trident Documentation

Release 1.1.0.dev1

Team Trident

Aug 12, 2017

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 two versions of Trident: the stable version, and the developent version. The stable version is tried, and tested, and it 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 installation steps are slightly different between the two 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*.

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, and INST_HG=1
$ ... if you want to use the dev version of yt and trident, mark 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 stable version of yt (for the stable version of trident), type:

```
$ conda install -c conda-forge yt
```

To get the nightly build of the development version of yt (for the development version of trident), 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 mercurial, which should be installed as part of your yt installation. If it isn't try: `conda install mercurial`. After that, you'll use pip to install the source directly. Go to your desired source code installation directory and run:

```
$ hg clone http://bitbucket.org/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>
$ hg pull
$ hg up
$ pip uninstall trident
$ 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, but 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:

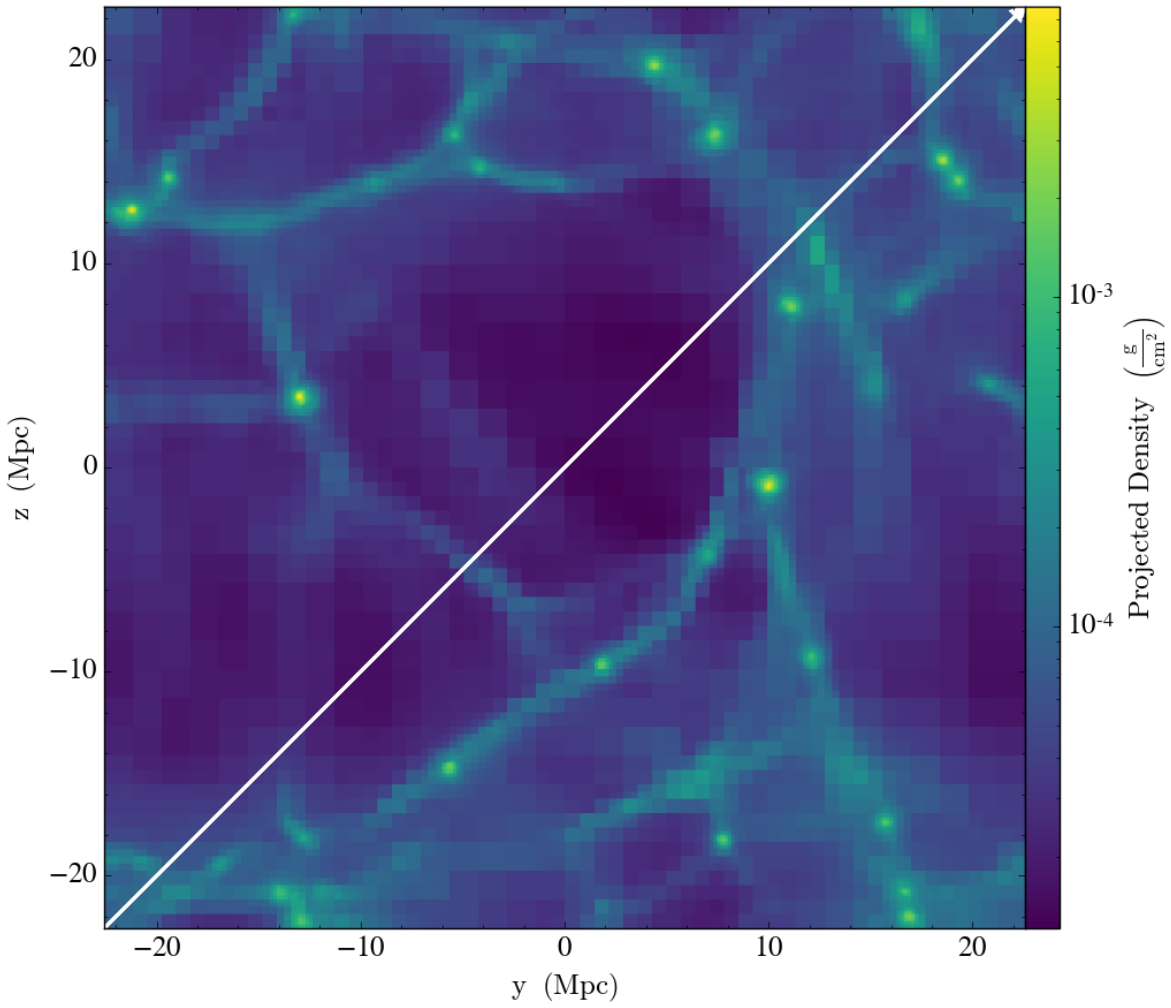
```
ray = trident.make_simple_ray(ds,
                              start_position=ray_start,
                              end_position=ray_end,
                              data_filename="ray.h5",
                              lines=line_list,
                              ftype='gas')
```

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')
```

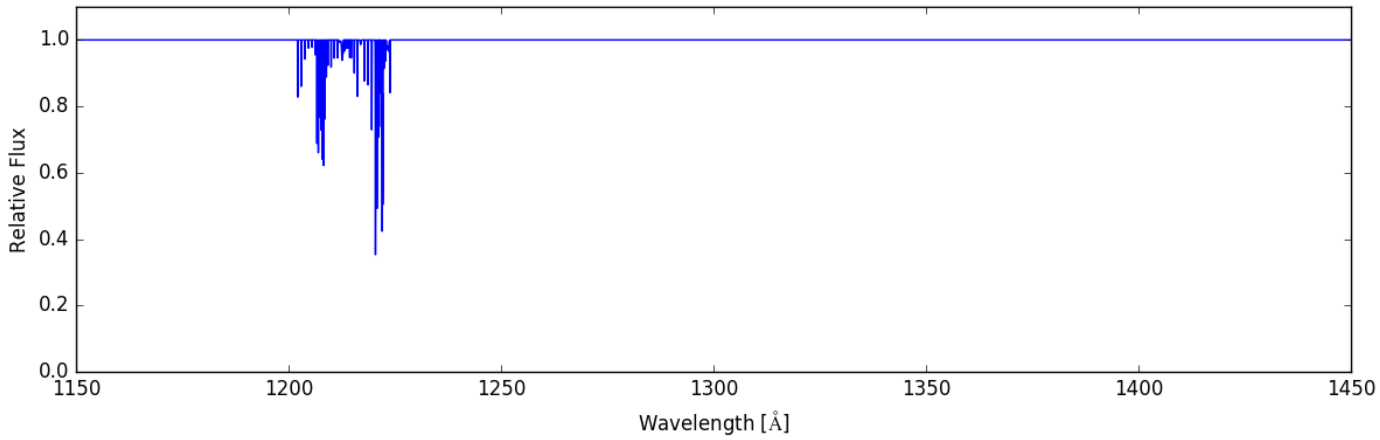


2.3 Spectrum Generation

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')
```



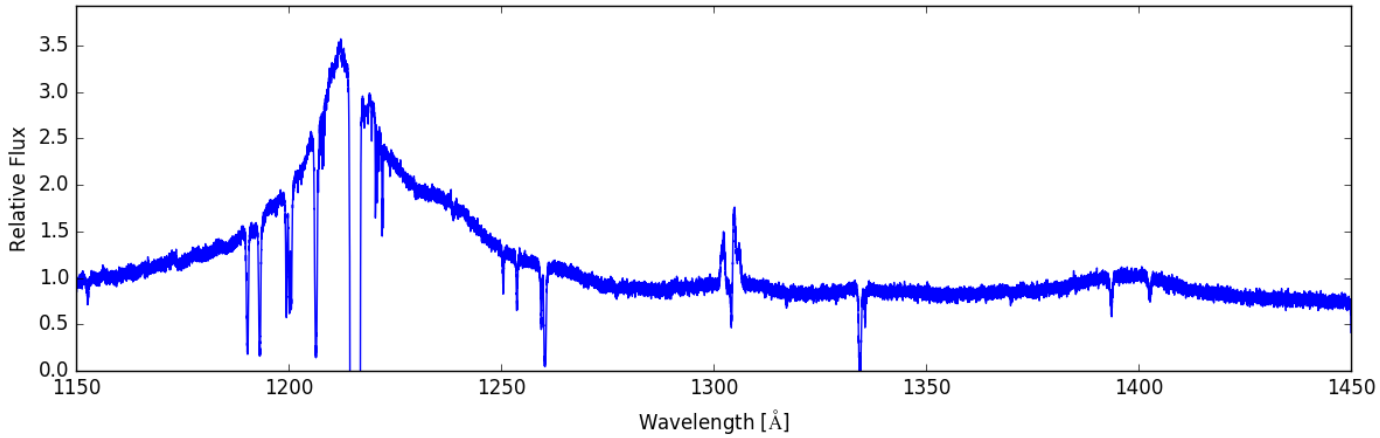
From here we can do some post-processing to the spectrum to include additional features that would be present in an actual observed spectrum. We add a background quasar spectrum, a Milky Way foreground, apply the COS line spread function, and add gaussian noise with SNR=30:

```
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 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)
```

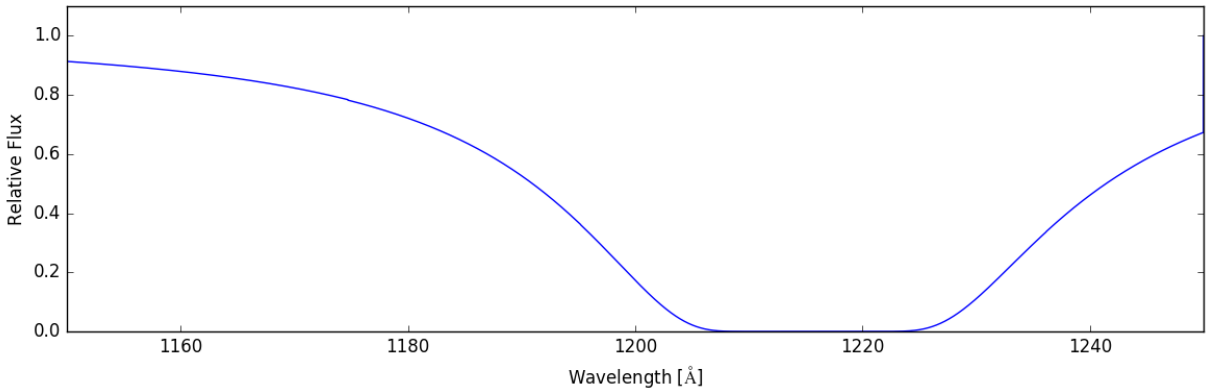
which is reading lines from the 'lines.txt' file present in the data directory (see *where is Trident installed?*) We can specify any subset of these spectral lines to use when creating the spectrum from our master line list. So if you're interested in just looking at neutral hydrogen lines in your spectrum,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

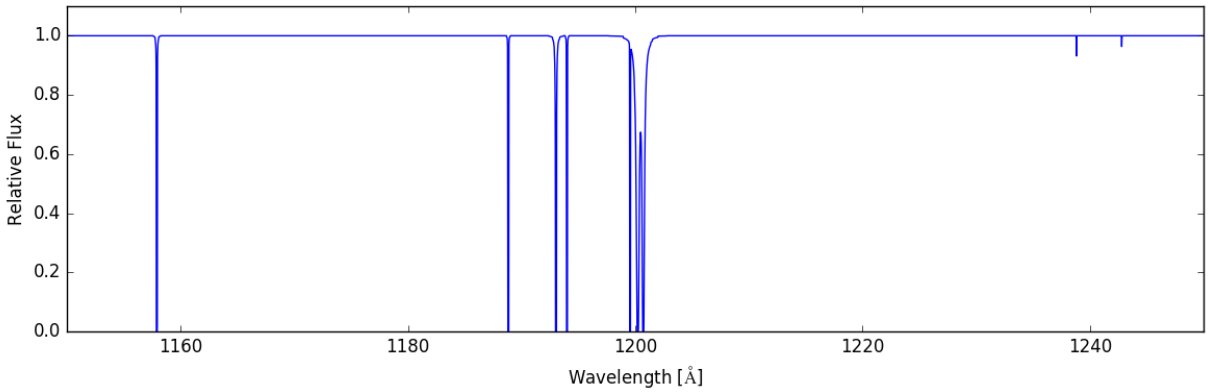
The resulting spectrum contains a nice, big Lyman-alpha feature.



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')
```

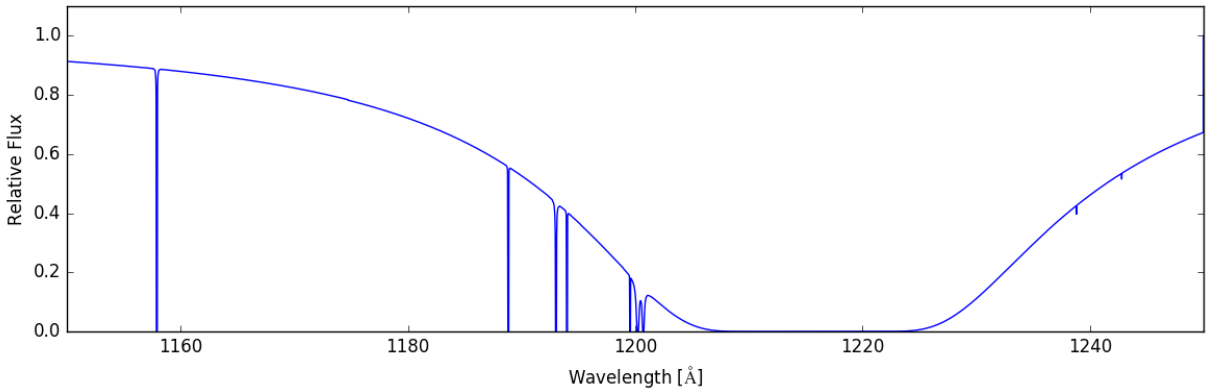
And now we have:



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')
```

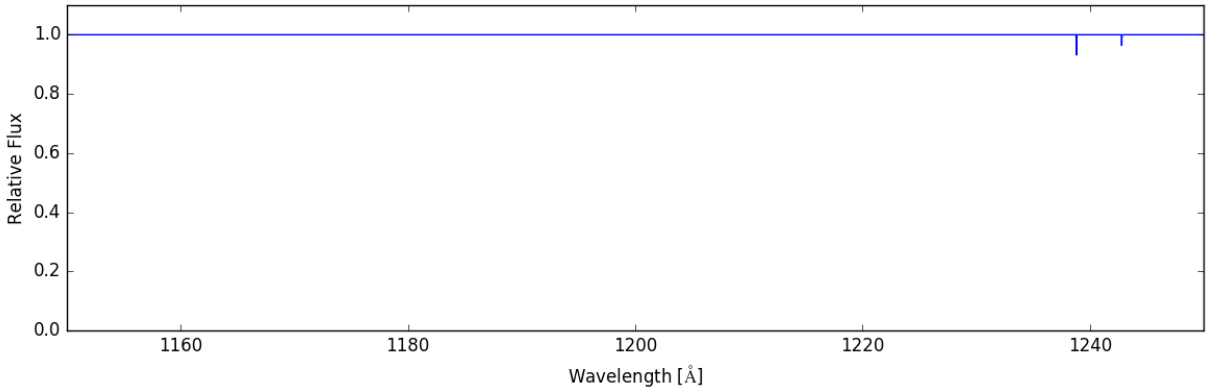
which gives:



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')
```

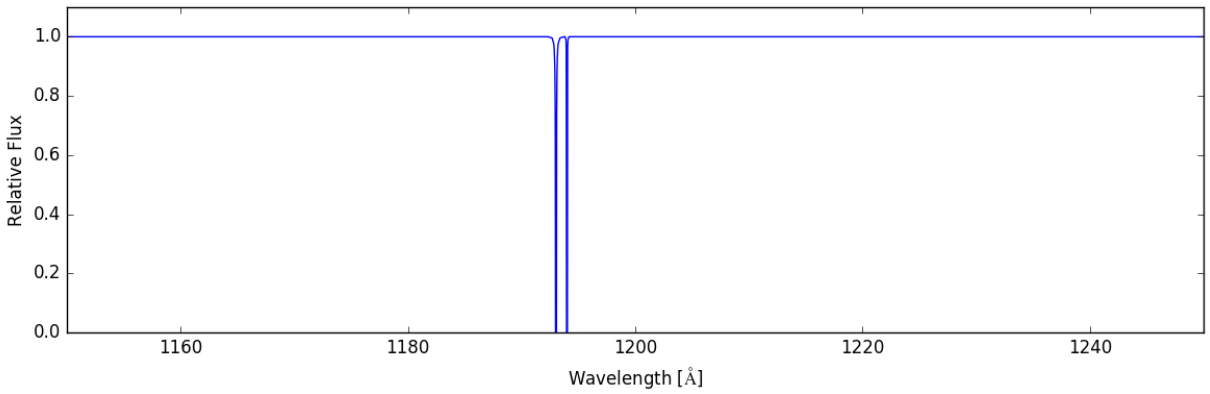
This spectrum only shows a couple of small lines on the right hand side.



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')
```

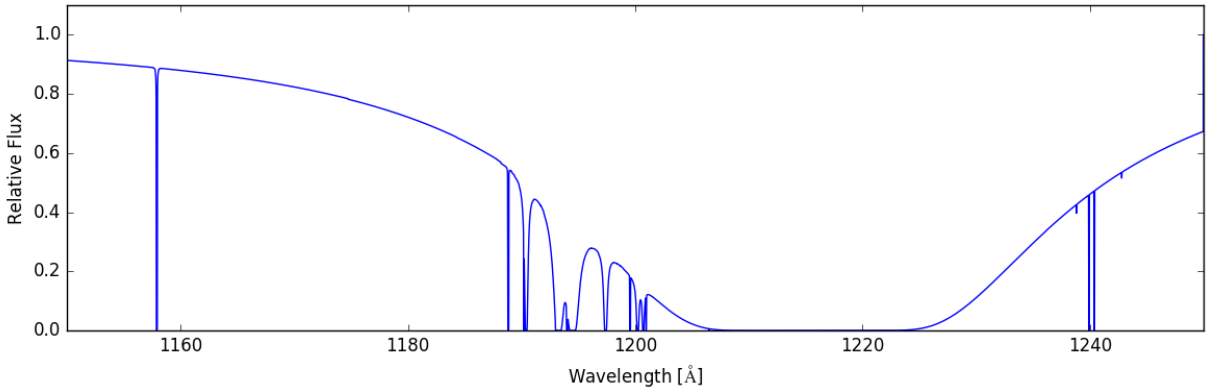
And we end up with:



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):

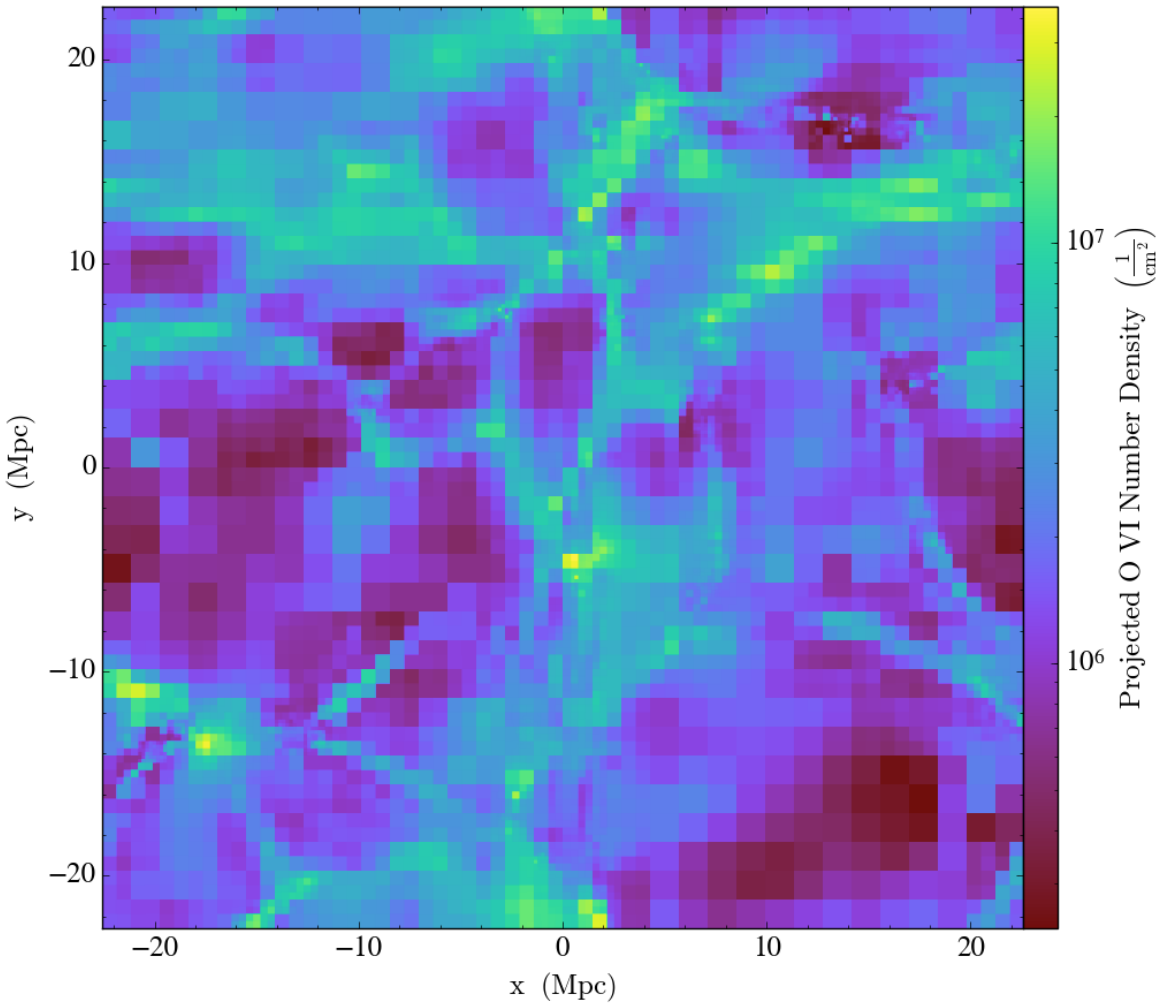
```
trident.add_ion_fields(ds, ions=['O VI'], ftype="gas")
```

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()
```

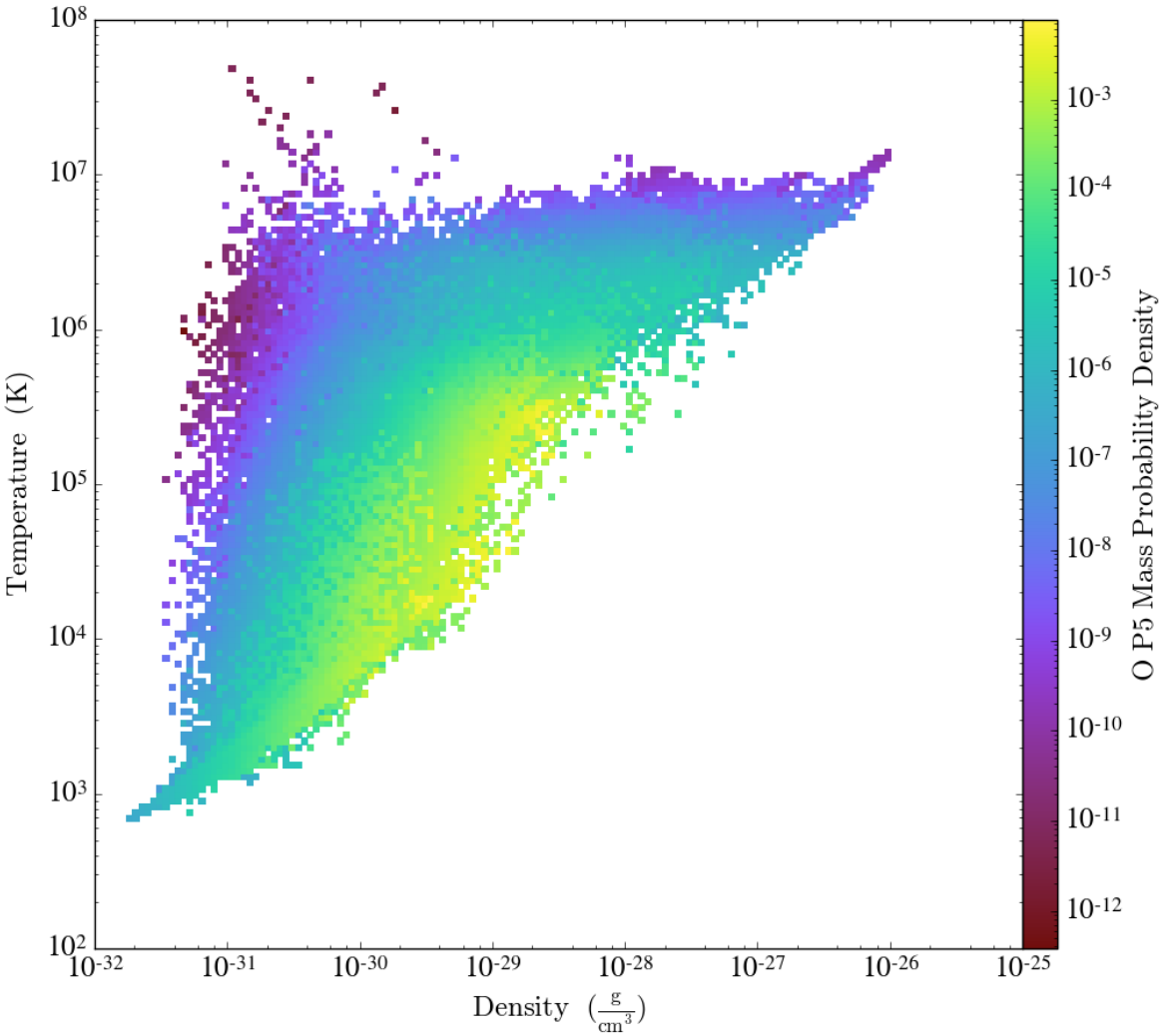
which produces:



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

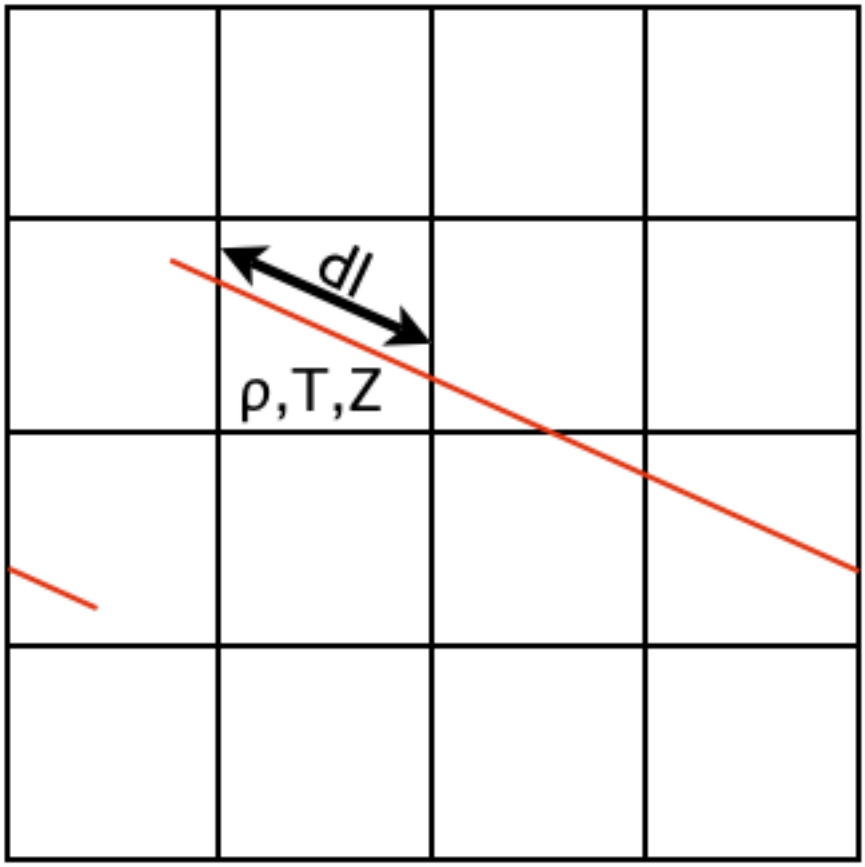
Internals and Extensions

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
```

```
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

Running the Test Suite

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

Trident maintains a suite of unit and answer tests to ensure that development doesn't change code behavior in unexpected ways. 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 as well as results files for answer comparison. 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. The helper script is located in the `tests` directory of the Trident source.

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

Once the test data has been downloaded, the test suite is run by calling `py.test` from within the `tests` directory.

```
$ 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 =========================
```

CHAPTER 7

Generating Test Results

If new tests have been added or the code's behavior has changed (in a good way) such that the tests no longer pass, new results must be generated. Before generating new results, be sure to update the results version number in `tests/test_results_version.txt`. Then, set the `TRIDENT_GENERATE_TEST_RESULTS` environment variable to 1 and rerun the tests:

```
$ cd tests
$ export TRIDENT_GENERATE_TEST_RESULTS=1
$ py.test
```

The results must then be tarred up and uploaded to the Trident website.

CHAPTER 8

Frequently Asked Questions

8.1 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>
$ hg id
```

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.

8.2 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`.

8.3 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

8.4 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.

8.5 How do I cite Trident in my research?

Check out our *citation* page.

CHAPTER 9

API Reference

9.1 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.

9.1.1 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` and `dredshift` to represent the path length in space and redshift 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')
```

9.1.2 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*, *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` and `dredshift` to represent the path length in space and redshift 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

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')
```

9.1.3 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.

parameter_filename [string or `yt.data_objects.static_output.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

9.2 Generating Spectra

SpectrumGenerator	Class for generating, storing, and plotting absorption-line 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.

9.2.1 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*)

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, optional

A text file listing the various lines to insert into the line database. The line database provides a list of all possible lines that could be added to the spectrum. The file should 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')
```

9.2.2 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

9.2.3 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)
```

9.2.4 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')
```

9.2.5 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)
```

9.3 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.

9.3.1 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')
```

9.3.2 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')
```

9.4 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.

9.4.1 trident.add_ion_fields

trident.**add_ion_fields**(*ds*, *ions*, *ftype='gas'*, *ionization_table=None*, *field_suffix=False*, *line_database=None*, *force_override=False*, *particle_type='auto'*)

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.

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.

Force_override boolean, optional

Set to True if you wish to clobber existing ion fields with any created with this functionality. Otherwise, existing fields will remain untouched. Default: False

Particle_type boolean, optional

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'])
```

9.4.2 trident.add_ion_fraction_field

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

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

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

---

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

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

Parameters

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

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

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

Ftype string, optional 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

Force_override boolean, optional

Set to True if you wish to clobber existing ion fields with any created with this functionality. Otherwise, existing fields will remain untouched. Default: False

Particle_type boolean, optional

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()
```

9.4.3 trident.add_ion_number_density_field

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

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

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

---

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

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

Parameters

Atom string

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

Ion integer

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

Ds yt dataset object

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

Ftype string, optional

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

Force_override boolean, optional

Set to True if you wish to clobber existing ion fields with any created with this functionality. Otherwise, existing fields will remain untouched. Default: False

Particle_type boolean, optional

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()
```

9.4.4 trident.add_ion_density_field

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

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.

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

Force_override boolean, optional

Set to True if you wish to clobber existing ion fields with any created with this functionality. Otherwise, existing fields will remain untouched. Default: False

Particle_type boolean, optional

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()
```

9.4.5 trident.add_ion_mass_field

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

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

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

---

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

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

Parameters

Atom string

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

Ion integer

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

Ds yt dataset object

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

Force_override boolean, optional

Set to True if you wish to clobber existing ion fields with any created with this functionality. Otherwise, existing fields will remain untouched. Default: False

Particle_type boolean, optional

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

9.5 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.

9.5.1 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'])
>>> sg = trident.SpectrumGenerator('COS')
>>> sg.make_spectrum(ray)
>>> sg.plot_spectrum('spec_raw.png')
```

9.5.2 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')
```

9.5.3 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)
```

9.5.4 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')
```

9.5.5 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())
```

9.5.6 trident.trident

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

9.5.7 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()
```

9.6 Internals and Extensions

trident.light_ray.LightRay
trident.light_ray.LightRay. make_light_ray
trident.absorption_spectrum. absorption_spectrum.AbsorptionSpectrum
trident.absorption_spectrum. absorption_spectrum.AbsorptionSpectrum. add_continuum

Continued on next page

Table 9.6 – continued from previous page

trident.absorption_spectrum. absorption_spectrum.AbsorptionSpectrum. add_line
trident.absorption_spectrum. absorption_spectrum.AbsorptionSpectrum. make_spectrum
trident.absorption_spectrum. absorption_spectrum_fit. generate_total_fit

CHAPTER 10

Citation

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

```
@ARTICLE{2016arXiv161203935H,
       author = {{Hummels}, C. and {Smith}, B. and {Silvia}, D.},
        title = "{Trident: a universal tool for generating synthetic absorption
↪spectra from astrophysical simulations}",
      journal = {ArXiv e-prints},
archivePrefix = "arXiv",
       eprint = {1612.03935},
 primaryClass = "astro-ph.IM",
     keywords = {Astrophysics - Instrumentation and Methods for Astrophysics,
↪Astrophysics - Astrophysics of Galaxies},
         year = 2016,
        month = dec,
       adsurl = {http://adsabs.harvard.edu/abs/2016arXiv161203935H},
      adsnote = {Provided by the SAO/NASA Astrophysics Data System}
}
```

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

We've tried to do a decent job of documenting Trident, but because Trident is still beta, there are definitely holes in the documentation. That said, give it a shot and search the docs for your problem using that 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

Index