NEAT

Nebular Empirical Analysis Tool

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1 Introduction

NEAT (Nebular empirical analysis tool) is a code designed for the quick analysis of emission line spectra of photoionised nebulae. It is designed to be very simple but to return robust and meaningful results. It has been used to determine abundances and conditions for several samples of ionized nebulae (e.g. Stock et al, 2011) and also as a testbed for investigating uncertainties (e.g. Wesson et al, 2012)

2 Installation

The easiest way to install NEAT is to use another program called GIT. GIT is a version control program which we have used to track our development of the code, as such you can ensure that you always have an up to date version of NEAT by "cloning" the got repository, e.g. in an empty directory type:

```
git clone http://github.com/rwesson/NEAT.
```

Presuming you actually have GIT installed, this will copy the latest version of the code into that empty directory. Subsequently you can issue the command 'git pull' in this directory and the latest version of NEAT which we have uploaded will be downloaded onto your machine.

If this sounds too complex, you can download everything you need as a tar.gz file from http://github.com/rwesson/NEAT, or from our website: http://www.rogerneedstomakeusawebsite.com.

You will also need the relevant atomic data[1]. This should be placed in a subdirectory 'NEAT/Atomic-data/' where 'NEAT/' contains the executable file etc. Links to files in the Atomic-data directory are currently hardcoded into the program, it is important that this data is in the correct place!

Once you've got the source code and the atomic data, you should be able to compile the code by typing `make`. Our makefile relies upon you having gfortran installed, if you don't have gfortran installed then any modern fortran compiler should work as well[2].

You should now see an executable 'abundances.exe' in the root neat directory. Congratulations, everything worked!

2.1 Potential Problems

- Is the atomic data in the correct place?

[1] available from http://github.com/rwesson/Atomic-data, substitute this address into the command above to obtain it.

[2] Although some alterations may be required given that dialects of Fortran do not necessarily overlap. We recommend that you use gfortran.

- do you have make, git etc installed before attemping this?
- Are you trying to do this on a windows machine?

3 Running the code

You can test that the code is working by typing

```
./abundances.exe -i examples/ngc6543.dat
```

You should see a lot of output to the terminal, ending with a section titled "Abundance Discrepancy Factors".

3.1 Inputs

In its simplest form, the code is run by typing

```
./abundances.exe -i filename
```

The filename should be a plain text file, containing three columns. The first is a rest wavelength, which the code will use to identify the line. The wavelengths should correspond exactly to those listed in source/Ilines_levs. The second column should be a flux per unit wavelength (any units are fine), and the third column should be the uncertainty on the flux, given in the same units.

We have introduced further command line options, '-n' and '-e' both of which fulfil important roles when running NEAT.

The first option '-n' controls the number of iterations to carry out. If this number is 1 (or the '-n' option is not specified) then the code simply calculates all of the temperatures, densities, ionic and total abundances that it can, using the line list provided. If it is greater than 1 e.g.

```
./abundances.exe -n 100 -i examples/ngc6543.dat
```

then the code will also calculate uncertainties using a Monte Carlo technique, in which the nebular parameters are calculated repeatedly, each time drawing the line flux randomly from a Gaussian distribution, centred on the quoted flux and with a standard deviation equal to the quoted uncertainty. The higher the number of iterations, the better sampled the uncertainty distribution of the output parameters will be. Around 10,000 iterations should be sufficient in most cases. See Wesson et al, 2012, for a full discussion of this technique. When doing large numbers of iterations, we strongly recommend that you use a unix redirect, such that the output (the results) end up in a large text file:

```
./abundances.exe -n 100 -i examples/ngc6543.dat > ngc6543_results.dat
```

3.2 Outputs

At the moment, the code simply outputs its results to the terminal. We appreciate that this is a somewhat inconvenient way of doing things, and we are working on more efficient ways of dealing with the data avalanche.

So how do you get results out of this potentially very large file? The best way is to use something like grep to pull out the quantities you're interested in such that you can then do statistics with the results. E.g. If you issued the command at the end of the previous section and created a file 'ngc56543_results.dat', then you could issue the following command to extract, for example, the [O II] density:

```
grep '\[O II\] dens' ngc6543_results.dat | awk '{print $5}'
```

We hope to include better tools to interpret the data produced by this process in future releases of NEAT.