PyNeb_manual_4

June 2, 2020

0.1 Recombination lines: the RecAtom class

This object is similar to **Atom**, but some methods differ due to the particularities of the recombination spectrum. It is instantiated with the following command:

[1]:
```
%matplotlib inline
import numpy as np
import matplotlib.pyplot as plt
import pyneb as pn
```

[2]:
```
H1 = pn.RecAtom('H', 1)
```

The data are read from a fits file and interpolated in temperature and density. The name of the file is retrievable through:

[3]:
```
pn.atomicData.getDataFile('H1', 'rec')
```

[3]:
```
'h_i_rec_SH95.hdf5'
```

In case the instantiation takes too much time (on some systems, the reading the fits fils is slow), you can use the data store in the hdf5 file using:

[4]:
```
pn.atomicData.setDataFile('h_i_rec_SH95.hdf5')
```

[5]:
```
H1 = pn.RecAtom('H', 1)
```

The ions for which recombination lines are available are listed with the command:

[6]:
```
pn.atomicData.getAllAtoms(coll=False, rec=True)
```

[6]:
```
['H1',
 'He1',
 'He2',
 'C1',
 'C2',
 'C3',
 'C4',
 'N1',
 'N2',
```

```
 'N3',
 'N4',
 'Ne2',
 'O1',
 'O2',
 'O3',
 'O4',
 'O5',
 'N5',
 'O6']
```

You can list all the available data files for a given ion by:

[7]:
```
pn.atomicData.getAllAvailableFiles('H1')
```

[7]:
```
['h_i_atom.chianti',
 'h_i_coll.chianti',
 'h_i_rec_P91.func',
 'h_i_rec_SH95-caseA.fits',
 'h_i_rec_SH95-caseA.hdf5',
 'h_i_rec_SH95.fits',
 'h_i_rec_SH95.hdf5',
 'h_i_trc_SH95-caseA.dat',
 'h_i_trc_SH95-caseB.dat']
```

The emissivities are obtained by, e.g.:

[8]:
```
Hbeta = H1.getEmissivity(tem=1e4, den=1e3, lev_i=4, lev_j=2)
Halpha = H1.getEmissivity(tem=1e4, den=1e3, lev_i=3, lev_j=2)
print(Halpha/Hbeta)
```

```
2.856911883589329
```

The argument used to identify the various lines in the data file depend on whether the atom is a hydrogenoid or not. In the first case, the transition can be specified either as a pair of levels **lev_i**, **lev_j**, or as a label (labels are descriptive of level pairs):

[9]:
```
print(H1.getEmissivity([1e4, 1.8e4], [1e4, 1e2], lev_i = 4, lev_j = 2))
```

```
[[1.24000000e-25 1.23500000e-25]
 [7.26633333e-26 7.25266667e-26]]
```

[10]:
```
print(H1.getEmissivity([1e4, 1.8e4], [1e4, 1e2], label='4_2'))
```

```
[[1.24000000e-25 1.23500000e-25]
 [7.26633333e-26 7.25266667e-26]]
```

As in the case of collisional lines, setting **product=False** modifies the input array of temperature and density values:

[11]:
```
print(H1.getEmissivity([1e4, 1.8e4], [1e4, 1e2], label='4_2', product=False))
```

```
[1.24000000e-25 7.25266667e-26]
```

In the case of non-hydrogenoids, the transition can be specified either as a wavelength or as a label (labels are descriptive of wavelengths):

[12]:
```
He1 = pn.RecAtom('He', 1)
print(He1.getEmissivity(1e4, 1e2, wave=4471.0))
print(He1.getEmissivity(1e4, 1e2, label='4471.0'))
```

```
6.11561306801098e-26
6.11561306801098e-26
```

Use **Atom.labels** to display the valid labels for both kind of recombiation atoms, i.e.:

[13]:
```
H1.labels[0:10]
```

[13]:
```
('2_1', '3_1', '3_2', '4_1', '4_2', '4_3', '5_1', '5_2', '5_3', '5_4')
```

[14]:
```
He1.labels[0:10]
```

[14]:
```
('2945.0',
 '3188.0',
 '3614.0',
 '3889.0',
 '3965.0',
 '4026.0',
 '4121.0',
 '4388.0',
 '4438.0',
 '4471.0')
```

As an example application, you can easily generate a 2D table of H alpha/ H Beta as a function of Te and Ne:

[15]:
```
tem = np.linspace(5000, 20000, 100)
den = np.logspace(2, 6, 50)
im_Hab = (H1.getEmissivity(tem, den, label='3_2') / H1.getEmissivity(tem, den,␣
 ↪label='4_2'))
print(im_Hab.shape)
print(np.min(im_Hab))
print(np.max(im_Hab))
```

```
(100, 50)
2.7245237375264586
3.040927694406548
```

By default, H1 emissivities are computed under case B; to compute Case A emissivities, the atomic data file must be changed:

[16]:
```
pn.atomicData.setDataFile('h_i_rec_SH95-caseA.hdf5')
```

[17]:
```
H1_A = pn.RecAtom('H', 1)
```

Note that the previously defined H1 atom is still available and use the default values.

[18]:
```
im_caseAoverB = (H1_A.getEmissivity(tem, den, label='4_2')/H1.
 ↪getEmissivity(tem, den, label='4_2'))
```

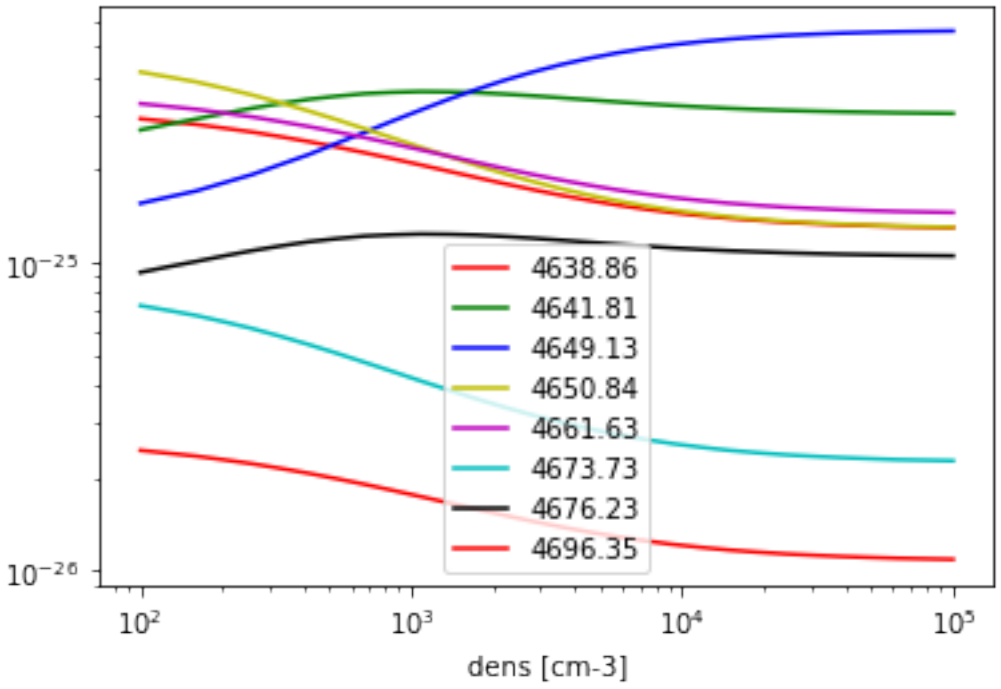
plt.imshow(im_caseAoverB) plt.colorbar();

0.1.1 Emissivities of OII recombination lines

[19]:
```
O2 = pn.RecAtom('O', 2)
```

[20]:
```
V1_mult = ('4638.86', '4641.81', '4649.13', '4650.84', '4661.63', '4673.73',␣
 ↪'4676.23', '4696.35')
```

[22]:
```
cols = 'rgbymckrgbymckr'
temps = 1e4
dens = np.logspace(2, 5, 30)
f, ax = plt.subplots()
for j, label in enumerate(V1_mult):
    ax.loglog(dens, O2.getEmissivity(temps, dens, label=label), label=label,␣
 ↪c=cols[j])
ax.set_xlabel('dens [cm-3]')
ax.legend(loc='best');
```



0.1.2 Ionic abundances from collisional and recombination lines, ADF

[23]:
```
O3c = pn.Atom('O',3)
O2r = pn.RecAtom('O',2)
tem = 1e4
den = 1e2
Opp_col = O3c.getIonAbundance(int_ratio=127, tem=tem, den=den, wave=5007)
Opp_rec = O2r.getIonAbundance(int_ratio=.023, tem=tem, den=den, label='4649.13')
print("""12+log(O++/H) from recombination line: {:.2f},
12+log(O++/H) from collisional line: {:.2f},
ADF: {:.1f}""".format(12+np.log10(Opp_rec), 12+np.log10(Opp_col), Opp_rec /␣
↪Opp_col))
```

```
12+log(O++/H) from recombination line: 8.09,
12+log(O++/H) from collisional line: 7.48,
ADF: 4.1
```