

RADEX Online Python Interface

(radexonline.py)

User Guide

Andrés Megías Toledano
Center for Astrobiology (CAB), Madrid

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1. Introduction

The RADEX Online Python Interface is a Python 3 script, `radexonline.py`, that uses RADEX Online tool¹ to make a non-LTE fit (LTE: *Local Thermodynamical Equilibrium*) to the observed lines and derive the column density of the species. Please, take into account that RADEX Online is discouraged for serious applications. For publication-quality results, the standalone version of RADEX should be used instead.

The script requires the modules `os`, `re`, `io`, `sys`, `copy`, `time`, `pickle`, `platform`, and `requests`, from the Python's standard library, and also the libraries `PyYAML`, `NumPy`, `Pandas`, `Matplotlib`, `SciPy`, `Beautiful Soup`, and `RichValues`.² In order to run the code, it is necessary to specify some options in a configuration file. For running the code we have to write the following command line in the terminal, being in the folder of the file `radexonline.py`:

```
python3 radexonline.py <path> .
```

The argument `<path>` is the path of the configuration file. If we do not specify it, the

1. <http://var.sron.nl/radex/radex.php>

2. <https://github.com/andresmegias/richvalues>

script will search in the current folder (./) for the configuration file specified inside the script in the variable `config_file`, at the beginning of the code; we can use this variable to run the script in a programming environment like Spyder. If the script `radexonline.py` is not in the current folder, but in a folder with path `<folder>`, we should write `<folder>/radexonline.py` instead of `radexonline.py`. Moreover, if the script is included in a folder of executable files, the term `python3` can be removed from the command line, and the script will be run from any path.

2. Input files

There are no mandatory input files needed to run this script. However, there are two files that can be used for each source to extract automatically some data, in which case they do not have to be explicitly written in the configuration file. Below is a description of each name, with the same names as the given ones in the configuration file:

- **MADCUBA table.** Transition lines table in .csv format generated by the tool SLIM from the software MADCUBA. To generate it in SLIM, select one of the species in the SimFit tab to open the transition table window, check the Spectral, Fit, and Phys. options, and click the save icon to export the table in .csv format. This variable is only needed if the values of the line widths, the temperature, and/or the initial column density are set to be chosen from SLIM.
- **spectra table.** Table in .csv format with information of the RMS noise and resolution of the spectra. Each row, which corresponds to one spectral range, must have a column called `rms noise (mK)`, with the value of the RMS noise of the spectral range. Such a file can be generated by the Python Reduction Pipeline for CLASS (`classpipeline.py`) once we have run the steps `--selection`, `--line_search`, and `--reduction`, adding the argument `--spectra_table` (for example: `python3 classpipeline.py config.yaml --spectra_table`). This variable is only needed if one does not specify the values of the RMS noise in the variable `RADEX` parameters.

3. Output files

After the running of the script, a file in YAML formatting style with the results of the calculations will be generated. It will contain a Python dictionary with name non-LTE molecules, containing one next-level dictionary for each molecule studied. For each of them, there will be three entries: one for the column density (column density (/cm²)), one for the kinetic temperature (kinetic temperature (K)), and one regarding the lines fit (lines (GHz)). Except for the last entry, this variable has the same structure as the corresponding variable for the SLIM Table Generator (`slimtables.py`), although the exact names of the species studied could vary a little bit, so they may need to be edited if you want to use this other script.

Plus, a plot will be generated for each species and each source studied, showing the loss function between the observed lines and the predicted ones by RADEX with respect to the column density.

4. Configuration file

The configuration file is a plain text document in the YAML formatting style. This way, we can specify the options of the script `radexonline.py` by defining different variables that can be nested.

In order to define the values of the variables, we have to write, in a single line, the name of the variable followed by a colon (:), and its value, separated with a space. For the logical variables, the possible values are yes/no. There are variables whose value can be a list of elements, in which case they can be written between brackets and separated by commas or in single lines preceded by a hyphen (-). Similarly, in the case of nested variables, which work like Python dictionaries, next level variables must be written in a different line and with an indent. Text variables can be written between simple quotation marks ('), but this is optional. If the definition of a variable is not written,³ its default value will be used (see Section 3).

Below is a list of all the variables with their meaning and possible values:

- **show RADEX plots.** Logical variable that makes the code show a plot of the loss function (the error) between the observed lines and the predicted ones by RADEX with respect to the column density.
- **save RADEX plots.** Logical variable that makes the code save the generated plots.
- **save individual plots.** Logical variable that makes the code save an individual image for each of the generated subplots.
- **load previous results.** Logical variable that makes the code try to load previous results from another RADEX calculation and just plot the results.
- **input files.** Nested variable for specifying the name of the input file.
 - **MADCUBA table.** Transition lines table in .csv format generated by the tool SLIM from the software MADCUBA. To generate it in SLIM, select one of the species in the SimFit tab to open the transition table window, check the Spectral, Fit, and Phys. options, and click the save icon to export the table in .csv format. If there are multiple sources, this variable should be a list. This variable is only needed if the values of the line widths, the temperature, and/or the initial column density are set to be chosen from SLIM.
 - **spectra table.** Table in .csv format with information of the RMS noise and resolution of the spectra used in MADCUBA. Each row, which corresponds to one spectral range, must have a column called rms noise (mK), with the value of the RMS noise of the spectral range. Such a file can be generated by the script `class-pipeline.py` once we have run the steps `--selection`, `--line_search`, and `--reduction`, adding the argument `--spectra_table`. If there are multiple sources, it should be a list. This variable is only needed if one does not specify the values of the RMS noise in the variable RADEX parameters.

3. Here, 'not written' means that neither the variable name nor its value are written in the configuration file. If the variable name is written (and the colon) but its value is not, the corresponding Python variable will get the value `None`.

- **output files.** Nested variable for specifying the names of the output file generated by the script.
 - **RADEX results.** Plain text file in YAML formatting style which contains the values of the minimized column density and its uncertainty for the input molecules, as well as the kinetic temperature which was introduced in the variable RADEX parameters.
- **lines margin (MHz).** Frequency range around the given value of the transitions that will be used by the script to identify each observed line from the lines produced by RADEX.
- **maximum iterations for optimization.** Maximum number of iterations for the optimization method to find the optimal values of the column density.
- **grid points.** Number of points used to calculate the difference between the modelled and observed lines around the optimized value of the column density, in order to estimate the uncertainties.
- **RADEX parameters.** Nested variable with the names of the molecules that will be modeled with RADEX, as they appear in its species catalogue. Each of the names must be also a nested variable with the following next level variables:
 - **MADCUBA name.** The name of the molecule in the transition lines table generated by SLIM, from MADCUBA. This is only needed if the line width, the temperature, and/or the initial column density is set to be taken from MADCUBA.
 - **observed lines.** Dictionary (or nested variable) with the following entries:
 - **frequency (MHz).** Array with the frequencies, in MHz, of the observed lines.
 - **intensity (K).** Array with the intensities, in K, of the observed lines. If there are multiple sources, it should be a list of arrays.
 - **RMS noise (mK).** Array with the values of the RMS noise, in mK, of the spectra in the surroundings of the observed lines. If the value is set to 'auto', the script will use the values from the given .csv table in the variable spectra table. If there are multiple sources, it should be a list of arrays.
 - **background temperature (K).** Background temperature of the source of the observations. If there are multiple sources, it should be a list.
 - **kinetic temperature (K).** Kinetic temperature of the molecule. If the value is set to 'auto', the script will use the value of the excitation temperature of the LTE model done by MADCUBA from the transition lines table of the variable MADCUBA table. If there are multiple sources, it should be a list.
 - **hydrogen number density (/cm³).** Number density of molecular hydrogen (H₂), in /cm³, in the source of the observations. If there are multiple sources, it should be a list.
 - **line width (km/s).** Velocity width, in km/s, of the observed lines. If the value is set to 'auto', the script will use the value of the LTE model done by MADCUBA from the transition lines table of the variable MADCUBA table. If there are multiple sources, it should be a list.

- **column density (/cm²).** Initial value of the column density of the molecule, in / cm², that will be used to minimize the column density with RADEX. If the value is set to 'auto', the script will use the value of the LTE model done by MADCUBA from the transition lines table of the variable MADCUBA table. If there are multiples sources, it should be a list.

Default variable values

Below are the default values of the variables of radexonline.py, that is, the values that they will take if they are not declared in the configuration file.

```
show RADEX plots: yes
save RADEX plots: no
save individual plots: no
load previous RADEX results: no
input files: []
output files:
    radex results: radex-output.yaml
RADEX parameters: []
lines margin (MHz): 0.2
maximum iterations for optimization: 200
grid points points: 21
```

5. Example case

Here we show a brief example to see how to use the script radexonline.py. We will study the two thermodynamical variants of methanol (CH₃OH) named A and E, for two different sources, and making use of the SLIM transition lines table.

5.1. Input files

For this example, we will use four files in .csv format, two for each source:

- **MADCUBA table.** It contains information of all the transitions of the studied species and can be exported in the transition table window in SLIM.
- **spectra table.** It contains information about the observations and can be generated by the Python Reduction Pipeline for CLASS (script classpipeline.py) with the argument --spectra_table.

5.2. Configuration file

Below is an example of configuration file for this example case.

```
show RADEX plots: yes
input files:
    MADCUBA table:
        - L1517B-madcuba.csv
        - L1517B0FF1-madcuba.csv
    spectra table:
        - L1517B-spectra.csv
        - L1517B0FF1-spectra.csv
output files:
    RADEX results: radex-output.yaml
```

```

RADEX parameters:
CH3OH-A:
  MADCUBA name: CH3OH-A,vt=0-2
  observed lines:
    frequency (MHz): [96741.371, 95914.310]
    intensity (K): [[0.63, 0], [0.73, 0]]
    rms noise (mK): ['auto', 'auto']
  background temperature (K): [2.73, 2.73]
  kinetic temperature (K): [10, 10]
  hydrogen number density (/cm3): [2.2e5, 1.235e5]
  line width (km/s): ['auto', 'auto']
  column density (/cm2): ['auto', 'auto']
CH3OH-E:
  MADCUBA name: CH3OH-E,vt=0-2
  observed lines:
    frequency (MHz): [96739.358, 96744.545]
    intensity (K): [[0.44, 0.03], [0.53, 0.04]]
    rms noise (mK): ['auto', 'auto']
  background temperature (K): [2.73, 2.73]
  kinetic temperature (K): [10, 10]
  hydrogen number density (/cm3): [2.2e5, 1.235e5]
  line width (km/s): ['auto', 'auto']
  column density (/cm2): ['auto', 'auto']

```

Note that this default values will only be used if neither the variable name nor its value are written in the configuration file. If the variable name is written (and the colon) but its value is not, the corresponding Python variable will get the value None.

5.3. Output plots

As we set the variable show RADEX plots to yes, a plot with different subplots will be generated for each species and each source. Figure 1 shows one of these plots for the previous configuration file.

5.4. Results of the calculations

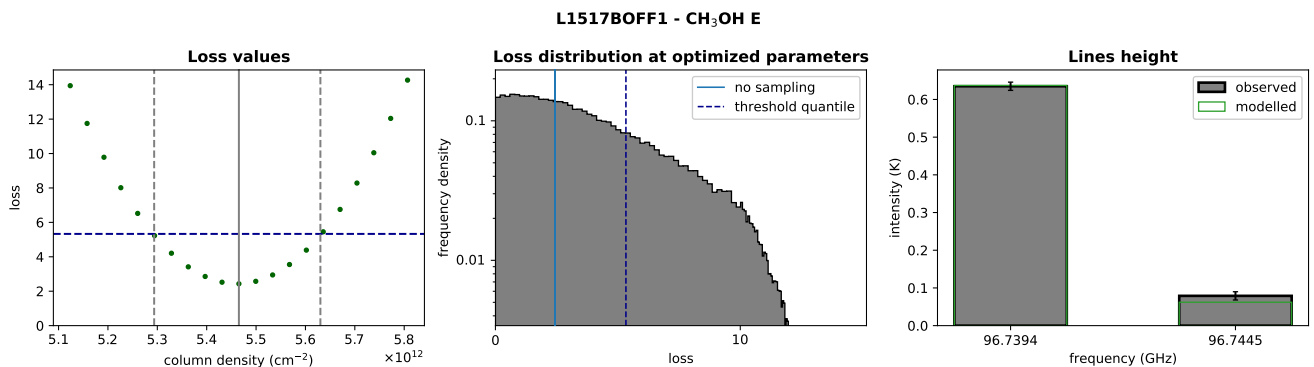


Figure 1. Plots generated for the RADEX calculations for an observation of the pre-stellar core L1517B and for the species methanol E (CH₃OH E). *Left:* Values of the difference between the observed lines and the lines generated by RADEX (the loss function) with respect to different values of the column density. The gray continuous line indicates the fitted value of the column density that minimizes the loss, and the gray dashed lines indicate the uncertainties on the column density. *Center:* Histogram of the values of the loss function obtained when varying the observed line intensities according to the noise (84 % percentile). The blue dashed line indicates the threshold value used to define the uncertainties in the previous plot. *Right:* Scheme of the height of the observed lines, comparing the observed height versus the modelled one.

Below is the content of the output file generated for the previous configuration file.

```

non-LTE molecules:
CH3OH-A:
  column density (/cm2):
  - 4.301-0.058+0.056 e12
  - 4.967+/-0.069 e12
  kinetic temperature (K):
  - 10
  - 10
  lines (GHz):
  '95.914310':
  - intensity (K): '0.003527'
    width (km/s): '0.283'
  - intensity (K): '0.002377'
    width (km/s): '0.283'
  '96.741371':
  - intensity (K): '0.6301'
    width (km/s): '0.283'
  - intensity (K): '0.7301'
    width (km/s): '0.283'
CH3OH-E:
  column density (/cm2):
  - 3.811-0.058+0.049 e12
  - 4.484-0.045+0.041 e12
  kinetic temperature (K):
  - 10
  - 10
  lines (GHz):
  '96.739358':
  - intensity (K): '0.4373'
    width (km/s): '0.283'
  - intensity (K): '0.5291'
    width (km/s): '0.283'
  '96.744545':
  - intensity (K): '0.05488'
    width (km/s): '0.283'
  - intensity (K): '0.05082'
    width (km/s): '0.283'

```

6. Using RADEX Online Python Interface along with SLIM Table Generator

The same configuration file can be used for both RADEX Online Python Interface (radexonline.py) and SLIM Table Generator (slimtables.py),⁴ as they share most of the variables of their configuration files. Basically, we can use the configuration file of slimtables.py and just add the variables show RADEX plots and RADEX parameters.

If we want to use the results of RADEX in the abundances table of slimtables.py, we can copy the results from the output file (named radex-output.yaml by default) to the configuration file. Then we would have to change the name of each molecule, which was its name as in the RADEX catalogue, to the name that will be shown in the table. For example, methanol A (CH₃OH A) is called CH3OH-A in RADEX catalogue, but we may want to name it CH3OH A, which will be displayed as CH₃OH A in the tables generated by slimtables.py. Additionally,

4. Which is part of the MADCUBA-SLIM Python Scripts: <https://github.com/andresmegias/madcuba-slim-scripts>.

the entry lines (GHz) can be deleted, as it is not used by `slimtables.py`.

7. Mathematical basis of the calculations

RADEX is a radiative transfer model that allows us to predict the line intensity of the selected molecule from the following parameters:

- **Molecule.** It has to be included in the molecule RADEX list, therefore having collisional cross-sections derived, experimentally or theoretically.
- **Spectral range.** Frequency range for the transitions to be predicted for the selected molecule.
- **Excitation conditions.**
 - Molecular hydrogen density.
 - Kinetic temperature of the molecule.
 - Background temperature.
- **Radiative transfer parameters.**
 - Column density.
 - Line width.

For each species, the results of the calculation would be a set of intensity lines, $\{\hat{I}_i\}$, where i is the index of the line. There is a set of observed intensities, $\{I_i\}$, from the configuration file, and an uncertainty for each line (the RMS noise), so we will also have a set of uncertainties, $\{\Delta I_i\}$. The rest of the parameters except the column density have to be specified in the configuration file.

The goal is to optimize the column density to minimize the difference between the observed lines, $\{I_i\}$, and the predicted ones, $\{\hat{I}_i\}$, taking into account the uncertainties, $\{\Delta I_i\}$. To measure that difference, one has to define a loss function, \mathcal{L} , which we choose to be the chi-square (χ^2) error:

$$\mathcal{L} = \sum_i \left(\frac{\hat{I}_i - I_i}{\Delta I_i} \right)^2 .$$

In this way we are measuring the quadratic error weighted with the inverse of the uncertainty, so that a difference between the observations and the model contributes less to the loss if the line uncertainty is greater.

Once the loss function is properly defined, it can be minimized with respect to the column density. This calculation is done with the library SciPy, using the function `minimize`. In particular, the script uses the method COBYLA with one variable and the method Nelder-Mead for two variables.

Finally, we have to estimate the uncertainty for the optimized value of the column density. To do so, we take a threshold for the loss, greater than the minimized value, which defines a lower and an upper uncertainty. In order to find a proper threshold, the script creates 10^5 sets of variations of the observed intensities, $\{I_{ij}\}$, so that the value of each intensity, I_{ij} , comes from a normal distribution with median I_i and standard deviation ΔI_i . Then, the loss, \mathcal{L} , is calculated for the optimized model for each set of intensities $\{I_{ij}\}$, obtaining a distribu-

tion of losses (see figure 1, lower-left plot). We choose the threshold so that the loss values less than it are the 68.27 % of the total values (similarly to the definition of 1σ confidence interval, but for an asymmetric distribution with a minimum value); that is, the threshold is the 68.27 percentile.

Now, the script will explore our parameter space of the column density around the minimized value in order to find when the loss function reaches our threshold value. It is only necessary to calculate the loss function in the surroundings of the minimized value until we reach the threshold value (see figure 2, upper plots). Therefore, the uncertainties are defined within the parameter space that make the loss lower than the threshold value.

Useful links

The following links may be of interest:

- **RADEX Online.**
<http://var.sron.nl/radex/radex.php>
- **MADCUBA.**
<https://cab.inta-csic.es/madcuba/>
- **MADCUBA-SLIM Python Scripts.**
<https://github.com/andresmegias/madcuba-slim-scripts>
- **Python Reduction Pipeline for CLASS.**
<https://github.com/andresmegias/gildas-class-python>
- **Python.**
<https://www.python.org/>
- **Python's standard library.**
<https://docs.python.org/3/library/>
- **PyYAML.**
<https://pyyaml.org/wiki/PyYAMLDocumentation/>
- **NumPy.**
<https://numpy.org/>
- **Pandas.**
<https://pandas.pydata.org/>
- **Matplotlib.**
<https://matplotlib.org/>
- **SciPy.**
<https://scipy.org/>
- **Beautiful Soup.**
<https://www.crummy.com/software/BeautifulSoup/>
- **RichValues.**
<https://github.com/andresmegias/richvalues/>

Credits

This software has been developed at the Center for Astrobiology (*Centro de Astrobiología*, CAB), in Madrid (Spain), within the subgroup of Astrochemistry and Chemical Complexity (Group of Interstellar and Circumstellar Medium, Department of Astrophysics).

Coding and testing

Andrés Megías Toledano

Supervising

Izaskun Jiménez Serra

License

The library RADEX Online Python Interface (`radexonline.py`) is published under a GNU General Public License (GPL) version 3.

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