs=None*, *line_database=None*, *ionization_table=None*)

Create a yt LightRay object for a single dataset (eg CGM). This is a wrapper function around yt's LightRay interface to reduce some of the complexity there.

A simple ray is a straight line passing through a single dataset where each gas cell intersected by the line is sampled for the desired fields and stored. Several additional fields are created and stored including `dl` to represent the path length in space for each element in the ray, `v_los` to represent the line of sight velocity along the ray, and `redshift`, `redshift_dopp`, and `redshift_eff` to represent the cosmological redshift, doppler redshift and effective redshift (combined doppler and cosmological) for each element of the ray.

A simple ray is typically specified by its start and end positions in the dataset volume. Because a simple ray only probes a single output, it lacks foreground absorbers between the observer at z=0 and the redshift of the dataset that one would naturally encounter. Thus it is usually only appropriate for studying the circumgalactic medium rather than the intergalactic medium.

This function can accept a yt dataset already loaded in memory, or it can load a dataset if you pass it the dataset's filename and optionally any load_kwargs or setup_function necessary to load/process it properly before generating the LightRay object.

The :lines: keyword can be set to automatically add all fields to the resulting ray necessary for later use with the SpectrumGenerator class. If the necessary fields do not exist for your line of choice, they will be added to your dataset before adding them to the ray.

If using the :lines: keyword with an SPH dataset, it is very important to set the :ftype: keyword appropriately, or you may end up calculating ion fields by interpolating on data already smoothed to the grid. This is generally not desired.

Parameters

Dataset_file string or yt Dataset object

Either a yt dataset or the filename of a dataset on disk. If you are passing it a filename, consider usage of the `load_kwargs` and `setup_function` kwargs.

Start_position, end_position list of floats or YTArray object

The coordinates of the starting and ending position of the desired ray. If providing a raw list, coordinates are assumed to be in code length units, but if providing a YTArray, any units can be specified.

lines=None, fields=None, solution_filename=None, data_filename=None, trajectory=None, redshift=None, line_database=None, ftype="gas", setup_function=None, load_kwargs=None, ionization_table=None):

Lines list of strings, optional

List of strings that determine which fields will be added to the ray to support line deposition to an absorption line 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 possible ions from H to Zn. :lines: can be used in conjunction with :fields: as they will not override each other. If using the :lines: keyword with an SPH dataset, it is very important to set the :ftype: keyword appropriately, or you may end up calculating ion fields by interpolating on data already smoothed to the grid. This is generally not desired. Default: None

Ftype string, optional

For use with the :lines: keyword. It is the field type of the fields to be added. It is the first string in the field tuple e.g. "gas" in ("gas", "O_p5_number_density"). For SPH datasets, it is important to set this to the field type of the gas particles in your dataset (e.g. 'PartType0'), as it determines the source data for the ion fields to be added. If you leave it set to "gas", it will calculate the ion fields based on the hydro fields already smoothed on the grid, which is usually not desired. Default: "gas"

Fields list of strings, optional

The list of which fields to store in the output LightRay. See :lines: keyword for additional functionality that will add fields necessary for creating absorption line spectra for certain line features. Default: None

Solution_filename string, optional

Output filename of text file containing trajectory of LightRay through the dataset. Default: None

Data_filename string, optional

Output filename for ray data stored as an HDF5 file. Note that at present, you *must* save a ray to disk in order for it to be returned by this function. If set to None, defaults to 'ray.h5'. Default: None

Trajectory list of floats, optional

The (r, theta, phi) direction of the LightRay. Use either end_position or trajectory, but not both. Default: None

Redshift float, optional

Sets the highest cosmological redshift of the ray. By default, it will use the cosmological redshift of the dataset, if set, and if not set, it will use a redshift of 0. Default: None

Setup_function function, optional

A function that will be called on the dataset as it is loaded but before the LightRay is generated. Very useful for adding derived fields and other manipulations of the dataset prior to LightRay creation. Default: None

Load_kwargs dict, optional

Dictionary of kwargs to be passed to the yt "load" function prior to creating the LightRay. Very useful for many frontends like Gadget, Tipsy, etc. for passing in "bounding_box", "unit_base", etc. Default: None

Line_database string, optional

For use with the :lines: keyword. If you want to limit the available ion fields to be added to those available in a particular subset, you can use a *LineDatabase*. This means when you set :lines:='all', it will only use those ions present in the corresponding LineDatabase. If :LineDatabase: is set to None, and :lines:='all', it will add every ion of every element up to Zinc. Default: None

Ionization_table string, optional

For use with the :lines: keyword. 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

Example

Generate a simple ray passing from the lower left corner to the upper right corner through some Gizmo dataset where gas particles are ftype='PartType0':

```
>>> import trident
>>> import yt
>>> ds = yt.load('path/to/dataset')
>>> ray = trident.make_simple_ray(ds,
... start_position=ds.domain_left_edge, end_position=ds.domain_right_edge,
... lines=['H', 'O', 'Mg II'], ftype='PartType0')
```

8.1.2 trident.make_compound_ray

trident.**make_compound_ray**(*parameter_filename*, *simulation_type*, *near_redshift*, *far_redshift*, *lines=None*, *ftype='gas'*, *fields=None*, *solution_filename=None*, *data_filename=None*, *use_minimum_datasets=True*, *max_box_fraction=1.0*, *deltaz_min=0.0*, *minimum_coherent_box_fraction=0.0*, *seed=None*, *setup_function=None*, *load_kwargs=None*, *line_database=None*, *ionization_table=None*)

Create a yt LightRay object for multiple consecutive datasets (eg IGM). This is a wrapper function around yt's LightRay interface to reduce some of the complexity there.

Note: The compound ray functionality has only been implemented for the Enzo and Gadget code. If you would like to help us implement this functionality for your simulation code, please contact us about this on the mailing

list.

A compound ray is a series of straight lines passing through multiple consecutive outputs from a single cosmological simulation to approximate a continuous line of sight to high redshift.

Because a single continuous ray traversing a simulated volume can only cover a small range in redshift space (e.g. 100 Mpc only covers the redshift range from z=0 to z=0.023), the compound ray passes rays through multiple consecutive outputs from the same simulation to approximate the path of a single line of sight to high redshift. By probing all of the foreground material out to any given redshift, the compound ray is appropriate for studies of the intergalactic medium and circumgalactic medium.

By default, it selects a random starting location and trajectory in each dataset it traverses, to assure that the same cosmological structures are not being probed multiple times from the same direction. In doing this, the ray becomes discontinuous across each dataset.

The compound ray requires the parameter_filename of the simulation run. This is *not* the dataset filename from a single output, but the parameter file that was used to run the simulation itself. It is in this parameter file that the output frequency, simulation volume, and cosmological parameters are described to assure full redshift coverage can be achieved for a compound ray. It also requires the simulation_type of the simulation.

Unlike the simple ray, which is specified by its start and end positions in the dataset volume, the compound ray requires the near_redshift and far_redshift to determine which datasets to use to get full coverage in redshift space as the ray propagates from near_redshift to far_redshift.

Like the simple ray produced by *make_simple_ray*, each gas cell intersected by the LightRay is sampled for the desired fields and stored. Several additional fields are created and stored including `dl` to represent the path length in space for each element in the ray, `v_los` to represent the line of sight velocity along the ray, and `redshift`, `redshift_dopp`, and `redshift_eff` to represent the cosmological redshift, doppler redshift and effective redshift (combined doppler and cosmological) for each element of the ray.

The :lines: keyword can be set to automatically add all fields to the resulting ray necessary for later use with the SpectrumGenerator class. If the necessary fields do not exist for your line of choice, they will be added to your datasets before adding them to the ray.

If using the :lines: keyword with SPH datasets, it is very important to set the :ftype: keyword appropriately, or you may end up calculating ion fields by interpolating on data already smoothed to the grid. This is generally not desired.

Parameters

Parameter_filename string

The simulation parameter file *not* the dataset filename

Simulation_type string

The simulation type of the parameter file. At present, this functionality only works with "Enzo" and "Gadget" yt frontends.

Near_redshift, far_redshift floats

The near and far redshift bounds of the LightRay through the simulation datasets.

Lines list of strings, optional

List of strings that determine which fields will be added to the ray to support line deposition to an absorption line 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 possible ions from H to Zn. :lines: can be used in conjunction with :fields: as they will not override each other. If using the :lines: keyword with an SPH dataset, it is very important to set the :ftype:

keyword appropriately, or you may end up calculating ion fields by interpolating on data already smoothed to the grid. This is generally not desired. Default: None

Ftype string, optional

For use with the :lines: keyword. It is the field type of the fields to be added. It is the first string in the field tuple e.g. "gas" in ("gas", "O_p5_number_density"). For SPH datasets, it is important to set this to the field type of the gas particles in your dataset (e.g. 'PartType0'), as it determines the source data for the ion fields to be added. If you leave it set to "gas", it will calculate the ion fields based on the hydro fields already smoothed on the grid, which is usually not desired. Default: "gas"

Fields list of strings, optional

The list of which fields to store in the output LightRay. See :lines: keyword for additional functionality that will add fields necessary for creating absorption line spectra for certain line features. Default: None

Solution_filename string, optional

Output filename of text file containing trajectory of LightRay through the dataset. Default: None

Data_filename string, optional

Output filename for ray data stored as an HDF5 file. Note that at present, you *must* save a ray to disk in order for it to be returned by this function. If set to None, defaults to 'ray.h5'. Default: None

Use_minimum_datasets bool, optional

Use the minimum number of datasets to make the ray continuous through the supplied datasets from the near_redshift to the far_redshift. If false, the LightRay solution will contain as many datasets as possible to enable the light ray to traverse the desired redshift interval. Default: True

Max_box_fraction float, optional

The maximum length a light ray segment can be in order to span the redshift interval from one dataset to another in units of the domain size. Values larger than 1.0 will result in LightRays crossing the domain of a given dataset more than once, which is generally undesired. Zoom-in simulations can use a value equal to the length of the high-resolution region so as to limit ray segments to that size. If the high-resolution region is not cubical, the smallest size should b used. Default: 1.0 (the size of the box)

Deltaz_min float, optional

The minimum delta-redshift value between consecutive datasets used in the LightRay solution. Default: 0.0

Minimum_coherent_box_fraction float, optional

When use_minimum_datasets is set to False, this parameter specifies the fraction of the total box width to be traversed before rerandomizing the ray location and trajectory. Default: 0.0

Seed int, optional

Sets the seed for the random number generator used to determine the location and trajectory of the LightRay as it traverses the simulation datasets. For consistent results between LightRays, use the same seed value. Default: None

Setup_function function, optional

A function that will be called on the dataset as it is loaded but before the LightRay is generated. Very useful for adding derived fields and other manipulations of the dataset prior to LightRay creation. Default: None

Load_kwargs dict, optional

Dictionary of kwargs to be passed to the yt "load" function prior to creating the LightRay. Very useful for many frontends like Gadget, Tipsy, etc. for passing in "bounding_box", "unit_base", etc. Default: None

Line_database string, optional

For use with the :lines: keyword. If you want to limit the available ion fields to be added to those available in a particular subset, you can use a *LineDatabase*. This means when you set :lines:='all', it will only use those ions present in the corresponding LineDatabase. If :LineDatabase: is set to None, and :lines:='all', it will add every ion of every element up to Zinc. Default: None

Ionization_table string, optional

For use with the :lines: keyword. 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

Example

Generate a compound ray passing from the redshift 0 to redshift 0.05 through a multi-output enzo simulation.

```
>>> import trident
>>> fn = 'path/to/simulation/parameter/file'
>>> ray = trident.make_compound_ray(fn, simulation_type='Enzo',
... near_redshift=0.0, far_redshift=0.05, ftype='gas',
... lines=['H', 'O', 'Mg II'])
```

Generate a compound ray passing from the redshift 0 to redshift 0.05 through a multi-output gadget simulation.

```
>>> import trident
>>> fn = 'path/to/simulation/parameter/file'
>>> ray = trident.make_compound_ray(fn, simulation_type='Gadget',
... near_redshift=0.0, far_redshift=0.05,
... lines=['H', 'O', 'Mg II'], ftype='PartType0')
```

8.1.3 trident.LightRay

class trident.**LightRay**(*parameter_filename*, *simulation_type=None*, *near_redshift=None*, *far_redshift=None*, *use_minimum_datasets=True*, *max_box_fraction=1.0*, *deltaz_min=0.0*, *minimum_coherent_box_fraction=0.0*, *time_data=True*, *redshift_data=True*, *find_outputs=False*, *load_kwargs=None*)

A 1D object representing the path of a light ray passing through a simulation. LightRays can be either simple, where they pass through a single dataset, or compound, where they pass through consecutive datasets from the same cosmological simulation. One can sample any of the fields intersected by the LightRay object as it passed through the dataset(s).

For compound rays, the LightRay stacks together multiple datasets in a time series in order to approximate a LightRay's path through a volume and redshift interval larger than a single simulation data output. The outcome is something akin to a synthetic QSO line of sight.

Once the LightRay object is set up, use LightRay.make_light_ray to begin making rays. Different randomizations can be created with a single object by providing different random seeds to make_light_ray.

Parameters

Parameter_filename string or Dataset

For simple rays, one may pass either a loaded dataset object or the filename of a dataset. For compound rays, one must pass the filename of the simulation parameter file.

Simulation_type optional, string

This refers to the simulation frontend type. Do not use for simple rays. Default: None

Near_redshift optional, float

The near (lowest) redshift for a light ray containing multiple datasets. Do not use for simple rays. Default: None

Far_redshift optional, float

The far (highest) redshift for a light ray containing multiple datasets. Do not use for simple rays. Default: None

Use_minimum_datasets optional, bool

If True, the minimum number of datasets is used to connect the initial and final redshift. If false, the light ray solution will contain as many entries as possible within the redshift interval. Do not use for simple rays. Default: True.

Max_box_fraction optional, float

In terms of the size of the domain, the maximum length a light ray segment can be in order to span the redshift interval from one dataset to another. If using a zoom-in simulation, this parameter can be set to the length of the high resolution region so as to limit ray segments to that size. If the high resolution region is not cubical, the smallest side should be used. Default: 1.0 (the size of the box)

Deltaz_min optional, float

Specifies the minimum Δz between consecutive datasets in the returned list. Do not use for simple rays. Default: 0.0.

Minimum_coherent_box_fraction optional, float

Use to specify the minimum length of a ray, in terms of the size of the domain, before the trajectory is re-randomized. Set to 0 to have ray trajectory randomized for every dataset. Set to np.inf (infinity) to use a single trajectory for the entire ray. Default: 0.

Time_data optional, bool

Whether or not to include time outputs when gathering datasets for time series. Do not use for simple rays. Default: True.

Redshift_data optional, bool

Whether or not to include redshift outputs when gathering datasets for time series. Do not use for simple rays. Default: True.

Find_outputs optional, bool

Whether or not to search for datasets in the current directory. Do not use for simple rays. Default: False.

Load_kwargs optional, dict

If you are passing a filename of a dataset to LightRay rather than an already loaded dataset, then you can optionally provide this dictionary as keywords when the dataset is loaded by yt with the "load" function. Necessary for use with certain frontends. E.g. Tipsy using "bounding_box" Gadget using "unit_base", etc. Default : None

Methods

__init__	Initialize self.
create_cosmology_splice	Create list of datasets capable of spanning a redshift interval.
make_light_ray	Actually generate the LightRay by traversing the desired dataset.
plan_cosmology_splice	Create imaginary list of redshift outputs to maximally span a redshift interval.

trident.LightRay.__init__

LightRay.**__init__**(*parameter_filename*, *simulation_type=None*, *near_redshift=None*, *far_redshift=None*, *use_minimum_datasets=True*, *max_box_fraction=1.0*, *deltaz_min=0.0*, *minimum_coherent_box_fraction=0.0*, *time_data=True*, *redshift_data=True*, *find_outputs=False*, *load_kwargs=None*)

Initialize self. See help(type(self)) for accurate signature.

trident.LightRay.create_cosmology_splice

LightRay.**create_cosmology_splice**(*near_redshift*, *far_redshift*, *minimal=True*, *max_box_fraction=1.0*, *deltaz_min=0.0*, *time_data=True*, *redshift_data=True*)

Create list of datasets capable of spanning a redshift interval.

For cosmological simulations, the physical width of the simulation box corresponds to some Delta z, which varies with redshift. Using this logic, one can stitch together a series of datasets to create a continuous volume or length element from one redshift to another. This method will return such a list

Parameters

- **near_redshift** (*float*) – The nearest (lowest) redshift in the cosmology splice list.
- **far_redshift** (*float*) – The furthest (highest) redshift in the cosmology splice list.
- **minimal** (*bool*) – If True, the minimum number of datasets is used to connect the initial and final redshift. If false, the list will contain as many entries as possible within the redshift interval. Default: True.
- **max_box_fraction** (*float*) – In terms of the size of the domain, the maximum length a light ray segment can be in order to span the redshift interval from one dataset to another. If using a zoom-in simulation, this parameter can be set to the length of the high resolution region so as to limit ray segments to that size. If the high resolution region is not cubical, the smallest side should be used. Default: 1.0 (the size of the box)
- **deltaz_min** (*float*) – Specifies the minimum delta z between consecutive datasets in the returned list. Default: 0.0.
- **time_data** (*bool*) – Whether or not to include time outputs when gathering datasets for time series. Default: True.
- **redshift_data** (*bool*) – Whether or not to include redshift outputs when gathering datasets for time series. Default: True.

Examples

```
>>> co = CosmologySplice("enzo_tiny_cosmology/32Mpc_32.enzo", "Enzo")
>>> cosmo = co.create_cosmology_splice(1.0, 0.0)
```

trident.LightRay.make_light_ray

LightRay.**make_light_ray**(*seed=None*, *periodic=True*, *left_edge=None*, *right_edge=None*, *min_level=None*, *start_position=None*, *end_position=None*, *trajectory=None*, *fields=None*, *setup_function=None*, *solution_filename=None*, *data_filename=None*, *get_los_velocity=None*, *use_peculiar_velocity=True*, *redshift=None*, *field_parameters=None*, *njobs=-1*)

Actually generate the LightRay by traversing the desired dataset.

A light ray consists of a list of field values for cells intersected by the ray and the path length of the ray through those cells. Light ray data must be written out to an hdf5 file.

Parameters

Seed optional, int

Seed for the random number generator. Default: None.

Periodic optional, bool

If True, ray trajectories will make use of periodic boundaries. If False, ray trajectories will not be periodic. Default : True.

Left_edge optional, iterable of floats or YTArray

The left corner of the region in which rays are to be generated. If None, the left edge will be that of the domain. If specified without units, it is assumed to be in code units. Default: None.

Right_edge optional, iterable of floats or YTArray

The right corner of the region in which rays are to be generated. If None, the right edge will be that of the domain. If specified without units, it is assumed to be in code units. Default: None.

Min_level optional, int

The minimum refinement level of the spatial region in which the ray passes. This can be used with zoom-in simulations where the high resolution region does not keep a constant geometry. Default: None.

Start_position optional, iterable of floats or YTArray.

Used only if creating a light ray from a single dataset. The coordinates of the starting position of the ray. If specified without units, it is assumed to be in code units. Default: None.

End_position optional, iterable of floats or YTArray.

Used only if creating a light ray from a single dataset. The coordinates of the ending position of the ray. If specified without units, it is assumed to be in code units. Default: None.

Trajectory optional, list of floats

Used only if creating a light ray from a single dataset. The (r, theta, phi) direction of the light ray. Use either end_position or trajectory, not both. Default: None.

Fields optional, list

A list of fields for which to get data. Default: None.

Setup_function optional, callable, accepts a ds

This function will be called on each dataset that is loaded to create the light ray. For, example, this can be used to add new derived fields. Default: None.

Solution_filename optional, string

Path to a text file where the trajectories of each subray is written out. Default: None.

Data_filename optional, string

Path to output file for ray data. Default: None.

Use_peculiar_velocity optional, bool

If True, the peculiar velocity along the ray will be sampled for calculating the effective redshift combining the cosmological redshift and the doppler redshift. Default: True.

Redshift optional, float

Used with light rays made from single datasets to specify a starting redshift for the ray. If not used, the starting redshift will be 0 for a non-cosmological dataset and the dataset redshift for a cosmological dataset. Default: None.

Njobs optional, int

The number of parallel jobs over which the segments will be split. Choose -1 for one processor per segment. Default: -1.

Examples

Make a light ray from multiple datasets:

```
>>> import yt
>>> from trident import LightRay
>>> my_ray = LightRay("enzo_tiny_cosmology/32Mpc_32.enzo", "Enzo",
...                   0., 0.1, time_data=False)
...
>>> my_ray.make_light_ray(seed=12345,
...                       solution_filename="solution.txt",
...                       data_filename="my_ray.h5",
...                       fields=["temperature", "density"],
...                       use_peculiar_velocity=True)
```

Make a light ray from a single dataset:

```
>>> import yt
>>> from trident import LightRay
>>> my_ray = LightRay("IsolatedGalaxy/galaxy0030/galaxy0030")
...
>>> my_ray.make_light_ray(start_position=[0., 0., 0.],
...                       end_position=[1., 1., 1.],
...                       solution_filename="solution.txt",
...                       data_filename="my_ray.h5",
...                       fields=["temperature", "density"],
...                       use_peculiar_velocity=True)
```

trident.LightRay.plan_cosmology_splice

LightRay.**plan_cosmology_splice**(*near_redshift*, *far_redshift*, *decimals=3*, *filename=None*, *start_index=0*)

Create imaginary list of redshift outputs to maximally span a redshift interval.

If you want to run a cosmological simulation that will have just enough data outputs to create a cosmology splice, this method will calculate a list of redshifts outputs that will minimally connect a redshift interval.

Parameters

- **near_redshift** (*float*) – The nearest (lowest) redshift in the cosmology splice list.
- **far_redshift** (*float*) – The furthest (highest) redshift in the cosmology splice list.
- **decimals** (*int*) – The decimal place to which the output redshift will be rounded. If the decimal place in question is nonzero, the redshift will be rounded up to ensure continuity of the splice. Default: 3.
- **filename** (*string*) – If provided, a file will be written with the redshift outputs in the form in which they should be given in the enzo dataset. Default: None.
- **start_index** (*int*) – The index of the first redshift output. Default: 0.

Examples

```
>>> from yt.extensions.astro_analysis.cosmological_observation.api import␣
↪CosmologySplice
>>> my_splice = CosmologySplice('enzo_tiny_cosmology/32Mpc_32.enzo', 'Enzo')
>>> my_splice.plan_cosmology_splice(0.0, 0.1, filename='redshifts.out')
```

8.2 Generating Spectra

SpectrumGenerator	Preferred class for generating, storing, and plotting absorption-line spectra.
AbsorptionSpectrum	Base class for generating absorption spectra.
Instrument	An instrument class for specifying a spectrograph/telescope pair
LSF	A class representing a spectrograph's line spread function.
Line	A class representing an individual atomic transition.
LineDatabase	Class for storing and selecting collections of spectral lines.

8.2.1 trident.SpectrumGenerator

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

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_min`, `lambda_max`, `dlambda` and `lsf_kernel``s appropriately. If you're going to set ``lambda_min`, `lambda_max`, et al manually, leave this set to None. Default: None

Lambda_min int

The wavelength extrema of the spectra in angstroms Defaults: None

Lambda_max int

The wavelength extrema of the spectra in angstroms Defaults: None

N_lambda int

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

Dlambda float

The desired wavelength bin width of the spectrum (in angstroms). Default: None

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.

```
>>> 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 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'.

```
>>> 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

__init__	Initialize self.
add_continuum	Add a continuum feature that follows a power-law.
add_gaussian_noise	Postprocess a spectrum to add gaussian random noise of a given SNR.
add_line	Add an absorption line to the list of lines included in the spectrum.
add_line_to_database	Adds desired line to the current *LineDatabase* object.
add_milky_way_foreground	Postprocess a spectrum to add a Milky Way foreground.
add_noise_vector	Add an array of noise to the spectrum.
add_qso_spectrum	Postprocess a spectrum to add a QSO spectrum background.
apply_lsf	Postprocess a spectrum to apply a line spread function.
clear_spectrum	Clear the current spectrum in the SpectrumGenerator.
error_func	Approximate the flux error for a spectrum.
load_spectrum	Load data arrays into an existing spectrum object.
make_spectrum	Make a spectrum from ray data depositing the desired lines.
plot_spectrum	Plot the current spectrum and save to disk.
save_spectrum	Save the current spectrum data to an output file.

trident.SpectrumGenerator.__init__

SpectrumGenerator.**__init__**(*instrument=None*, *lambda_min=None*, *lambda_max=None*, *n_lambda=None*, *dlambda=None*, *lsf_kernel=None*, *line_database='lines.txt'*, *ionization_table=None*)

Initialize self. See help(type(self)) for accurate signature.

trident.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.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.

```
>>> 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.

```
>>> 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.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 gamme value.

Atomic_mass float

mass of atom in amu.

trident.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

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.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.

```
>>> 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.

```
>>> import trident
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.add_milky_way_foreground()
>>> sg.plot_spectrum('spec_mw.png')
```

trident.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

```
>>> 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.SpectrumGenerator.add_qso_spectrum

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

Postprocess a spectrum to add a QSO spectrum background. Uses data from Telfer et al., ApJ, 565, 773 "The Rest-Frame Extreme Ultraviolet Spectral Properties of QSO". HST Radio Quiet composite for < 1275 Ang, SDSS composite > 2000 Ang, mean in between 8251 0

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.

```
>>> 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.SpectrumGenerator.apply_lsf

SpectrumGenerator.**apply_lsf**(*function=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.SpectrumGenerator.clear_spectrum

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.SpectrumGenerator.error_func

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.SpectrumGenerator.load_spectrum

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:

```
>>> 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.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 or dataset

Ray dataset filename or a loaded ray dataset

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 A) not at formal Lyman Limit (911.76 A) 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 applied 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.

```
>>> 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.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 postprocessing. 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 [$rmAA$]', '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.

```
>>> 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.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.

```
>>> 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')
```

8.2.2 trident.absorption_spectrum.absorption_spectrum.AbsorptionSpectrum

class trident.absorption_spectrum.absorption_spectrum.**AbsorptionSpectrum**(*lambda_min*, *lambda_max*, *n_lambda*)

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.

Note: The preferred method for generating spectra is using *SpectrumGenerator*.

Parameters

Lambda_min float

lower wavelength bound in angstroms.

Lambda_max float

upper wavelength bound in angstroms.

N_lambda int

number of wavelength bins.

Methods

__init__	Initialize self.
add_continuum	Add a continuum feature that follows a power-law.
add_line	Add an absorption line to the list of lines included in the spectrum.
error_func	Approximate the flux error for a spectrum.
make_spectrum	Make spectrum from ray data using the line list.

trident.absorption_spectrum.absorption_spectrum.AbsorptionSpectrum.__init__

AbsorptionSpectrum.**__init__**(*lambda_min*, *lambda_max*, *n_lambda*)

Initialize self. See help(type(self)) for accurate signature.

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.

trident.absorption_spectrum.absorption_spectrum.AbsorptionSpectrum.add_line

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.

trident.absorption_spectrum.absorption_spectrum.AbsorptionSpectrum.error_func

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_file*, *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_file string or dataset

path to input ray data or a loaded ray dataset

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"

8.2.3 trident.Instrument

class trident.**Instrument**(*lambda_min*, *lambda_max*, *n_lambda=None*, *dlambda=None*, *lsf_kernel=None*, *name=None*)

An instrument class for specifying a spectrograph/telescope pair

Parameters

Lambda_min int

Minimum desired wavelength for generated spectrum in angstroms

Lambda_max int

Maximum desired wavelength for generated spectrum in angstroms

N_lambda int

Number of desired wavelength bins for the spectrum Setting dlambda overrides n_lambda value Default: None

Dlambda float

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

Name string

Name assigned to the *Instrument* object Default: None

Methods

__init__	Initialize self.

trident.Instrument.__init__

`Instrument.`**`__init__`**(*lambda_min*, *lambda_max*, *n_lambda=None*, *dlambda=None*, *lsf_kernel=None*, *name=None*)

Initialize self. See help(type(self)) for accurate signature.

8.2.4 trident.LSF

class `trident.`**`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.

Parameters

Function string, optional

The function defining the LSF kernel. valid functions are "boxcar" or "gaussian"

Width int, optional

The width of the LSF kernel in bins.

Filename string, optional

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.__path__/data/lsf_kernels` Trident searches for these files either in the aforementioned directory or in the execution directory.

Examples

Generate an LSF based on a text file:

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

Generate a boxcar-based LSF:

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

Generate a gaussian-based LSF:

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

Methods

__init__	Initialize self.

trident.LSF.__init__

LSF.**__init__**(*function=None*, *width=None*, *filename=None*)
Initialize self. See help(type(self)) for accurate signature.

8.2.5 trident.Line

class trident.**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.

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

Methods

__init__	Initialize self.

trident.Line.__init__

Line.**__init__**(*element*, *ion_state*, *wavelength*, *gamma*, *f_value*, *field=None*, *identifier=None*)
Initialize self. See help(type(self)) for accurate signature.

8.2.6 trident.LineDatabase

class trident.**LineDatabase**(*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

Input_file string, optional

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:

element, ion_state, wavelength, gamma, f_value, (name)

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

Example

```
>>> # 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)
```

Methods

__init__	Initialize self.
add_line	Manually add a line to the *LineDatabase*.
load_line_list_from_file	Load a line list from a file into the LineDatabase.

Continued on next page

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

trident.LineDatabase.__init__

LineDatabase.**__init__**(*input_file=None*)

Initialize self. See help(type(self)) for accurate signature.

trident.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

```
>>> # 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)
```

trident.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.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 LineDatabase, 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", "Mg" * Ion - Examples: "H I", "H II", "C IV", "Mg II" * Line - Examples: "H I 1216", "C II 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.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

List strings matching possible lines. Strings can be of the form: * Atom - Examples: “H”, “C”, “Mg” * Ion - Examples: “H I”, “H II”, “C IV”, “Mg II” * Line - Examples: “H I 1216”, “C II 1336”, “Mg II 1240” * Identifier - Examples: “Ly a”, “Ly b”

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

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

trident.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')
```

8.3 Plotting Spectra

load_spectrum	Load a previously saved spectrum from disk.
plot_spectrum	Plot a spectrum or a collection of spectra and save to disk.

8.3.1 trident.load_spectrum

trident.**load_spectrum**(*filename*, *format='auto'*, *instrument=None*, *lsf_kernel=None*, *line_database='lines.txt'*, *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.

```
>>> 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')
```

8.3.2 trident.plot_spectrum

trident.**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 postprocessing. 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 [$rmAA$]', 'Relative Flux'). Default: None

Returns

Matplotlib Figure object for further processing

Example

Plot a flat spectrum

```
>>> 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.

```
>>> 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')
```

8.4 Adding Ion Fields

add_ion_fields	Preferred method for adding ion fields to a yt dataset.
add_ion_fraction_field	Add ion fraction field to a yt dataset for the desired ion.
add_ion_number_density_field	Add ion number density field to a yt dataset for the desired ion.
add_ion_density_field	Add ion mass density field to a yt dataset for the desired ion.
add_ion_mass_field	Add ion mass field to a yt dataset for the desired ion.

8.4.1 trident.add_ion_fields

trident.**add_ion_fields**(*ds*, *ions*, *ftype='gas'*, *ionization_table=None*, *field_suffix=False*, *line_database=None*, *sampling_type='auto'*, *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. (ftype, 'Mg_p1_ion_fraction')
- Number density field. e.g. (ftype, 'Mg_p1_number_density')
- Density field. e.g. (ftype, 'Mg_p1_density')
- Mass field. e.g. (ftype, '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.

WARNING: The "ftype" must match the field type that you're using for the field interpolation. So for particle-based codes, this must be the ftype of the gas particles (e.g., *PartType0*, *Gas*). Using the default of *gas* in this instance will interpolate on the grid-based fields, which will give the wrong answers for particle-based codes, since the ion field interpolation will take place on the already deposited grid-based fields.

Parameters

Ds yt dataset object

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

Ions list of strings

List of strings matching possible lines. Strings can be of the form: * Atom - Examples: "H", "C", "Mg" * Ion - Examples: "H I", "H II", "C IV", "Mg II" * Line - Examples: "H I 1216", "C II 1336", "Mg II 1240"

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*.

Ftype string, optional

The field type of the field to add. it is the first string in the field tuple e.g. "gas" in ("gas", "O_p5_ion_fraction") ftype must correspond to the ftype of the 'density', and 'temperature' fields in your dataset you wish to use to generate the ion field. 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. 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.

Sampling_type string, optional

Set to 'particle' if the field should be for particles. Set to 'cell' if the field should be for grids/cells. Set to 'auto' for this to be determined automatically. Default: 'auto'

Particle_type boolean, optional

This is deprecated in favor of 'sampling_type'. Set to True if you are adding ion fields to particles, as specified by the 'ftype'. Set to False if you are not. Set to 'auto', if you want the code to autodetermine if the field specified by the 'ftype' is particle or not. Default: 'auto'

Example

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

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

8.4.2 trident.add_ion_fraction_field

trident.**add_ion_fraction_field**(*atom*, *ion*, *ds*, *ftype='gas'*, *ionization_table=None*, *field_suffix=False*, *sampling_type='auto'*, *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.

WARNING: The "ftype" must match the field type that you're using for the field interpolation. So for particle-based codes, this must be the ftype of the gas particles (e.g., *PartType0*, *Gas*). Using the default of *gas* in this instance will interpolate on the grid-based fields, which will give the wrong answers for particle-based codes, since the ion field interpolation will take place on the already deposited grid-based fields.

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 The field type of the field to add. it is the first string in the field tuple e.g. "gas" in ("gas", "O_p5_ion_fraction") ftype must correspond to the ftype of the 'density', and 'temperature' fields in your dataset you wish to use to generate the ion field. 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

Set to 'particle' if the field should be for particles. Set to 'cell' if the field should be for grids/cells. Set to 'auto' for this to be determined automatically. Default: 'auto'

Particle_type boolean, optional

This is deprecated in favor of 'sampling_type'. Set to True if you are adding ion fields to particles, as specified by the 'ftype'. Set to False if you are not. Set to 'auto', if you want the code to autodetermine if the field specified by the 'ftype' is particle or not. Default: 'auto'

Example

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

```
>>> 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()
```

8.4.3 trident.add_ion_number_density_field

trident.**add_ion_number_density_field**(*atom*, *ion*, *ds*, *ftype='gas'*, *ionization_table=None*, *field_suffix=False*, *sampling_type='auto'*, *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.

WARNING: The "ftype" must match the field type that you're using for the field interpolation. So for particle-based codes, this must be the ftype of the gas particles (e.g., *PartType0*, *Gas*). Using the default of *gas* in this instance will interpolate on the grid-based fields, which will give the wrong answers for particle-based codes, since the ion field interpolation will take place on the already deposited grid-based fields.

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

The field type of the field to add. it is the first string in the field tuple e.g. "gas" in ("gas", "O_p5_ion_fraction") ftype must correspond to the ftype of the 'density', and 'temperature' fields in your dataset you wish to use to generate the ion field. 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

Set to 'particle' if the field should be for particles. Set to 'cell' if the field should be for grids/cells. Set to 'auto' for this to be determined automatically. Default: 'auto'

Particle_type boolean, optional

This is deprecated in favor of 'sampling_type'. Set to True if you are adding ion fields to particles, as specified by the 'ftype'. Set to False if you are not. Set to 'auto', if you want the code to autodetermine if the field specified by the 'ftype' is particle or not. Default: 'auto'

Example

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

```
>>> 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()
```

8.4.4 trident.add_ion_density_field

trident.**add_ion_density_field**(*atom*, *ion*, *ds*, *ftype='gas'*, *ionization_table=None*, *field_suffix=False*, *sampling_type='auto'*, *particle_type=None*)

Add ion mass 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_density_field('O', 6, ds) creates a field called O_p5_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.

WARNING: The "ftype" must match the field type that you're using for the field interpolation. So for particle-based codes, this must be the ftype of the gas particles (e.g., *PartType0*, *Gas*). Using the default of *gas* in this instance will interpolate on the grid-based fields, which will give the wrong answers for particle-based codes, since the ion field interpolation will take place on the already deposited grid-based fields.

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

The field type of the field to add. it is the first string in the field tuple e.g. "gas" in ("gas", "O_p5_ion_fraction") ftype must correspond to the ftype of the 'density', and 'temperature' fields in your dataset you wish to use to generate the ion field. 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

Set to 'particle' if the field should be for particles. Set to 'cell' if the field should be for grids/cells. Set to 'auto' for this to be determined automatically. Default: 'auto'

Particle_type boolean, optional

This is deprecated in favor of 'sampling_type'. Set to True if you are adding ion fields to particles, as specified by the 'ftype'. Set to False if you are not. Set to 'auto', if you want the code to autodetermine if the field specified by the 'ftype' is particle or not. Default: 'auto'

Example

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

```
>>> 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()
```

8.4.5 trident.add_ion_mass_field

trident.**add_ion_mass_field**(*atom*, *ion*, *ds*, *ftype='gas'*, *ionization_table=None*, *field_suffix=False*, *sampling_type='auto'*, *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.

WARNING: The "ftype" must match the field type that you're using for the field interpolation. So for particle-based codes, this must be the ftype of the gas particles (e.g., *PartType0*, *Gas*). Using the default of *gas* in this instance will interpolate on the grid-based fields, which will give the wrong answers for particle-based codes, since the ion field interpolation will take place on the already deposited grid-based fields.

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. will be added.

Ftype string, optional

The field type of the field to add. it is the first string in the field tuple e.g. "gas" in ("gas", "O_p5_ion_fraction") ftype must correspond to the ftype of the 'density', and 'temperature' fields in your dataset you wish to use to generate the ion field. 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

Set to 'particle' if the field should be for particles. Set to 'cell' if the field should be for grids/cells. Set to 'auto' for this to be determined automatically. Default: 'auto'

Particle_type boolean, optional

This is deprecated in favor of 'sampling_type'. Set to True if you are adding ion fields to particles, as specified by the 'ftype'. Set to False if you are not. Set to 'auto', if you want the code to autodetermine if the field specified by the 'ftype' is particle or not. Default: 'auto'

Example

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

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

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```
>>> trident.add_ion_mass_field('C', 4, ds)
>>> yt.ProjectionPlot(ds, 'x', 'C_p3_mass').save()
```

8.5 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.

8.5.1 trident.make_onezone_dataset

trident.**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.

```
>>> 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'])
```

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

8.5.2 trident.make_onezone_ray

trident.**make_onezone_ray**(*density=1e-26*, *temperature=1000*, *metallicity=0.3*, *length=10*, *redshift=0*, *filename='ray.h5'*, *column_densities=None*)

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.

```
>>> 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.

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

8.5.3 trident.to_roman

trident.**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

```
>>> num = to_roman(5)
```

8.5.4 trident.from_roman

trident.**from_roman**(*s*)

Convert a Roman numeral to an integer.

Parameters

S string

String representing Roman numeral. Examples: 'I', "II", 'XI', "MCMXC".

Returns

Integer value equivalent to **s** Roman numeral argument.

Example

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

8.5.5 trident.trident_path

trident.**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())
```

8.5.6 trident.trident

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

8.5.7 trident.verify

trident.**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()
```

8.5.8 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.

CHAPTER 9

Citation

If you use Trident for a research application, please cite the Trident method paper in your work with the bibtex entry below:

```
@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}
}
```

CHAPTER 10

Changelog

This document summarizes changes to the codebase with time for Trident.

10.1 Contributors

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

10.2 Version 1.1

- 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()`*. This may cause slight backwards-incompatible changes when applying line spread functions to post-process spectra.
- Replaced internal instances of `particle_type` with `sampling_type` to match similar yt conversion.

10.3 Version 1.0

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.

CHAPTER 11

Help

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.

11.1 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.

11.2 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.

11.3 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
```

11.4 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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