

RADEX Python Interface

(radex.py)

User Guide

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1. Introduction

The RADEX Python Interface is a Python 3 script, `radex.py`, that uses RADEX software¹ to make a non-LTE fit (LTE: *Local Thermodynamical Equilibrium*) to the observed lines and derive the column density of the species, and optionally also the molecular hydrogen (H₂) number density or the kinetic temperature of the molecule.

First of all, the script requires the software RADEX to be installed locally in your computer.¹ With regard to Python, the script requires the modules `os`, `re`, `io`, `sys`, `copy`, `time`, `pickle`, and `platform`, from the Python's standard library, and also the libraries `PyYAML`, `NumPy`, `Pandas`, `Matplotlib`, `SciPy`, 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 `radex.py`:

```
python3 radex.py <path> .
```

The argument `<path>` is the path of the configuration file. If we do not specify it, the script will search in the current folder (`./`) for the configuration file specified inside the script

1. <https://personal.sron.nl/~vdtak/radex/index.shtml>

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

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 `radex.py` is not in the current folder, but in a folder with path `<folder>`, we should write `<folder>/radex.py` instead of `radex.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

In order to run calculations for a certain species, you need a file containing physical and thermodynamical information about the species. It can be downloaded from the LAMDA database³ (Leiden Atomic and Molecular Database). Once downloaded, it has to be placed inside the subdirectory `data/` inside the RADEX local folder. Lastly, it should have the same name as in the RADEX Online species list,⁴ so you may have to rename the file.

Additionally, 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.
- **processing 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_tables`). 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 four entries: one for the column density (column density (/cm²)), one for the kinetic temperature (kinetic temperature (K)), other for the molecular hydrogen number density (hydrogen number density (/cm³)), and another regarding the lines fit (lines (GHz)). Except for the

3. <https://home.strw.leidenuniv.nl/~moldata/>

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

last entry, this variable has the same structure as the corresponding variable for the SLIM Table Generator (tablegenerator.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, several plots may 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, and showing also the intensity of the predicted lines versus the observed ones.

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 radex.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,⁵ 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.

5. 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.

- **processing 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 classpipeline.py once we have run the steps --selection, --line_search, and --reduction, adding the argument --spectra_tables. 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.
- **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.
- **RADEX fit parameters.** Text variable that indicates which parameters should be optimized when minimizing the difference between the observed and modelled lines. Possible values, which are self-explanatory, are 'column density', 'column density, H2 number density', and 'column density, kinetic temperature'.
- **maximum iterations for optimization.** Maximum number of iterations for the optimization method to find the optimal values of the variable/s.
- **grid points.** In case that two variables are being optimized, this variable sets the number of points that will have one side of the grid used to explore the parameter space to calculate 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 processing table. If there are multiple sources, it should be a list of arrays.
 - **background temperature (K).** Background temperature of the source of the obser-

variations. If there are multiples 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 multiples 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 multiples 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 multiples 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.
- **fit parameters**. Text variable that indicates which parameters should be optimized when minimizing the difference between the observed and modelled lines, but only for this specific species. Possible values are 'column density', 'column density, H2 number density', and 'column density, kinetic temperature'.

Default variable values

Below are the default values of the variables of radex.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: []
RADEX fit parameters: 'column density'
lines margin (MHz): 0.2
maximum iterations for optimization: 200
grid points: 15
```

5. Example case

Here we show a brief example to see how to use the script radex.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. For methanol A, we will only fit the column density, but for methanol E we will also fit the H₂ number density, as we have two observed transitions.

5.1. Input files

For this example, we need to download the molecular data files for methanol A and E from the LAMDA database.⁶ The files are named `ch3oh_a.dat` and `e-ch3oh.dat`, so we have to rename the first one to `a-ch3oh.dat` and place both files inside the subdirectory `data/` inside the RADEX directory. Moreover, 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.
- **processing 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_tables`.

5.2. Configuration file

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

```
show RADEX plots: yes
save RADEX plots: yes
save individual plots: yes
RADEX fit parameters: 'column density, H2 column density'
input files:
  MADCUBA table:
  - L1517B-madcuba.csv
  - L1517B0FF1-madcuba.csv
  processing table:
  - L1517B-processing.csv
  - L1517B0FF1-processing.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]]
    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']
    fit parameters: 'column density'
  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]]
    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']
```

6. <https://home.strw.leidenuniv.nl/~moldata/>

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 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

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

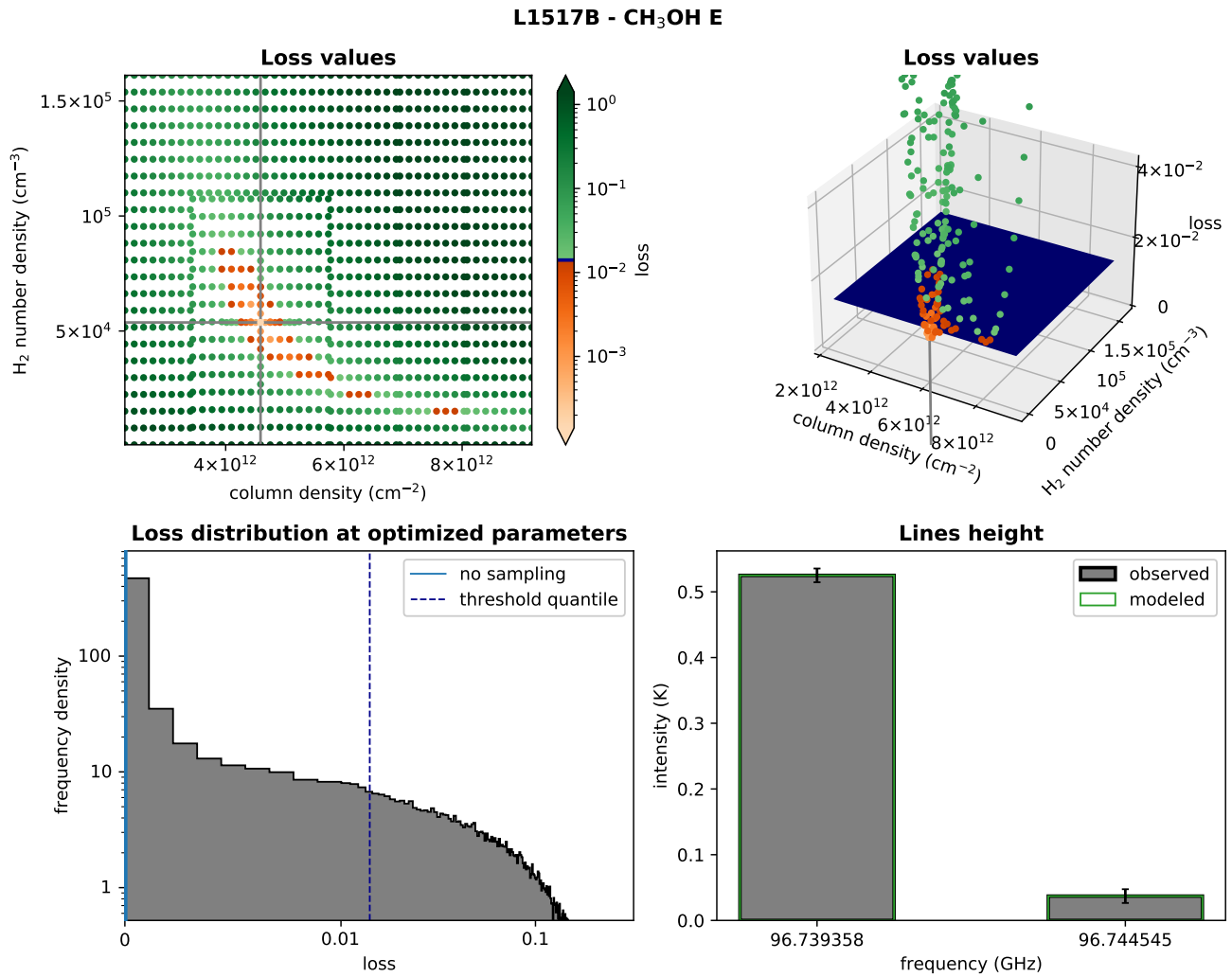


Figure 1. Plots generated for the RADEX calculations for an observation of the pre-stellar core L1517B and for the species methanol E (CH₃OH E). *Upper-left:* Values of the difference between the observed lines and the lines generated by RADEX (the loss function) with respect to different values of the column density. The gray lines indicates the fitted values of the column density and H₂ number density that minimize the loss. *Upper-right:* Same as the previous plot, but in 3 dimensions. *Lower-left:* Histogram of the values of the loss function obtained when varying the observed line intensity according to the noise. The blue dashed line indicates the threshold value used to define the uncertainties in the previous plot. *Lower-right:* Scheme of the height of the observed lines, comparing the observed height versus the modelled one.

```

non-LTE molecules:
CH3OH-A:
  column density (/cm2):
  - 4.705-0.035+0.033 e12
  - 5.476-0.037+0.036 e12
  hydrogen number density (/cm3):
  - 2.2e5
  - 1.235e5
  kinetic temperature (K):
  - 10
  - 10
  lines (GHz):
    '96.741371':
      - intensity (K): '0.6872'
        width (km/s): '0.283'
      - intensity (K): '0.8001'
        width (km/s): '0.283'
CH3OH-E:
  column density (/cm2):
  - 4.59-0.66+3.29 e12
  - 5.62+/-0.30 e12
  hydrogen number density (/cm3):
  - 5.4-3.9+3.1 e4
  - 2.05+/-0.29 e5
  kinetic temperature (K):
  - 10
  - 10
  lines (GHz):
    '96.739358':
      - intensity (K): '0.525'
        width (km/s): '0.283'
      - intensity (K): '0.635'
        width (km/s): '0.283'
    '96.744545':
      - intensity (K): '0.037'
        width (km/s): '0.283'
      - intensity (K): '0.079'
        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 Python Interface (`radex.py`) and SLIM Table Generator (`slimtables.py`)⁷ as they share most of the variables of their configuration files. Basically, we can use the configuration file of `tablegenerator.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,

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

which will be displayed as CH₃OH A in the tables generated by slimtables.py. Additionally, the entry lines (GHz) can be deleted, as it is not used by slimtables.py.

Useful links

The following links may be of interest:

- **RADEX Online.**
<https://personal.sron.nl/~vdtak/radex/index.shtml>
- **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/>
- **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

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License

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