



# **RMG-Py and Arkane Documentation**

*Release 3.2.0*

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RMG is an automatic chemical reaction mechanism generator that constructs kinetic models composed of elementary chemical reaction steps using a general understanding of how molecules react. This documentation is for the newer Python version of RMG that we call RMG-Py.

I want to...	Resource
analyze models & search databases	<a href="#">RMG website resources</a> (no download needed)
create mechanisms automatically	Download RMG with the RMG User's Guide
make transition state theory calculations	Run Arkane after downloading RMG. See the Arkane User's Guide
post an issue with RMG	<a href="#">GitHub issues page</a>
contribute to the RMG project	<a href="#">RMG developer's wiki</a>

Arkane is developed and distributed as part of RMG-Py, but can be used as a stand-alone application for Thermochemistry, Transition State Theory, and Master Equation chemical kinetics calculations. Its user guide is also included.

The last section of this documentation covers some of the more in depth theory behind RMG and Arkane.

Please visit <https://reactionmechanismgenerator.github.io/RMG-Py/> for the most up to date documentation and source code. You may refer to the separate *RMG-Py API Reference* document to view the details of RMG-Py's modules and subpackages.



## RMG USER'S GUIDE

For any questions related to RMG and its usage and installation, please post an issue at <https://github.com/ReactionMechanismGenerator/RMG-Py/issues> and the RMG developers will get back to you as soon as we can. You can also search for your problem on the issues page to see if there are already solutions in development. Alternatively, you can email us at [rmg\\_dev@mit.edu](mailto:rmg_dev@mit.edu).

### 1.1 Introduction

**Reaction Mechanism Generator (RMG)** is an automatic chemical reaction mechanism generator that constructs kinetic models composed of elementary chemical reaction steps using a general understanding of how molecules react. This version is written in Python, and called RMG-Py.

#### 1.1.1 License

RMG is an open source program, available to the general public free of charge. The primary RMG code is distributed under the terms of the [MIT/X11 License](#). However, RMG has a number of dependencies of various licenses, some of which may be more restrictive. **It is the user's responsibility to ensure these licenses have been obtained.**

Copyright (c) 2002-2022 Prof. William H. Green ([whgreen@mit.edu](mailto:whgreen@mit.edu)),  
Prof. Richard H. West ([r.west@neu.edu](mailto:r.west@neu.edu)) and the RMG Team ([rmg\\_dev@mit.edu](mailto:rmg_dev@mit.edu))

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## 1.2 Overview of Features

### Thermodynamics estimation using group additivity.

Group additivity based on Benson's groups provide fast and reliable thermochemistry estimates. A standalone utility for estimating heat of formation, entropy, and heat capacity is also included.

### Rate-based model enlargement

Reactions are added to the model based on their rate, fastest first.

### Rate-based termination.

The model enlargement stops when all excluded reactions are slower than a given threshold. This provides a controllable error bound on the kinetic model that is generated.

### Extensible libraries

Ability to include reaction models on top of the provided reaction families.

### Pressure-dependent reaction networks.

Dissociation, combination, and isomerization reactions have the potential to have rate coefficients that are dependent on both temperature and pressure, and RMG is able to estimate both for networks of arbitrary complexity with a bounded error.

### Simultaneous mechanism generation for several conditions.

Concurrent generation of a reaction mechanism over multiple temperature and pressure conditions. Mechanisms generated this way are valid over a range of reaction conditions.

### Dynamic simulation to a target conversion or time.

Often the desired simulation time is not known *a priori*, so a target conversion is preferred.

### Transport properties estimation using group additivity

The Lennard-Jones sigma and epsilon parameters are estimated using empirical correlations (based on a species' critical properties and acentric factor). The critical properties are estimated using a group-additivity approach; the acentric factor is also estimated using empirical correlations. A standalone application for estimating these parameters is provided, and the output is stored in CHEMKIN-readable format.

## 1.3 Installation

---

**Note:** It is recommended that RMG be installed with Python 3.7. Legacy releases compatible with Python 2.7 are also available.

---

For any questions related to RMG and its usage and installation, please post an issue at <https://github.com/ReactionMechanismGenerator/RMG-Py/issues> and the RMG developers will get back to you as soon as we can. You can also search for your problem on the issues page to see if there are already solutions in development. Alternatively, you can email us at [rmg\\_dev@mit.edu](mailto:rmg_dev@mit.edu)



### 1.3.1 Installation on a Windows Platform

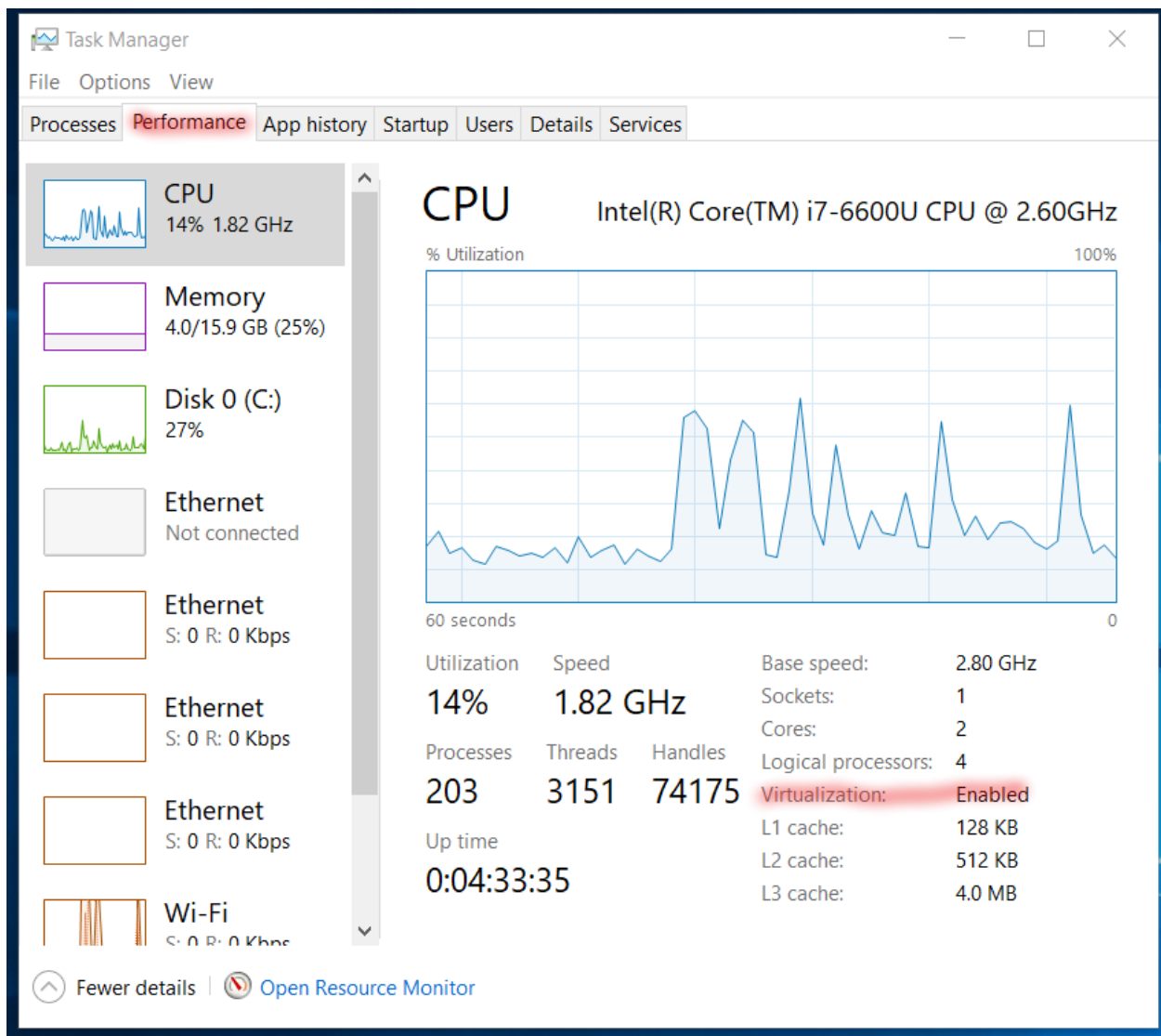
Due to difficulties with dependencies, installation on Windows directly is no longer supported. Instead, it is recommended to run a Linux virtual machine from Windows and follow either the instructions for basic users (binary installation using Anaconda) or the instructions for developers. Alternatively, it is also possible to install RMG in the Ubuntu subsystem now available on Windows 10.

#### Setting up a Linux Virtual Machine from Windows

##### Checking if Virtualization Technology is Enabled

While most PCs have CPUs that support running virtual machines (i.e. virtualization technology), it is possible that this feature has been disabled in your BIOS settings. If this is the case, then you will have to enable this technology in your BIOS settings.

First, check to see if virtualization technology is currently enabled on your computer by opening the Task Manager in Windows 8/10. Click on the Performance tab—from here you can see if virtualization technology is enabled.



For Windows 7 or earlier you can download and run [Microsoft's Virtualization Detection Tool](#).

If enabled, you can continue on with installing a virtual machine on your PC. If virtualization is currently disabled, though, you will have to enable this from the BIOS setting on your computer. How to do this varies from PC to PC (we recommend doing a quick google search for your make/model, as there are many instructions for this online), but the basic steps are as follows:

1. Restart the PC. As soon as the PC turns back on, enter the BIOS settings (this usually involves pressing the F2 or F12 keys, but will depend on your make/model). If you see the computer loading Windows then you have missed the opportunity, and should restart the PC to try again. If Secure Boot is enabled on your PC then there may be additional steps to reaching the BIOS settings (for example see these [instructions](#)).
2. From the BIOS settings, find the section on virtualization, and enable the virtualization technology. Save these changes and restart the PC.

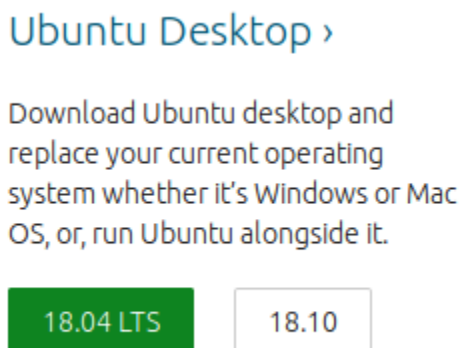
For more information, please see online tutorials like [this one here](#).

**Note that changing your BIOS settings can be risky, so follow online tutorials carefully.** If you are unsure of what to do even after looking for online tutorials, consider following the instructions for installing RMG inside the Linux subsystem in Windows 10 (*[Installing RMG in the Linux Subsystem on Windows 10](#)*)

### Downloading a Linux .iso File

If this is your first time using a Linux operating system, we recommend using Ubuntu 18.04, as it is one of the most popular Linux distributions out there, with plenty of support available online. Otherwise you are welcome to try out any other Linux distribution you like (see [Linux DistroWatch](#)).

1. Go to the [Ubuntu](#) website and click on the download link for 18.04 LTS (Desktop, not Server). Note that newer versions of Ubuntu might be available, but we recommend downloading only the LTS (long term support) versions. Note that Ubuntu is completely free to download and use, so you do not need to make a donation if prompted.



2. The .iso file is typically around 2 GB in size, so the file will take a while to download. While this is happening, feel free to proceed with the remaining sections.

## Choosing a VM Software

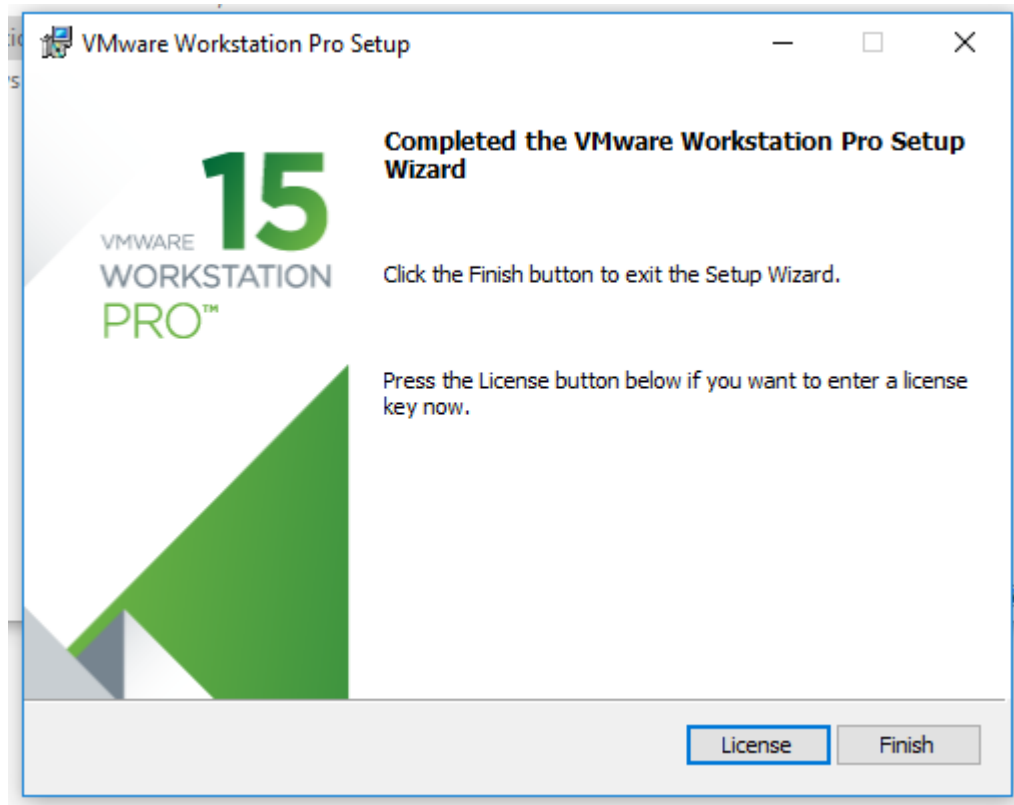
There are quite a few software options for running a virtual machine from Windows, including [VMware Workstation Pro](#) and [Oracle VirtualBox](#). VMware Workstation Pro is the recommended choice, though check to see if your institution has access to it (since it is not free). If not, VirtualBox (which is free) runs well and will work just as fine. Use the hyperlinks below to jump ahead to the setup instructions for the virtual machine software of your choice.

*[Setting up a Linux Virtual Machine using Workstation Pro](#)*

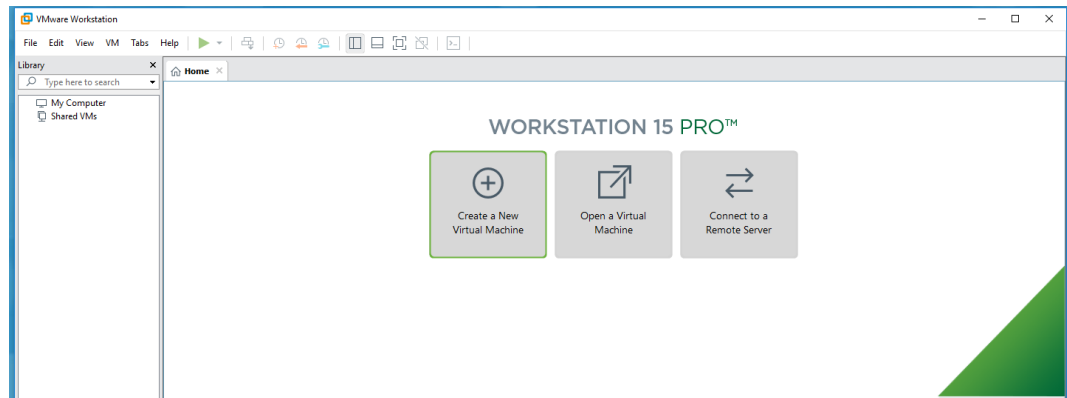
*[Setting up a Linux Virtual Machine using VirtualBox](#)*

## Setting up a Linux Virtual Machine using Workstation Pro

1. Follow your institution's instructions for downloading VMware Workstation Pro and obtaining the required license key.
2. At the end of the installation process for Workstation Pro, remember to enter in the required license key.



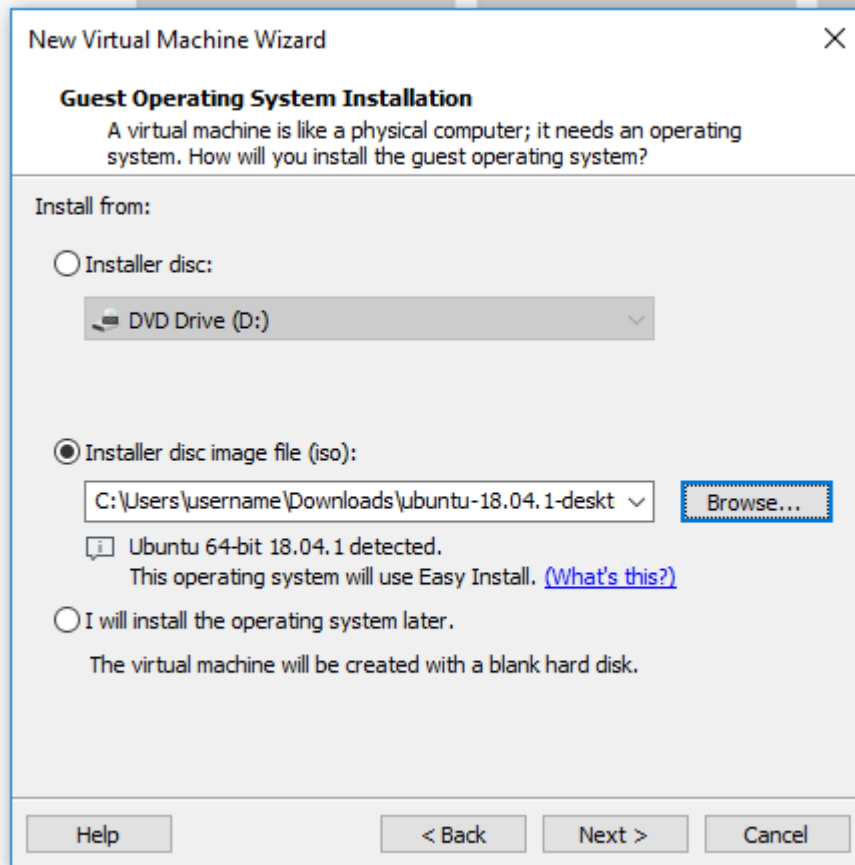
3. From Workstation Pro click on the Create a New Virtual Machine icon.



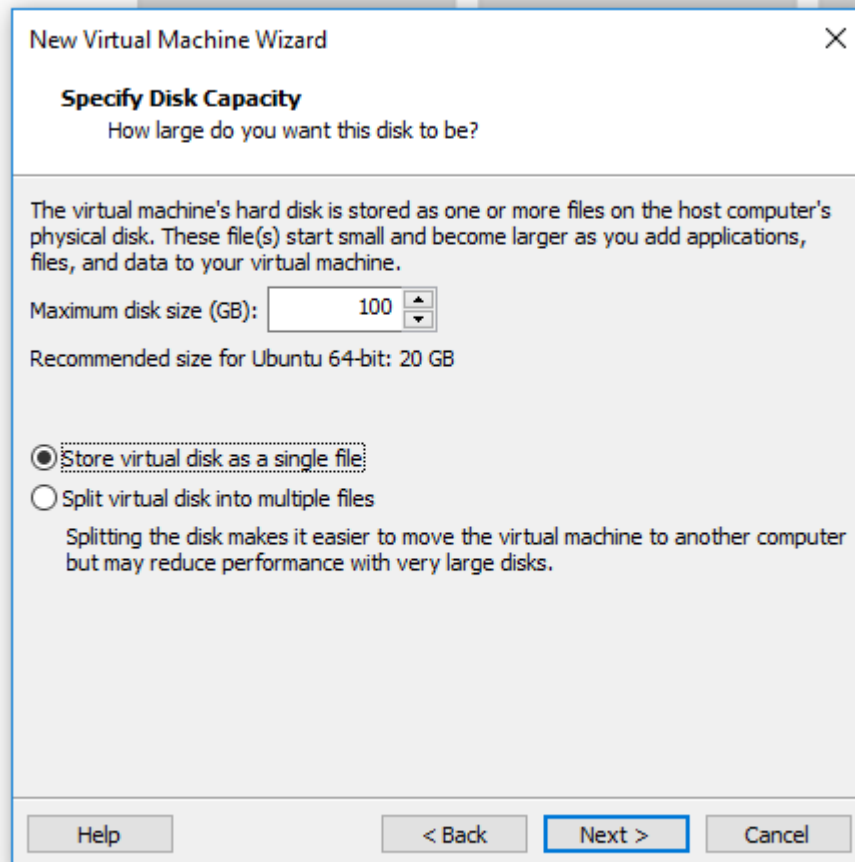
4. Choose a typical installation.



5. On the Guest Operating System Installation page, choose Installer disc image file (iso) and browse for the Ubuntu .iso file you downloaded previously. If found correctly you should see a message indicating that an Ubuntu operating system was detected.



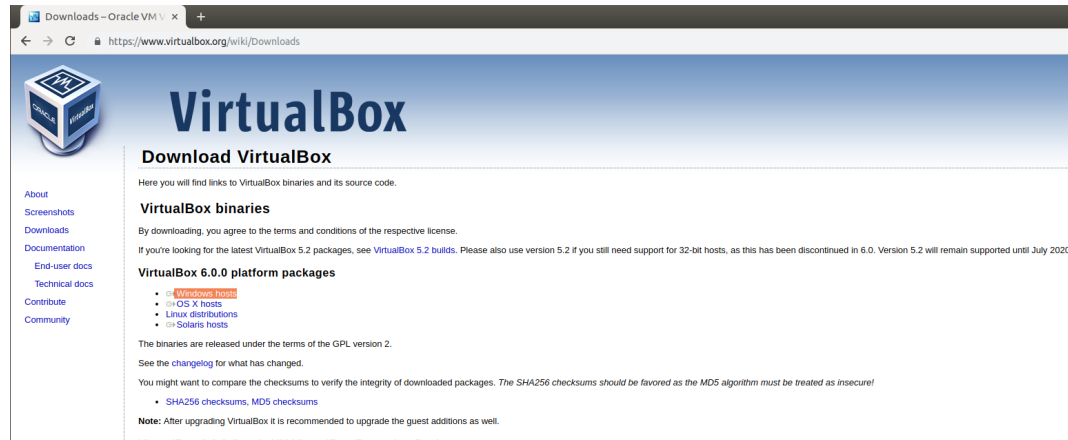
6. On the Specify Disk Capacity page create a disk with **no smaller than 50 GB**.



7. At some point after finishing the install, you will want to go into the settings of the VM and increase the number of CPUs allocated to the VM as well as increasing the memory.
8. To continue with installing RMG, follow the instructions for Linux and Mac OSX systems.

### Setting up a Linux Virtual Machine using VirtualBox

1. Go to the [Oracle VirtualBox](#) website and click on the download link for “Windows hosts” (highlighted orange in the image below)

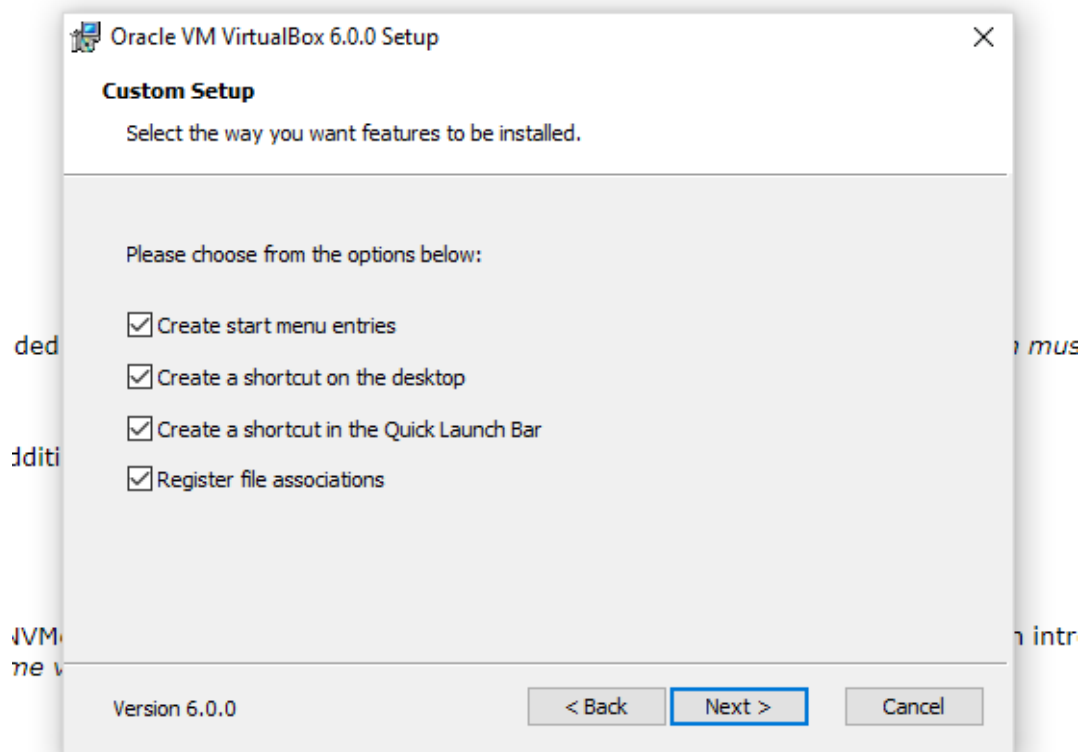
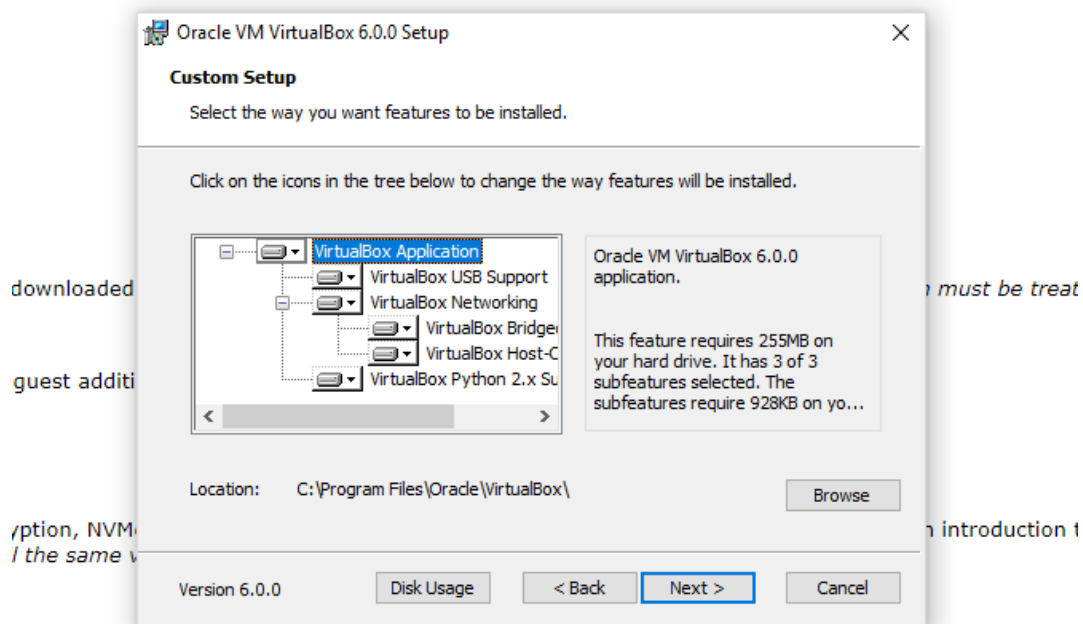


2. Once the download is complete, launch the executable. Select the “Next” button a few times to install VirtualBox with the default settings. If prompted download any necessary drivers. After installation, launch VirtualBox.

**5.2 builds.** Please also use version 5.2 if you still need support for 32-bit hosts, as this h

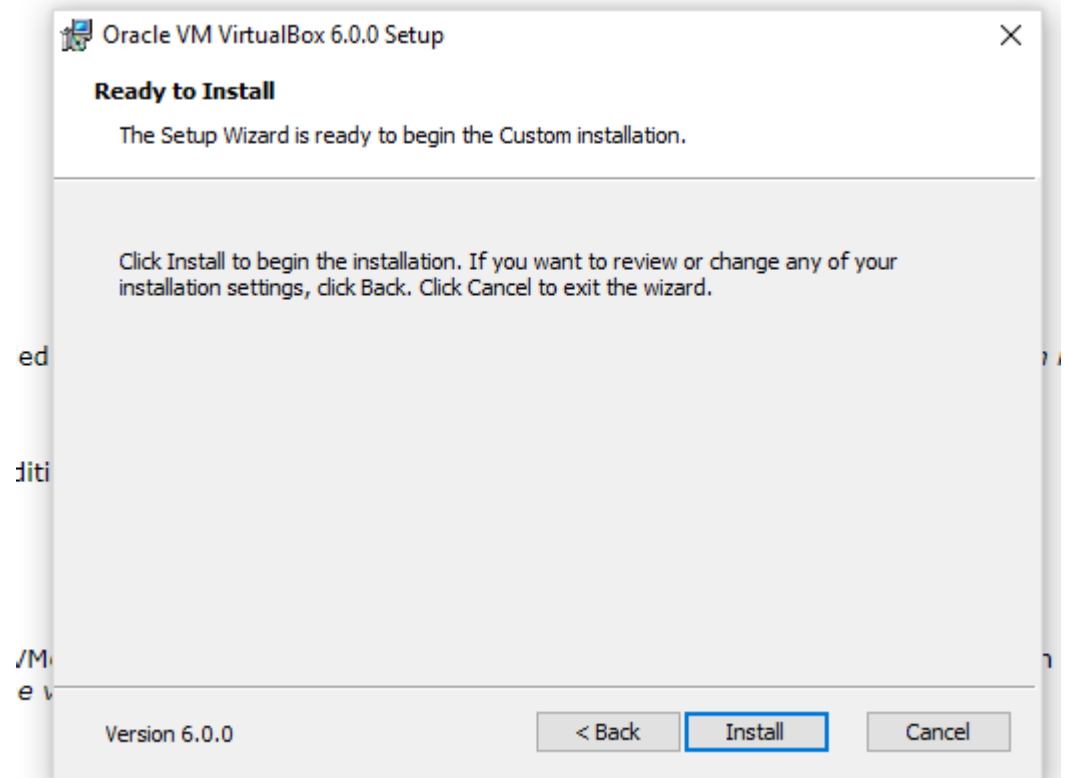
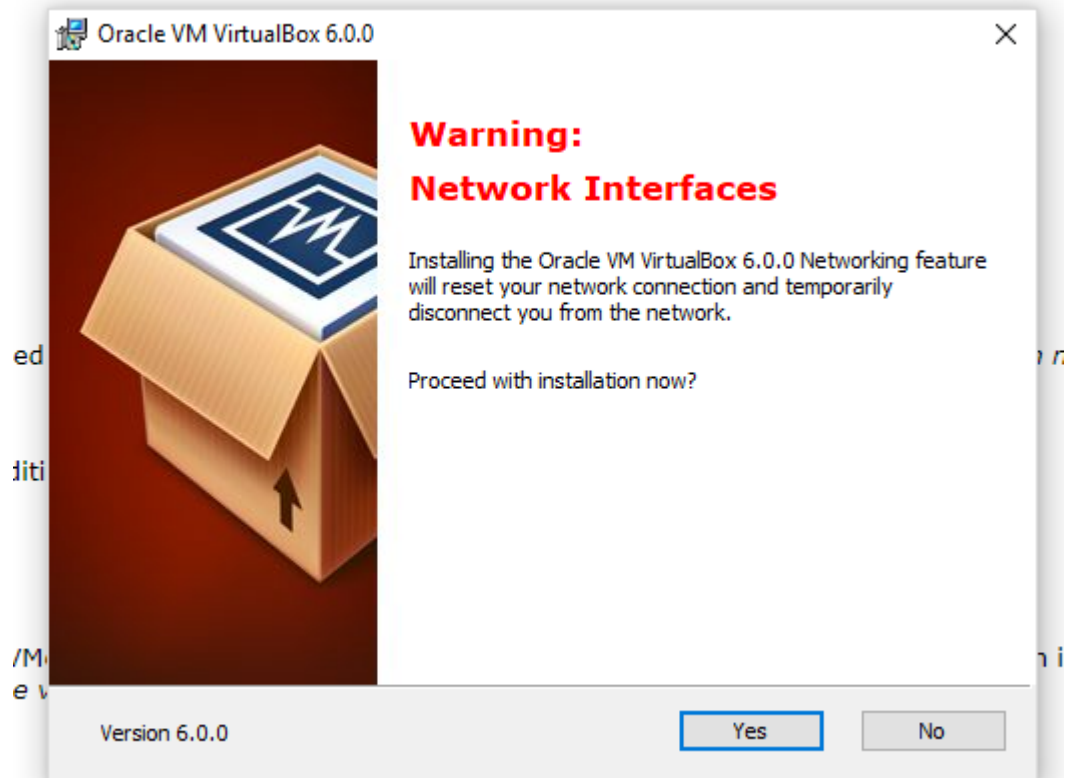


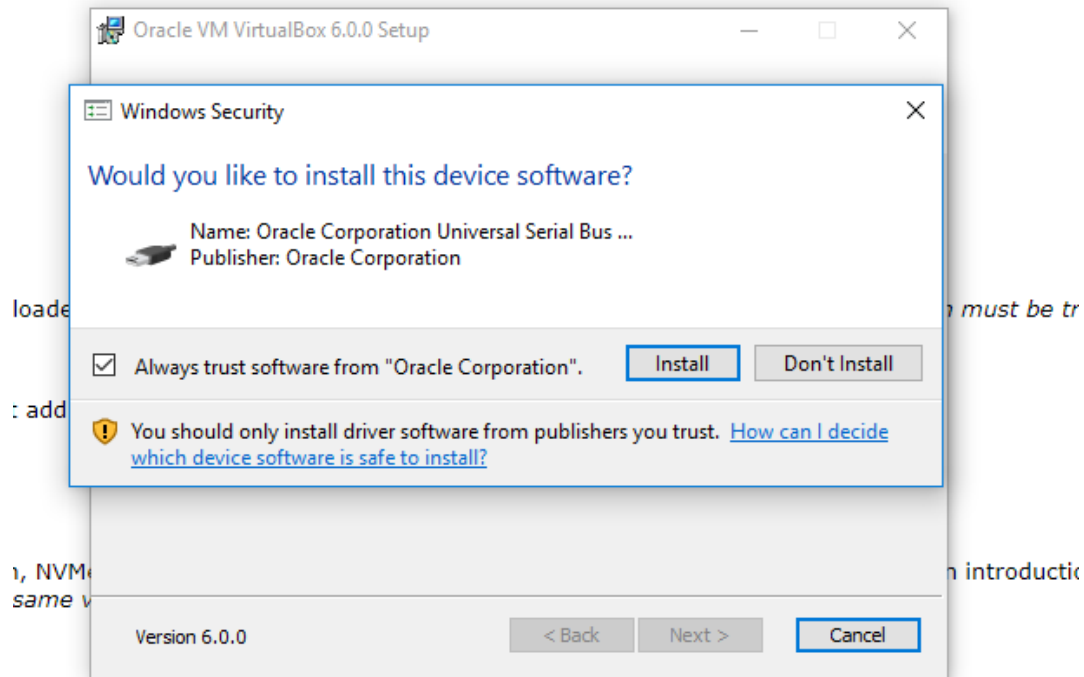
or 5.2 builds. Please also use version 5.2 if you still need support for 32-bit hosts, as this has been dis



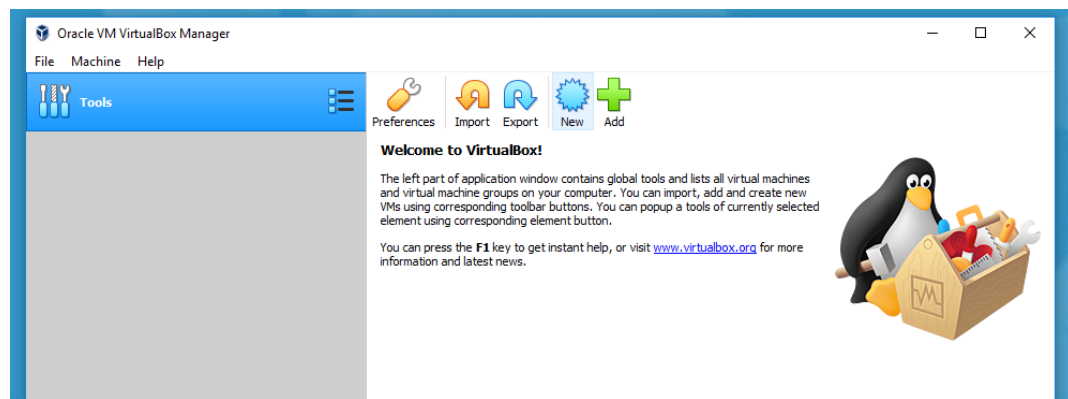


...Please also use Version 6.0.0 if you can (see support for 6.0.0 below), as this

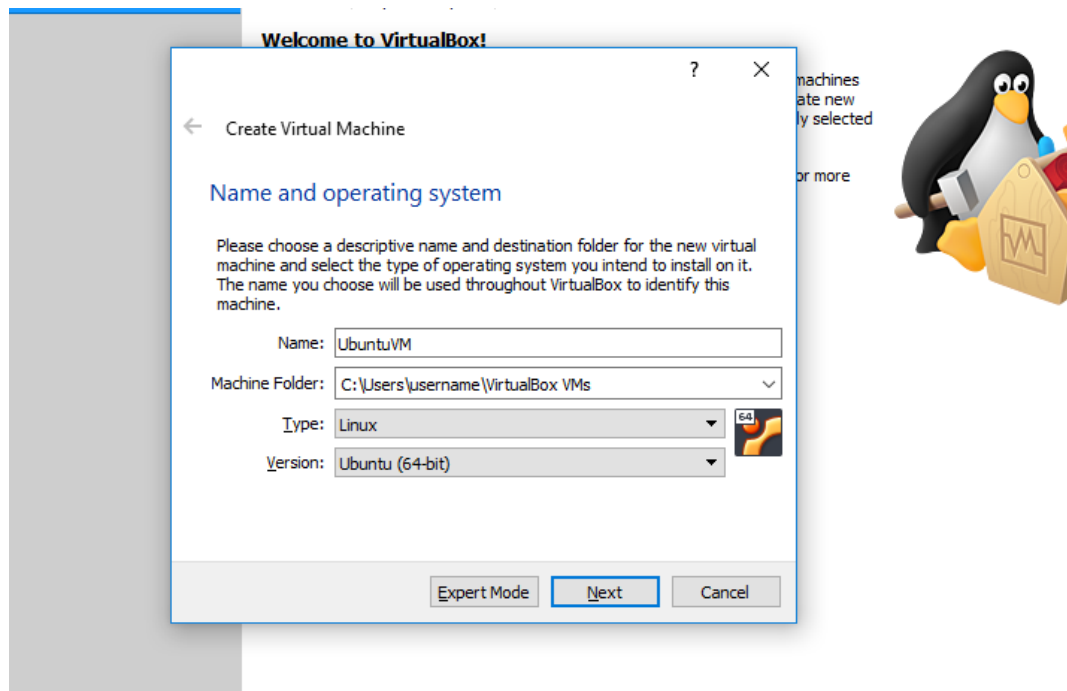




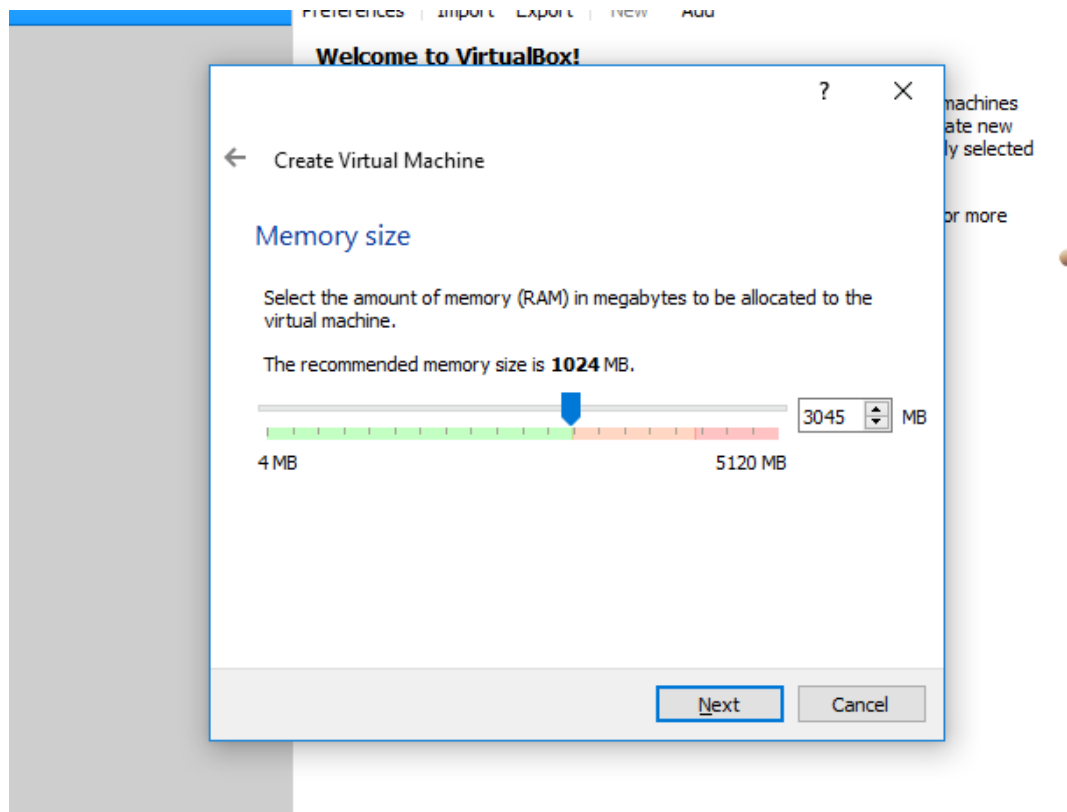
3. From the VirtualBox Manager window, click on the blue star labeled “New” to begin creating your Linux virtual machine.



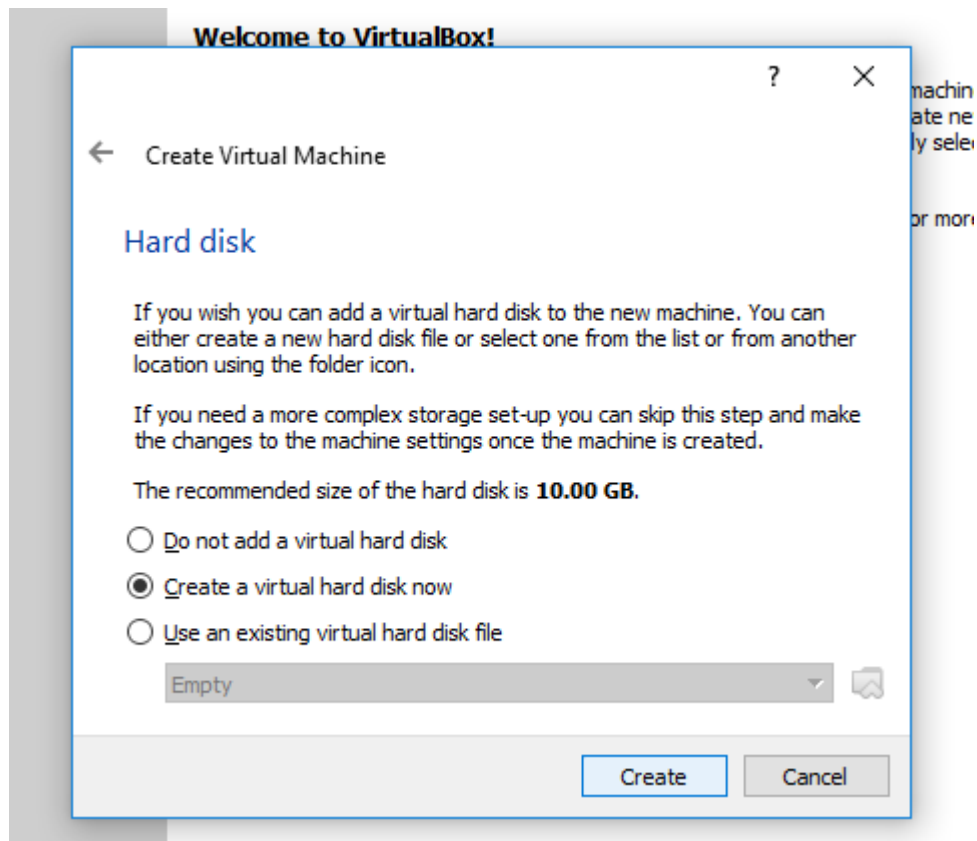
4. Give your new virtual machine a name (it can be anything you want, so long as you can recognize it by its name). Make sure that the Type is set to Linux and that the version is set to Ubuntu (64-bit). Then click “Next”.



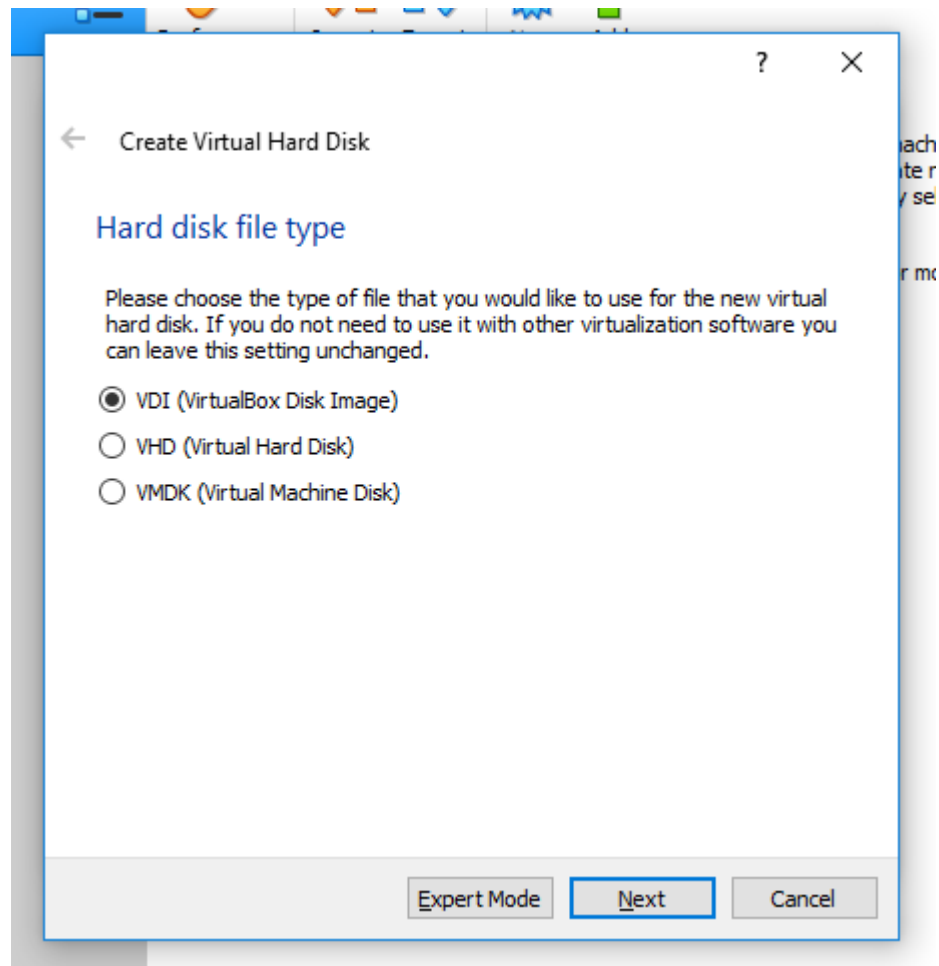
5. Move the slider for the memory size to the far right of the green section, giving your VM as much memory as you can without leaving too little for the host (Windows) OS.



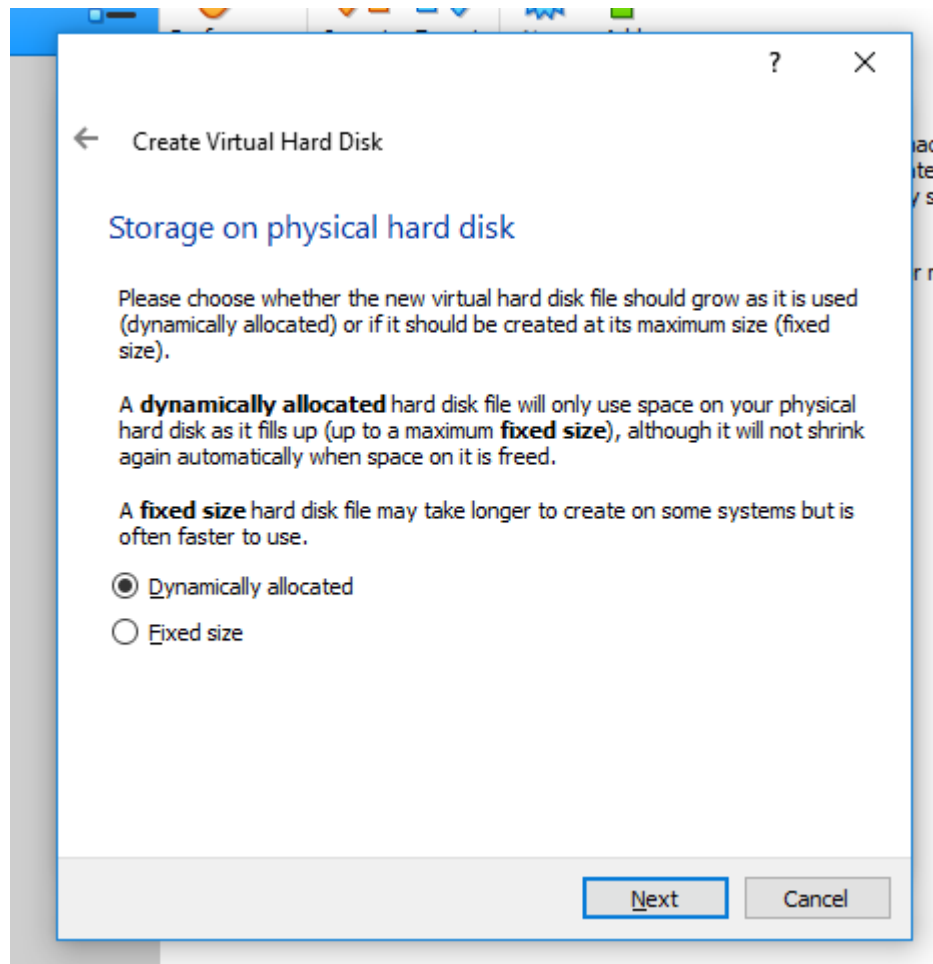
6. Create a virtual hard disk to store the data for your Linux VM by selecting Create a virtual hard disk now.



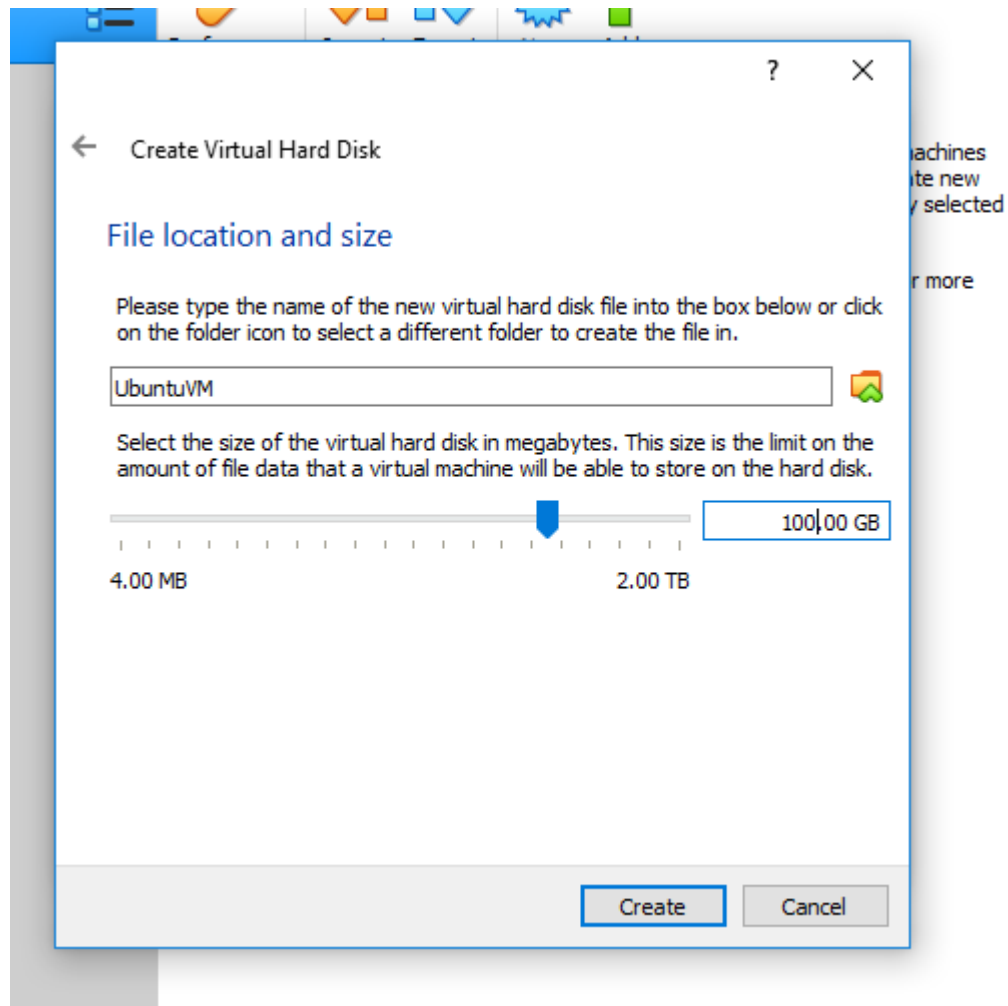
7. Choose VDI as the virtual hard disk type.



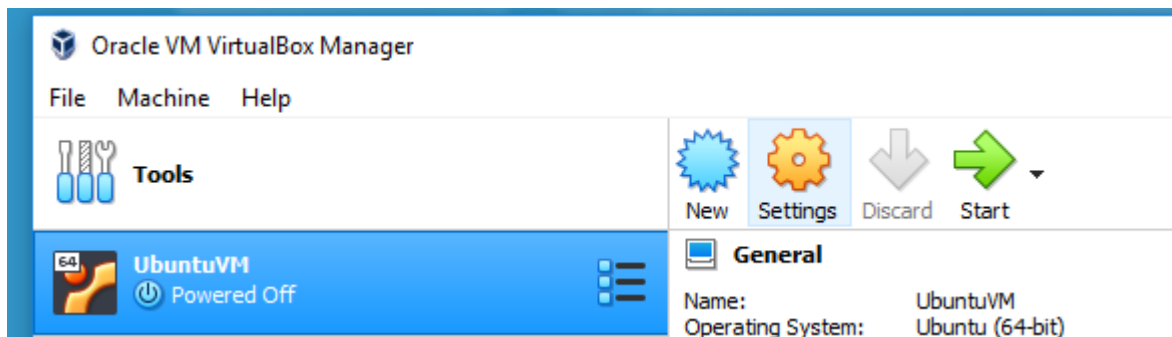
8. Choose Dynamically allocated as the storage type, so that your virtual hard disk does not take up more space than it needs to.



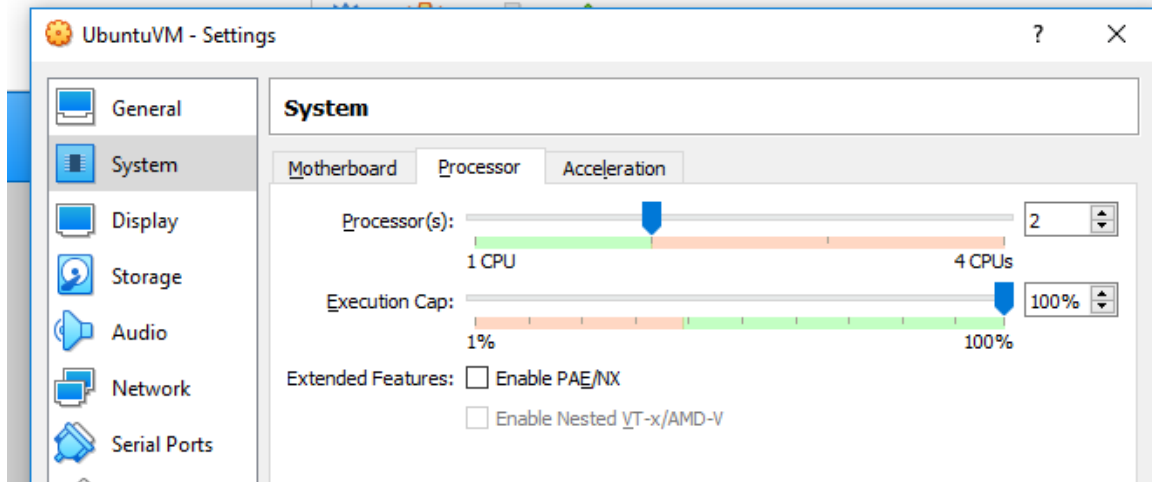
9. Set the size of the virtual hard disk to be **no smaller than 50 GB**. If you chose dynamically allocated in the previous step the full 50 GB won't be used initially anyways.



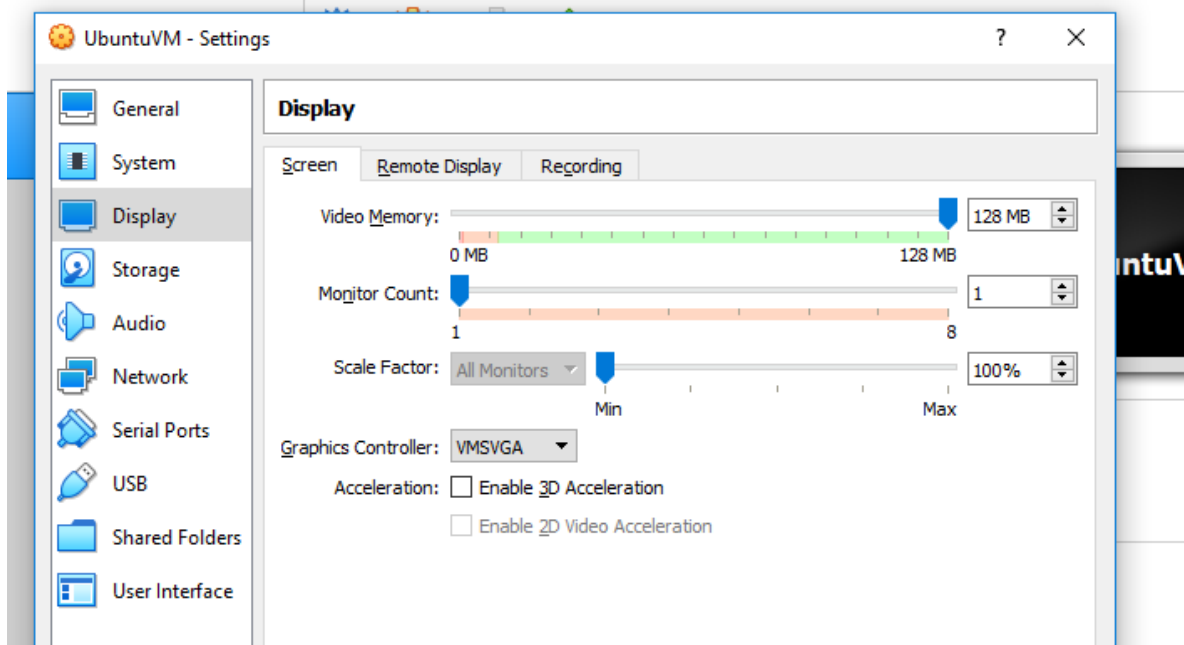
10. Click on the yellow gear labeled Settings.



11. From the System menu (left column), go to the Processor tab and increase the number of CPUs all the way to the right side of the green region.

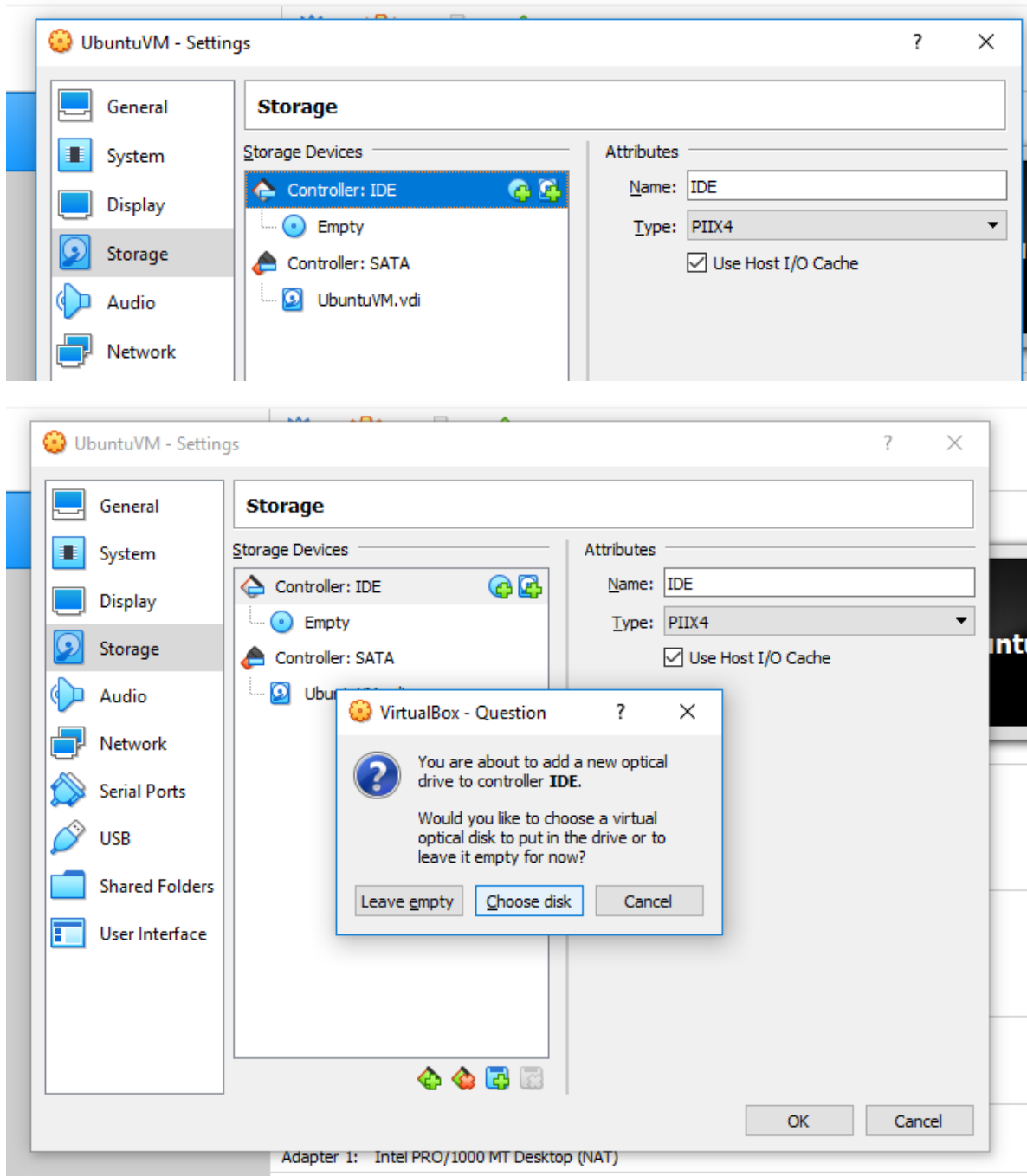


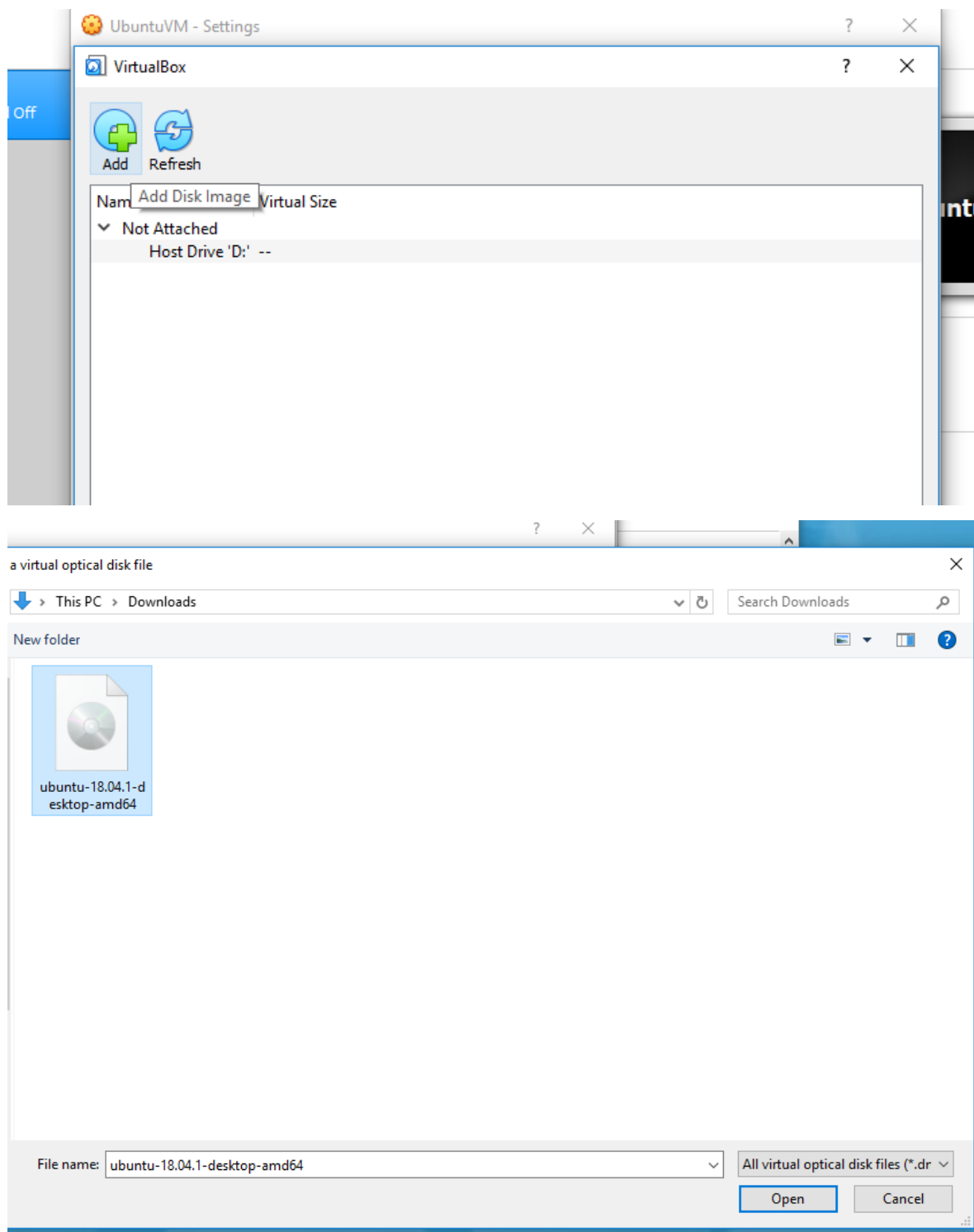
12. From the Display menu, go to the Screen tab and max out the video memory.



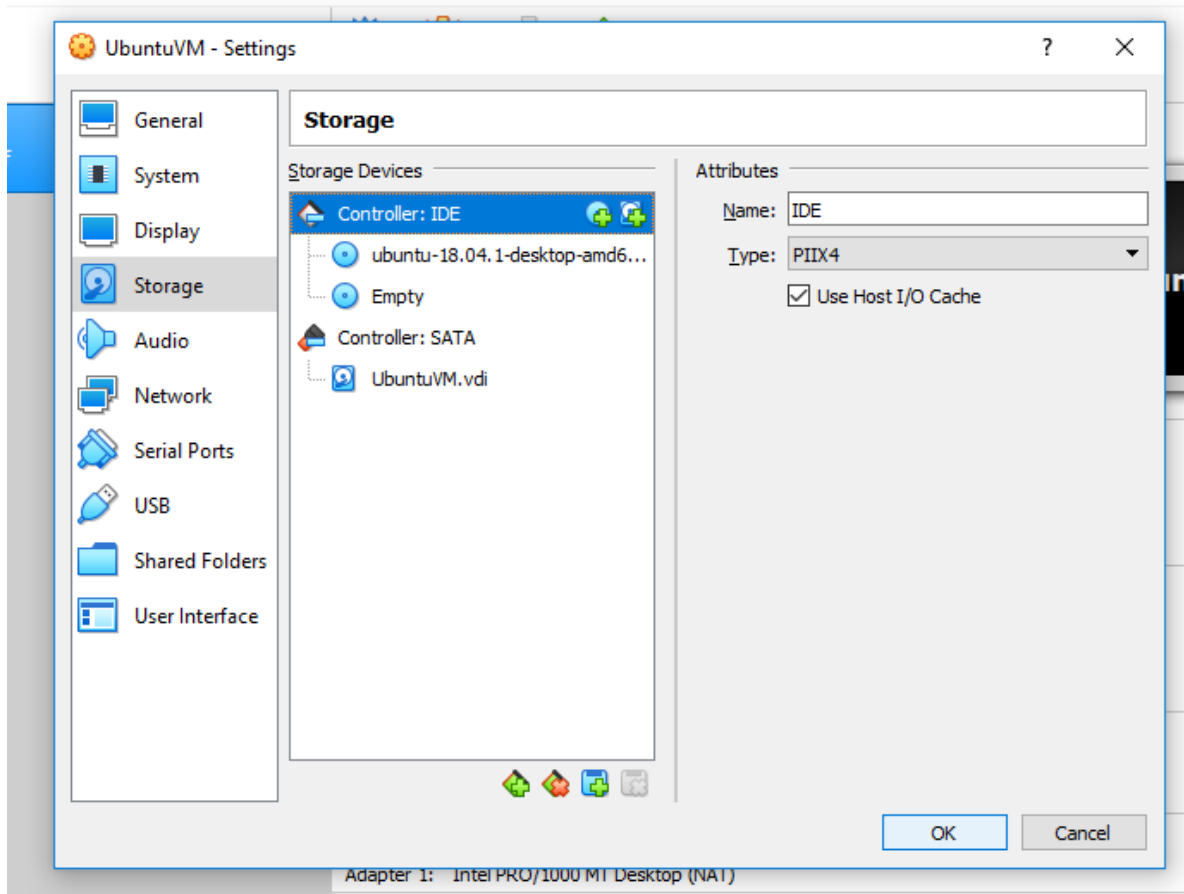
13. From the Storage menu, click on the Add optical drive icon (blue circle right next to Controller: IDE) to add the Ubuntu .iso file to the virtual machine.



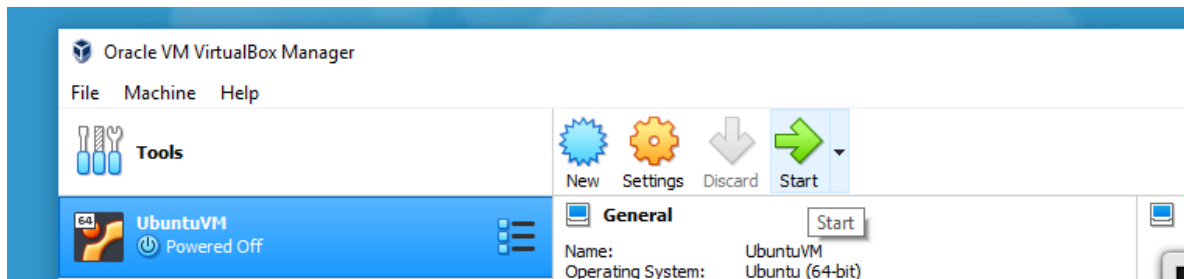




14. Click “OK” to save all of the changes.

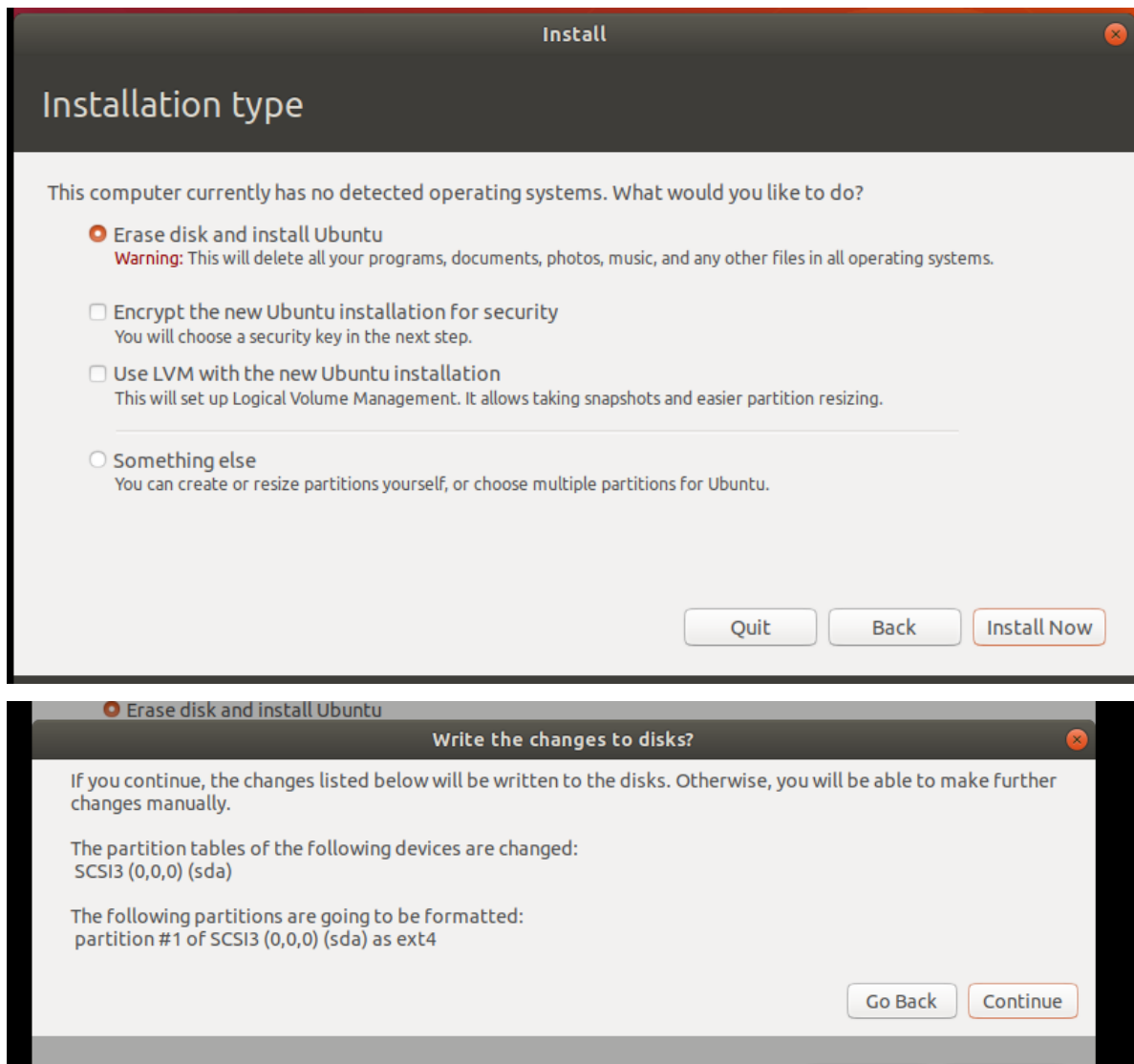


15. Click on the green “Start” arrow to begin installing the Linux OS in your virtual machine





16. When you get to the page below, choose the option to Erase disk and install Ubuntu. You can safely ignore the warning about this deleting all of your programs and data. This warning pertains ONLY to the blank virtual hard disk you created earlier. There is nothing you can do here that will delete your data on your host (Windows) system.



17. Continue with the installation, choosing a good username (we recommend choosing the same username as the one you use on your host OS or for your institution for example) and password (you may optionally select to login automatically on startup).
18. After installation is complete, the virtual machine should be up and running. To continue with installing RMG, follow the instructions either for binary (*Binary Installation Using Anaconda for Unix-Based Systems: Linux and Mac OSX*) or source installation (*Installation by Source Using Anaconda Environment for Unix-based Systems: Linux and Mac OSX*) for the Linux Operating system.

## Installing RMG in the Linux Subsystem on Windows 10

### Requirements

In order to install the Linux Subsystem, you need to be running Windows 10 build 16215 or later. The build can be determined from the “About” tab in the system settings (see the “OS build” line).

### Installing the Linux Subsystem

1. Follow the instructions provided by Microsoft to install the Linux subsystem, available [here](#). The basic steps include enabling the Windows Linux subsystem from a powershell **run as an administrator**, and downloading the latest LTS version of Ubuntu *from the Windows store*. We recommend Ubuntu (for which these instructions were made) over the other Linux distributions.
2. Once the Linux subsystem is installed, open a web browser in Windows and go to the [Anaconda Python Platform Downloads Page](#). Go to the tab for the **Linux Installer**, and **right click** on the download icon for Python to copy the link location. Open an Ubuntu terminal (type in Ubuntu into the Windows search bar if you are unsure where to find it) and paste the link into the terminal immediately after typing the `wget` command, so that your terminal looks like the following:

```
wget https://repo.anaconda.com/archive/Anaconda3-2021.05-Linux-x86_64.sh
```

Your exact link will look similar to the one above, but may be a more recent version of the installer. Execute this command in the terminal to begin downloading the installer.

3. Once the Anaconda installer has downloaded, execute the following commands in the Ubuntu terminal, changing the name of `Anaconda3-2021.05-Linux-x86_64.sh` to match the name of the script you downloaded.

```
bash Anaconda3-2021.05-Linux-x86_64.sh
```

Install the `anaconda3` folder inside your home directory (it should be the default location when it asks for a location to install). **When prompted to append Anaconda to your PATH, select or type Yes**. When prompted, do NOT install Microsoft VSCode. If you are interested in this lightweight IDE then you will want to install this into Windows 10 instead of inside the linux subsystem.

4. Execute the following commands to make sure that all of the required packages in Ubuntu are also installed:

```
sudo apt install gcc g++ make graphviz
```

Note: installing `graphviz` as a system package makes sure that rendering libraries that are not included in the WSL version of Ubuntu are installed. Unfortunately, the `graphviz` conda package does not install these dependencies in the RMG conda environment (later in the installation), instead relying on system libraries even in native Linux installations.

5. Follow the instructions for either the binary (*Binary Installation Using Anaconda for Unix-Based Systems: Linux and Mac OSX*) or source installation (*Installation by Source Using Anaconda Environment for Unix-based Systems: Linux and Mac OSX*) for the Linux Operating system. Follow these instructions from the point directly after installing Anaconda.

For users unfamiliar with bash or Linux, we recommend looking at [online Linux tutorials](#). To start out with, we recommend looking at the following tutorials: [Linux vs. Windows](#), [Terminal vs File Manager](#), and [Must Know Linux/Unix Commands](#).

### 1.3.2 For Basic Users: Binary Installation Using Anaconda

It is highly recommended to use the Python platform Anaconda to perform the installation of RMG-Py. A binary installation is recommended for users who want to use RMG out of the box, and are not interested in changing or recompiling the RMG code or making many additions to RMG's thermodynamic and kinetics databases.

#### Binary Installation Using Anaconda for Unix-Based Systems: Linux and Mac OSX

1. Download and install the [Anaconda Python Platform](#) for Python 3.7.

The download will be a .sh file with a name like Anaconda3-2019.07-Linux-x86\_64.sh. Open a terminal in the same directory as this file, and type the following to install Anaconda (replace the name of your .sh file below).

```
bash Anaconda3-2019.07-Linux-x86_64.sh
```

**When prompted to append Anaconda to your PATH, select or type Yes.** Install the Anaconda folder inside your home directory (typically /home/YourUsername/ in Linux and /Users/YourUsername in Mac). When prompted, you do not need to install Microsoft VSCode (but feel free to if you are looking for a lightweight IDE).

2. Install both RMG and the RMG-database binaries through the terminal. Dependencies will be installed automatically. It is safest to make a new conda environment for RMG and its dependencies. Type the following command into the terminal to create the new environment named 'rmg\_env' containing the latest stable version of the RMG program and its database.

```
conda create -c defaults -c rmg -c rdkit -c cantera -c pytorch -c conda-forge --  
→name rmg_env rmg rmgdatabase
```

Whenever you wish to use it you must first activate the environment:

```
source activate rmg_env
```

3. Optional: If you wish to use the [QMTP interface](#) with [MOPAC](#) to run quantum mechanical calculations for improved thermochemistry estimates of cyclic species, please obtain a legal license through the [MOPAC License Request Form](#). Once you have it, type the following into your terminal

```
mopac password_string_here
```

4. You may now run an RMG test job. Save the [Minimal Example Input File](#) to a local directory. Use the terminal to run your RMG job inside that folder using the following command

```
rmg.py input.py
```

You may now use RMG-Py, Arkane, as well as any of the [Standalone Modules](#) included in the RMG-Py package.

## Updating your binary installation of RMG in Linux or Mac OSX

If you had previously installed a binary version of the RMG package, you may check and update your installation to the latest stable version available on Anaconda by typing the following command on the terminal

```
source activate rmg_env
conda update rmg rmgdatabase -c rmg
```

### 1.3.3 For Developers: Installation by Source Using Anaconda Environment

RMG-Py can now be built by source using the Anaconda Python Platform to assist in installing all necessary dependencies. This is recommended for a developer who may be altering the RMG source code or someone who expects to manipulate the databases extensively. You will also be able to access the latest source code updates and patches through Github.

#### Installation by Source Using Anaconda Environment for Unix-based Systems: Linux and Mac OSX

1. Download and install *Anaconda Individual Edition* <<https://www.anaconda.com/products/individual#Downloads>>.

The download will be a .sh file with a name like `Anaconda3-2021.05-Linux-x86_64.sh`. Open a terminal in the same directory as this file, and type the following to install Anaconda (replace the name of your .sh file below).

```
bash Anaconda3-2021.05-Linux-x86_64.sh
```

**When prompted to append Anaconda to your PATH, select or type Yes.** Install the Anaconda folder inside your home directory (typically `/home/YourUsername/` in Linux and `/Users/YourUsername` in Mac). When prompted, you do not need to install Microsoft VSCode (but feel free to if you are looking for a lightweight IDE).

Note that you should restart your terminal in order for the changes to take effect, as the installer will tell you.

2. There are a few system-level dependencies which are required and should not be installed via Anaconda. These include [Git](#) for version control, [GNU Make](#), and the C and C++ compilers from the [GNU Compiler Collection \(GCC\)](#) for compiling RMG.

For Linux users, you can check whether these are already installed by simply calling them via the command line, which will let you know if they are missing. To install any missing packages, you should use the appropriate package manager for your system.

On Ubuntu and Debian the package manager is `apt`

```
sudo apt install git gcc g++ make
```

On Fedora and Red Hat derivatives (RHEL 8+) the package manager is `dnf`

```
sudo dnf install git gcc gcc-c++ make
```

Replace `dnf` with `yum` in the preceding for Red Hat 7 and lower.

On openSUSE the package manager is `zypper`:

```
sudo zypper install git gcc gcc-c++ make
```

On Manjaro or Arch Linux the package manager is `pacman`



```
sudo pacman -S git gcc make
```

For MacOS users, the above packages will not come preinstalled, but can be easily obtained by installing the XCode Command Line Tools. These are a set of packages relevant for software development which have been bundled together by Apple. The easiest way to install this is to simply run one of the commands in the terminal, e.g. `git`. The terminal will then prompt you on whether or not you would like to install the Command Line Tools.

For MacOS users only, download and install the latest macOS julia from here: <https://julialang.org/downloads/>. Then add julia to PATH by running the following command replacing 1.6 with the first two numbers in the Julia version designation (ex: 1.6.2->1.6, 1.1.1->1.1)

```
echo 'export PATH="/Applications/Julia-1.6.app/Contents/Resources/julia/bin:$PATH"
↪' >> ~/.bash_profile

export PATH="/Applications/Julia-1.6.app/Contents/Resources/julia/bin:$PATH"
```

Note that this julia install will not respect conda environmental boundaries this means only one conda environment can be linked to it at a time. For linux users julia will be installed automatically.

3. Install the latest versions of RMG and RMG-database through cloning the source code via Git. Make sure to start in an appropriate local directory where you want both RMG-Py and RMG-database folders to exist. Github has deprecated password authentication from the command line, so it is preferred to clone the repositories using ssh:

```
git clone git@github.com:ReactionMechanismGenerator/RMG-Py.git
git clone git@github.com:ReactionMechanismGenerator/RMG-database.git
```

It is still possible to clone the repositories using https if you are unfamiliar with ssh:

```
git clone https://github.com/ReactionMechanismGenerator/RMG-Py.git
git clone https://github.com/ReactionMechanismGenerator/RMG-database.git
```

For information on using ssh with GitHub see the [Connecting to GitHub with SSH](#)

4. Now create the conda environment for RMG-Py

```
cd RMG-Py
conda env create -f environment.yml
```

If the command returns an error due to being unable to find the conda command, try to either close and reopen your terminal to refresh your environment variables or type the following command.

If on Linux or pre-Catalina MacOS

```
source ~/.bashrc
```

If on MacOS Catalina or later

```
source ~/.zshrc
```

5. Activate conda environment

```
conda activate rmg_env
```

Note regarding differences between conda versions: Prior to Anaconda 4.4, the command to activate an environment was `source activate rmg_env`. It has since been changed to `conda activate rmg_env` due to

underlying changes to standardize operation across different operating systems. However, a prerequisite to using the new syntax is having run the `conda init` setup routine, which can be done at the end of the install procedure if the user requests.

6. Compile RMG-Py after activating the conda environment

```
make
```

7. Modify environment variables. Add RMG-Py to the `PYTHONPATH` to ensure that you can access RMG modules from any folder. Also, add your RMG-Py folder to `PATH` to launch `rmg.py` from any folder.

In general, these commands should be placed in the appropriate shell initialization file. For Linux users using bash (the default on distributions mentioned here), these should be placed in `~/.bashrc`. For MacOS users using bash (default before MacOS Catalina), these should be placed in `~/.bash_profile`, which you should create if it doesn't exist. For MacOS users using zsh (default beginning in MacOS Catalina), these should be placed in `~/.zshrc`.

```
export PYTHONPATH=YourFolder/RMG-Py/:$PYTHONPATH
export PATH=YourFolder/RMG-Py/:$PATH
```

NOTE: Make sure to change `YourFolder` to the path leading to the RMG-Py code. Not doing so will lead to an error stating that python cannot find the module `rmgpy`.

Be sure to either close and reopen your terminal to refresh your environment variables (`source ~/.bashrc` or `source ~/.zshrc`).

8. Install and Link Julia dependencies

```
python -c "import julia; julia.install(); import diffeqpy; diffeqpy.install()"

julia -e 'using Pkg; Pkg.add(PackageSpec(name="ReactionMechanismSimulator",
↪version="0.4")); using ReactionMechanismSimulator;'
```

Note that this links your python to python-jl enabling calls to Julia through pyjulia. Occasionally programs will interact with python-jl differently than the default python. If this occurs for you we recommend doing that operation in a different conda environment. However, if convenient you can undo this linking by replacing `python-jl` with `python3` in the second command above. Just make sure to rerun the linking command once you are done.

9. Finally, you can run RMG from any location by typing the following (given that you have prepared the input file as `input.py` in the current folder).

```
python-jl replace/with/path/to/rmg.py input.py
```

10. Optional: If you wish to use the *QMTP interface* with *MOPAC* to run quantum mechanical calculations for improved thermochemistry estimates of cyclic species, please obtain a legal license through the [MOPAC License Request Form](#). Once you have it, type the following into your terminal

```
mopac password_string_here
```

You may now use RMG-Py, Arkane, as well as any of the *Standalone Modules* included in the RMG-Py package.

## Test Suite

There are a number of basic tests you can run on the newly installed RMG. It is recommended to run them regularly to ensure the code and databases are behaving normally. Make sure that the environment is active before running the tests: `conda activate rmg_env`.

1. **Unit test suite:** this will run all the unit tests in the `rmgpy` and `arkane` packages

```
cd RMG-Py
make test
```

2. **Functional test suite:** this will run all the functional tests in the `rmgpy` and `arkane` packages

```
cd RMG-Py
make test-functional
```

3. **Database test suite:** this will run the database unit tests to ensure that groups, rate rules, and libraries are well-formed

```
cd RMG-Py
make test-database
```

## Running Examples

A number of basic examples can be run immediately. Additional example input files can be found in the `RMG-Py/examples` folder. Please read more on [Example Input Files](#) in the documentation.

1. **Minimal Example:** this will run an Ethane pyrolysis model. It should take less than a minute to complete. The results will be in the `RMG-Py/testing/minimal` folder:

```
cd RMG-Py
make eg1
```

2. **Hexadiene Example:** this will run a Hexadiene model with pressure dependence and QMTP. Note that you must have MOPAC installed for this to run. The results will be in the `RMG-Py/testing/hexadiene` folder:

```
cd RMG-Py
make eg2
```

3. **Liquid Phase Example:** this will run a liquid phase RMG model. The results will be in the `RMG-Py/testing/liquid_phase` folder

```
cd RMG-Py
make eg3
```

4. **ThermoEstimator Example:** this will run the [Thermo Estimation Module](#) on a few molecules. Note that you must have MOPAC installed for this to run completely. The results will be in the `RMG-Py/testing/thermoEstimator` folder

```
cd RMG-Py
make eg4
```

## Updating the RMG-Py Source Code

It is recommended to keep yourself up to date with the latest patches and bug fixes by RMG developers, which is maintained on the official repository at <https://github.com/ReactionMechanismGenerator/RMG-Py/>. You can view the latest changes by viewing the commits tab on the repository. To update your source code, you can “pull” the latest changes from the official repo by typing the following command in the Command Prompt

```
cd RMG-Py
git pull git@github.com:ReactionMechanismGenerator/RMG-Py.git main
```

If you are not using ssh (yet), it is still possible to pull the code using https:

```
git pull https://github.com/ReactionMechanismGenerator/RMG-Py.git main
```

We also recommend updating the RMG-database regularly. The repo itself can be found at <https://github.com/ReactionMechanismGenerator/RMG-database/>

```
cd RMG-database
git pull git@github.com:ReactionMechanismGenerator/RMG-database.git main
```

Again, for those (still) using https, the command is instead:

```
git pull https://github.com/ReactionMechanismGenerator/RMG-database.git main
```

For more information about how to use the Git workflow to make changes to the source code, please refer to the handy [Git Tutorial](#)

For information on updating your local repository from https to ssh, please see [Managing remote repositories](#)

## 1.3.4 Archive of Unsupported Installation Methods

Below are old installation techniques that are no longer supported, including instructions for installation without using Anaconda and the old installation instructions for Windows. These instructions are no longer maintained, and are not recommended for use.

### Linux Installation

RMG-Py and all of its dependencies may be easily installed through a short series of Terminal commands. The instructions listed below were written for Ubuntu 12.04 and should generally apply to other distributions.

Warning: This installation method is no longer actively maintained, and is not guaranteed to work as written. Please refer to [`installation`\\_](#) for more up-to-date instructions.

- Install compilers and libraries:

```
sudo apt-get install git g++ gfortran python-dev liblapack-dev
sudo apt-get install python-openbabel python-setuptools python-pip
```

- After creating a [Github account](#), generate your public key:

```
cd ~; ssh-keygen          # press enter to save to the default directory
                           # create a password if desired
cat .ssh/id_rsa.pub
```

Copy this public key to your [Github profile](#).

- Install dependencies:

```
sudo apt-get install libpng-dev libfreetype6-dev graphviz

sudo pip install numpy          # install NumPy before other packages

sudo pip install scipy cython nose matplotlib quantities sphinx psutil xlwt

cd ~
git clone https://github.com/ReactionMechanismGenerator/PyDAS.git
git clone https://github.com/ReactionMechanismGenerator/PyDQED.git
cd PyDAS; make F77=gfortran; sudo make install; cd ..
cd PyDQED; make F77=gfortran; sudo make install; cd ..
```

- Install RDKit

Full installation instructions: <https://www.rdkit.org/docs/Install.html> Be sure to **build it with InChI support**. Here's a synopsis:

```
cd ~
sudo apt-get install flex bison build-essential python-numpy cmake python-dev_
↳sqlite3
sudo apt-get install libsqlite3-dev libboost-dev libboost-python-dev libboost-
↳regex-dev
git clone https://github.com/rdkit/rdkit.git
cd rdkit
export RDBASE=`pwd`
export LD_LIBRARY_PATH=$LD_LIBRARY_PATH:$RDBASE/lib
export PYTHONPATH=$PYTHONPATH:$RDBASE
cd External/INCHI-API
./download-inchi.sh
cd ../../
mkdir build
cd build
cmake .. -DRDK_BUILD_INCHI_SUPPORT=ON
make
make install
```

You'll need various environment variables set (you may want to add these to your `.bash_profile` file), eg.:

```
export RDBASE=$HOME/rdkit # CHECK THIS (maybe you put RDKit somewhere else)
export LD_LIBRARY_PATH=$LD_LIBRARY_PATH:$RDBASE/lib
export PYTHONPATH=$PYTHONPATH:$RDBASE # (or some other way to make sure it's on_
↳your Python path)
```

- The following dependencies are also required for core RMG functions and must be installed from source before building RMG:

**pyrdl:** RingDecomposerLib, used for ring perception. Download from <https://github.com/rareylab/RingDecomposerLib>. Requires CMAKE to compile.

**lpsolve:** Mixed integer linear programming solver. Download from <https://sourceforge.net/projects/lpsolve/>. Python extension also required.

- Install RMG-Py:

```
cd ~
git clone https://github.com/ReactionMechanismGenerator/RMG-database.git
git clone https://github.com/ReactionMechanismGenerator/RMG-Py.git
sudo pip install -r RMG-Py/requirements.txt
cd RMG-Py
make
```

- Run an example:

```
python rmg.py examples/rmg/minimal/input.py
```

Verify your installation by opening the resulting output.html file under the “examples/rmg/minimal” directory.

You can also use the Makefile targets to test and run examples:

```
make test
make eg1
make eg2
```

- Compiling RMG-Py with Sensitivity Analysis:

Running sensitivity analysis in RMG-Py requires the prerequisite DASPK solver and DASPK compiled wrapper in PyDAS. To do so first compile daspk in PyDAS and agree to download the daspk31.tgz file when prompted.

```
cd PyDAS/
make
make install
```

Then compile RMG-Py normally. It will automatically be compiled with sensitivity analysis if DASPK is found.

```
cd RMG-Py
make clean-solver
make
```

Note that using this option will allow RMG to both run with and without sensitivity.

## MacOS X Installation

Warning: This installation method is no longer maintained, and is unlikely to work as written. Please refer to [`installation`](#) for more up-to-date instructions.

There are a number of dependencies for RMG-Py. This page will guide you through installing them. You will need the Command Line Tools for XCode. If you are not using Anaconda to install RMG-Py, we highly recommend the [Homebrew](#) package manager. The following instructions assume that you have [installed Homebrew and its requirements](#). We recommend using a [Virtual Environment](#) for your Python packages, but this is optional (without it you may need to add *sudo* before some commands to solve permission errors).

You will also need gfortran, Python, Numpy and Scipy. We typically install them using homebrew-python (which used to be at <https://github.com/Homebrew/homebrew-python>) but other methods may work as well.

- For example:

```
brew tap homebrew/python
brew install numpy
brew install scipy
brew install matplotlib --with-cairo --with-ghostscript --with-tcl-tk --with-
↳pyqt --with-pygtk --withgtk3
```

(continues on next page)

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- Install git if you don't already have it (you may also like some graphical interfaces like [GitX](#) or [GitUp](#) or dozens more):

```
brew update
brew install git
```

- Optional (but recommended for Nitrogen-chemistry nomenclature): install [OpenBabel](#):

```
brew install open-babel --with-python --HEAD
```

- Install [RDKit](#):

```
brew tap rdkit/rdkit
brew install rdkit --with-inchi
brew link --overwrite rdkit
```

You'll need to set an environment variable to use it, eg. put this in your `~/.bash_profile` file:

```
export RDBASE=/usr/local/share/RDKit
```

- The following dependencies are also required for core RMG functions and must be installed from source before building RMG:

**pyrdl:** RingDecomposerLib, used for ring perception. Download from <https://github.com/rareylab/RingDecomposerLib>. Requires CMAKE to compile.

**lpsolve:** Mixed integer linear programming solver. Download from <https://sourceforge.net/projects/lpsolve/>. Python extension also required.

- Make a directory to put everything in:

```
mkdir ~/Code
```

- Get the RMG-Py source code and the RMG-database from GitHub:

```
cd ~/Code
git clone https://github.com/ReactionMechanismGenerator/RMG-database.git
git clone https://github.com/ReactionMechanismGenerator/RMG-Py.git
```

- Install the Python dependencies listed in the `RMG-Py/requirements.txt` file using *pip* (do `easy_install pip` if you don't already have it):

```
pip install -r RMG-Py/requirements.txt
```

- Get and build [PyDQED](#):

```
cd ~/Code
git clone https://github.com/ReactionMechanismGenerator/PyDQED.git
cd PyDQED
export LIBRARY_PATH=$(dirname $(gfortran -print-file-name=libgfortran.a))
make
make install
```

- Get and build [PyDAS](#):

```
cd ~/Code
git clone https://github.com/ReactionMechanismGenerator/PyDAS.git
cd PyDAS
export LIBRARY_PATH=$(dirname $(gfortran -print-file-name=libgfortran.a))
make
make install
```

- Build RMG-Py:

```
cd ~/Code/RMG-Py
make -j4
```

- Run an example:

```
cd ~/Code/RMG-Py/
python rmg.py examples/rmg/minimal/input.py
```

Verify your installation by opening the resulting output.html file under the “examples/rmg/minimal” directory.

You can also use the Makefile targets to test and run examples:

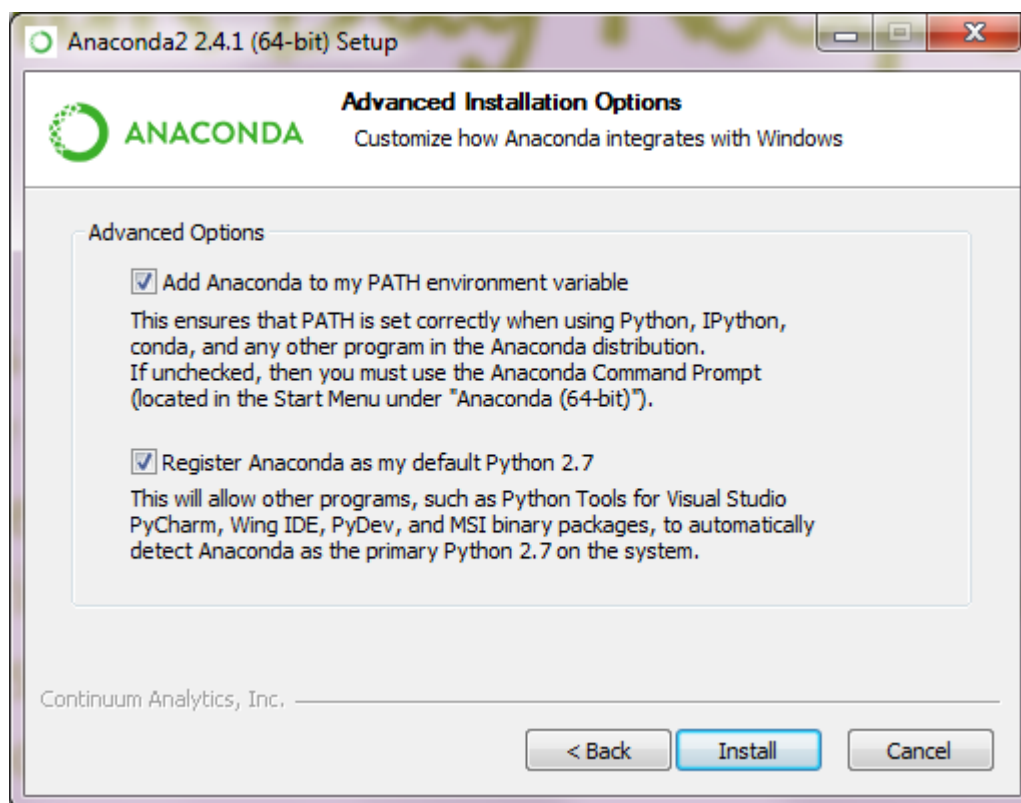
```
cd ~/Code/RMG-Py/
make test
make eg1
make eg2
```

To run with on-the-fly Quantum Mechanics calculations, you will also need to install [MOPAC](#) or [Gaussian](#), then run *make QM*.

## Binary Installation Using Anaconda for Windows

1. Download and install the [Anaconda Python Platform](#) for Python 2.7 (make sure not to install Python 3.0+, which is incompatible with RMG). We recommend changing the default install path to C:\Anaconda\ in order to avoid spaces in the install path and be easily accessible. It is recommended to append Anaconda to your PATH as well as setting it as your default Python executable. All other settings can remain as their defaults.





- Now we want to install both RMG and the RMG-database binaries via the command prompt. Dependencies will be installed automatically. It is safest to make a new Anaconda environment for RMG and all its dependencies. Open a command prompt (either by finding it in your Program Files or by searching for `cmd.exe`. You may need to run the command prompt as an administrator: to do this open up a file explorer and navigate to `C:\Windows\System32` and find the file `cmd.exe`; right click on this file and select “run as administrator”) and type the following to create the new environment named ‘`rmg_env`’ containing the latest stable version of the RMG program and its database.

```
conda create -c rmg --name rmg_env rmg rmgdatabase
```

- Whenever you wish to use it you must first activate the environment in the command prompt by typing:

```
activate rmg_env
```

- Optional: If you wish to use the *QMTP interface* with **MOPAC** to run quantum mechanical calculations for improved thermochemistry estimates of cyclic species, please obtain a legal license through the [MOPAC License Request Form](#). Once you have it, type the following into your command prompt (while the environment is activated)

```
mopac password_string_here
```

- Now you must *set the RMG environment variable in Windows* to allow your system to find the RMG python files more easily.
- If you set any new environment variables, you must now close and reopen the command prompt so that those environment variables can be refreshed and used.
- You may now run an RMG test job. Save the [Minimal Example Input File](#) to a local directory. Use the command prompt to run your RMG job inside that folder by using the following command

```
activate rmg_env
python %RMGPy%\rmg.py input.py
```

You may now use RMG-Py, Arkane, as well as any of the *Standalone Modules* included in the RMG-Py package.

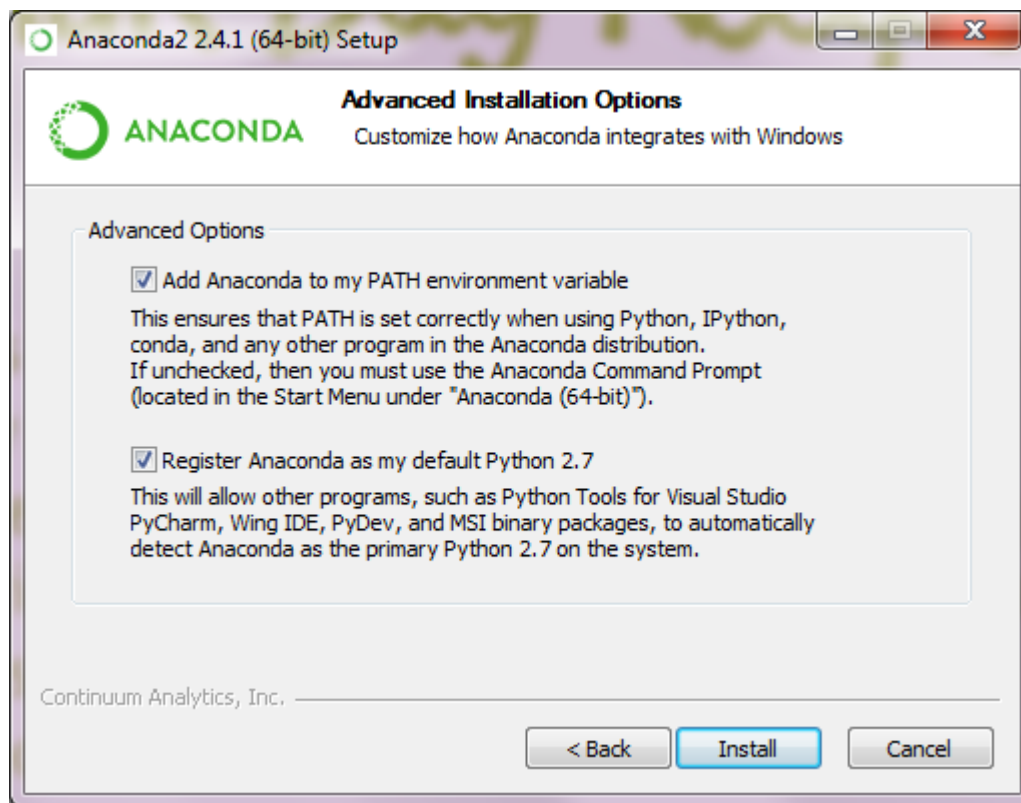
## Updating your binary installation of RMG for Windows

If you had previously installed a binary version of the RMG package, you may check and update your installation to the latest stable version available on Anaconda by typing the following command in a Command Prompt

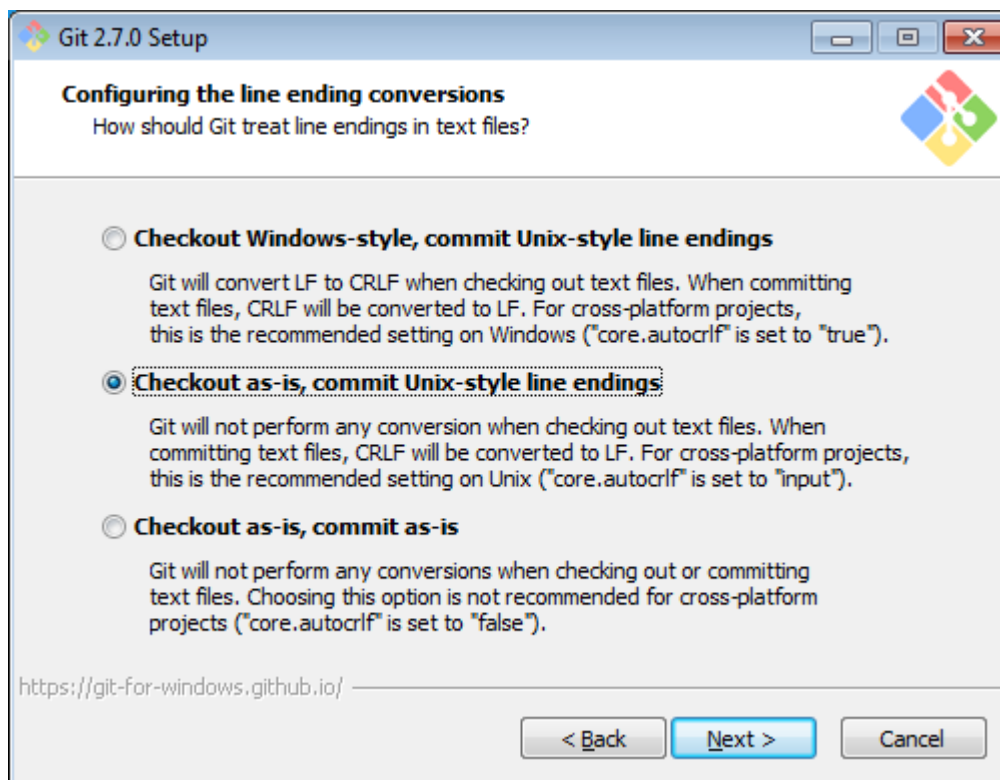
```
source activate rmg_env
conda update rmg rmgdatabase -c rmg
```

## Installation by Source Using Anaconda Environment for Windows

1. Download and install the [Anaconda Python Platform](#) for Python 2.7 (make sure not to install Python 3.0+, which is incompatible with RMG). We recommend changing the default install path to C:\Anaconda\ in order to avoid spaces in the install path and be easily accessible. It is recommended to append Anaconda to your PATH as well as setting it as your default Python executable. All other settings can remain as their defaults.



2. Install [Git](#), the open source version control package. When asked, append Git tools to your Command Prompt. It is also recommended to commit Unix-style line endings:



3. Open Git CMD or a command prompt (either by finding it in your Program Files or by searching for `cmd.exe`. You may have to run the command prompt as an administrator. To do so right click on `cmd.exe`. and select Run as Administrator). Install the latest versions of RMG and RMG-database through cloning the source code via Git. Make sure to start in an appropriate local directory where you want both RMG-Py and RMG-database folders to exist. We recommend creating a folder such as `C:\Code\`

```
git clone https://github.com/ReactionMechanismGenerator/RMG-Py.git
git clone https://github.com/ReactionMechanismGenerator/RMG-database.git
```

4. Create and activate the RMG Anaconda environment

```
cd RMG-Py
conda env create -f environment_windows.yml
activate rmg_env
```

Every time you open a new command prompt and want to compile or use RMG, you must reactivate this environment by typing

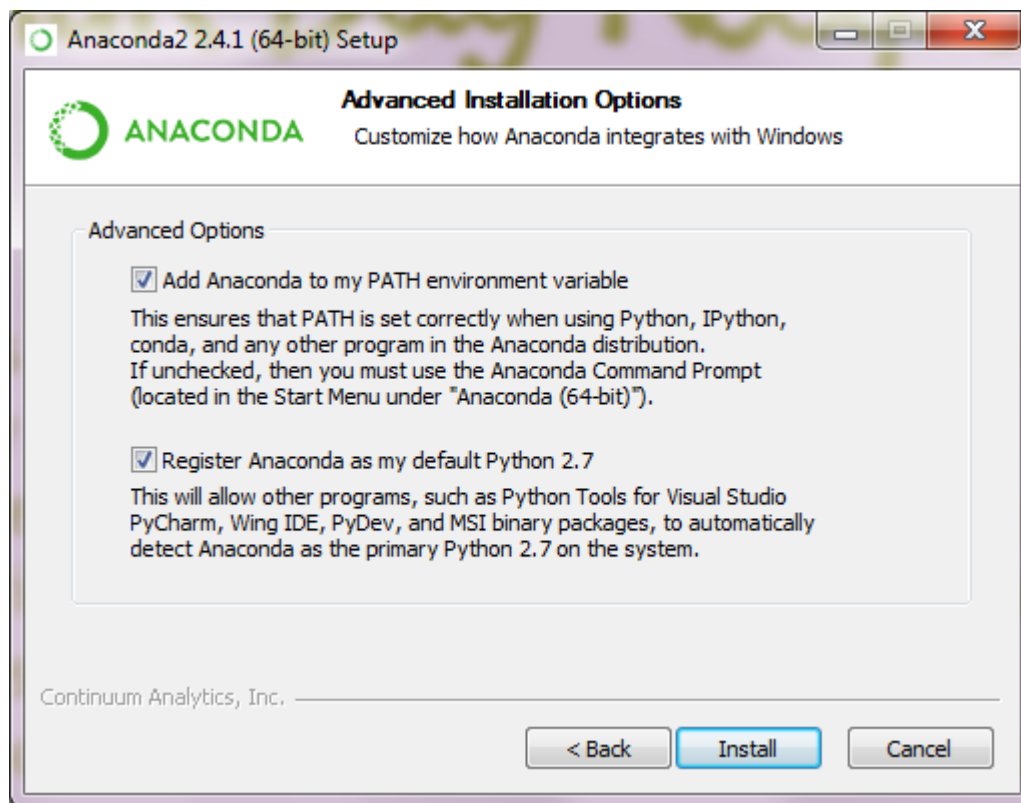
```
activate rmg_env
```

5. Now you can compile RMG-Py

```
cd RMG-Py
mingw32-make
```

6. Now it is recommended to modify your system's environment variables. Please see *Setting the RMG environment variable in Windows* for more information.

Additionally, set the `PYTHONPATH` environment variable to the path of your RMG-Py source folder to ensure that you can access RMG modules from any python prompt. The prompt might look like this:



7. If you set any new environment variables, you must now close and reopen the command prompt so that those environment variables can be refreshed and used.
8. Optional: If you wish to use the *QMTP interface* with MOPAC to run quantum mechanical calculations for improved thermochemistry estimates of cyclic species, please obtain a legal license through the [MOPAC License Request Form](#). Once you have it, type the following into your command prompt

```
mopac password_string_here
```

You may now use RMG-Py, Arkane, as well as any of the *Standalone Modules* included in the RMG-Py package.

## Test Suite

There are a number of basic tests you can run on the newly installed RMG. It is recommended to run them regularly to ensure the code and databases are behaving normally.

1. **Unit test suite:** this will run all the unit tests in the `rmgpy` package

```
cd RMG-Py
mingw32-make test
```

2. **Database test suite:** this will run the database unit tests to ensure that groups, rate rules, and libraries are well formed

```
cd RMG-Py
mingw32-make test-database
```

## Running Examples

A number of basic examples can be run immediately. Additional example input files can be found in the RMG-Py\examples folder. Please read more on *Example Input Files* in the documentation.

1. **Minimal Example:** this will run an Ethane pyrolysis model. It should take less than a minute to complete. The results will be in the RMG-Py\testing\minimal folder:

```
cd RMG-Py
mingw32-make eg1
```

2. **Hexadiene Example:** this will run a Hexadiene model with pressure dependence and QMTP. Note that you must have MOPAC installed for this to run. The results will be in the RMG-Py\testing\hexadiene folder:

```
cd RMG-Py
mingw32-make eg2
```

3. **Liquid Phase Example:** this will run a liquid phase RMG model. The results will be in the RMG-Py\testing\liquid\_phase folder

```
cd RMG-Py
mingw32-make eg3
```

4. **ThermoEstimator Example:** this will run the *Thermo Estimation Module* on a few molecules. Note that you must have MOPAC installed for this to run completely. The results will be in the RMG-Py\testing\thermoEstimator folder

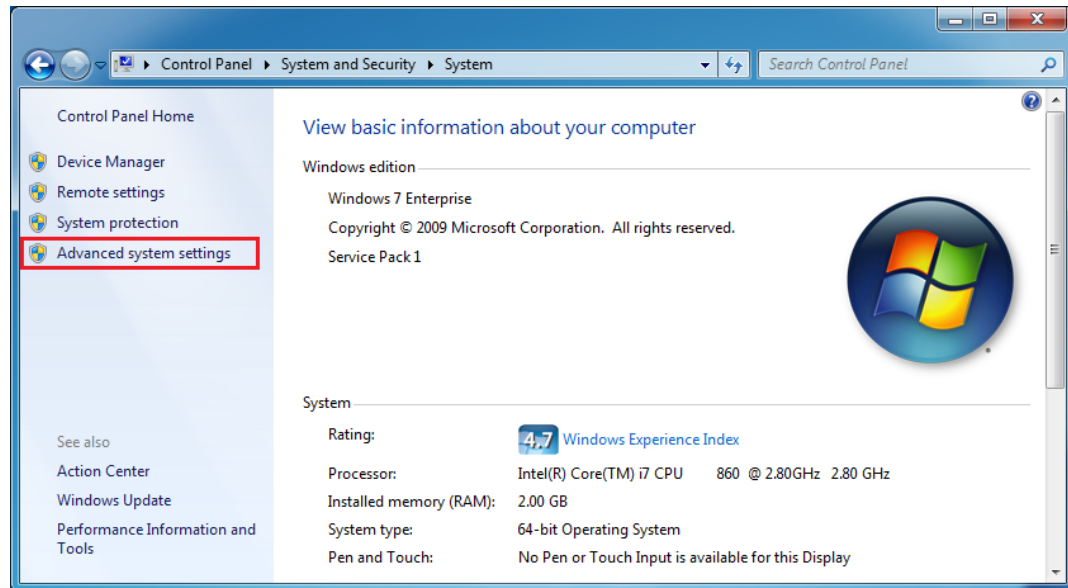
```
cd RMG-Py
mingw32-make eg4
```

## Setting up Windows Environment Variables for RMG

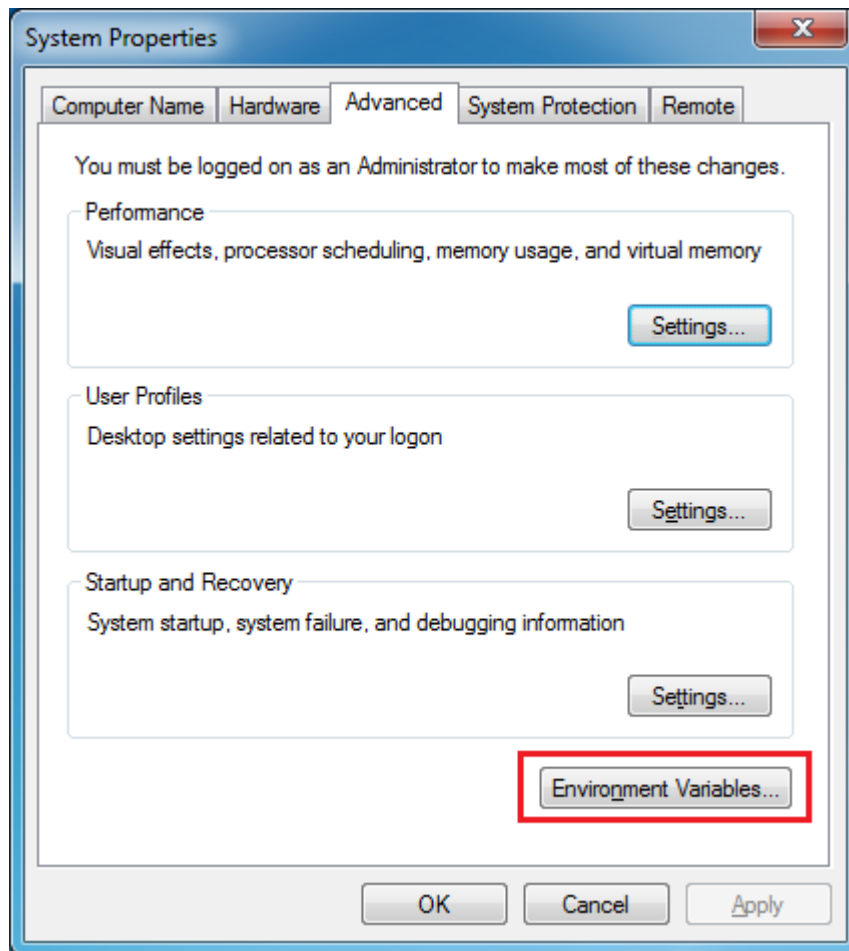
Setting environment variables in Windows allows for easier shortcutting and usage of RMG scripts and packages.

## Setting the RMGPy variable

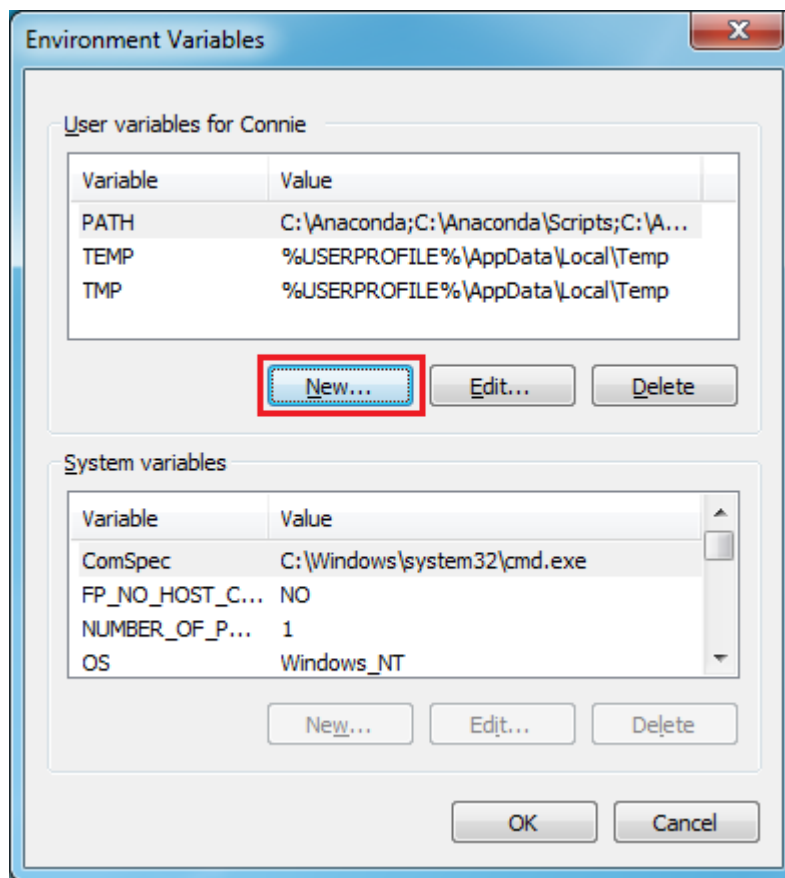
1. If you have a search bar available in your start menu, search for “environment variables” and select “Edit environment variables for your account”. Alternatively, navigate to this settings window by first going to “Control Panel > System”, then clicking “Advanced system settings”.



2. Once the “System Properties” window opens, click on “Environment Variables...” in the “Advanced” tab.



3. Once the “Environment Variables” window opens, click on “New” under the “User variables”.



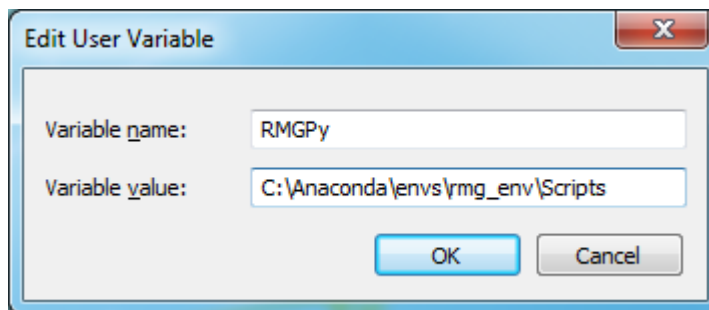
4. Set a new variable with the name RMGPy with the appropriate value directed at your RMG path.

If you installed the binary version of RMG, the environment value should be set to:

```
C:\Anaconda\envs\rmg_env\Scripts\
```

where C:\Anaconda can be replaced by wherever your Anaconda was installed.

Your screen might look like this:



If you are installing RMG by source, you can similarly set your RMGPy variable to the source directory, such as

```
C:\Code\RMG-Py
```

5. Click “Ok” on all screens to confirm the changes.

**Note:** If you set any new environment variables, you must close and reopen any command prompts previously open



before the changes can take effect.

---

### Optional: Setting a Permanent Anaconda Environment for RMG

If you use Anaconda solely for RMG, it may be more convenient to set your PATH variable to be permanently directed to the RMG environment. This will allow you to run RMG easily without having to type `activate rmg_env` in the command prompt every time.

Similarly to setting the environment variable for RMGPy, go to “Edit environment variables for your account” and click edit on the PATH variable. Replace the paths containing the Anaconda main directory with the RMG environment in Anaconda.

For example a path such as

C:\Anaconda\Scripts\

should be changed to:

C:\Anaconda\envs\rmg\_env\Scripts\

Note that C:\Anaconda should be wherever your Anaconda was installed.

## 1.3.5 Dependencies

Please visit the page below for detailed information on all of RMG’s dependencies and their license restrictions

### Dependencies

#### List of Dependencies

Briefly, RMG depends on the following packages, almost all of which can be found in the [RMG anaconda channel](#) as binary packages.

- **boost:** portable C++ source libraries
- **cairo:** a 2D vector graphics library with support for multiple backends including image buffers, PNG, PostScript, PDF, and SVG file output. Used for molecular diagram generation
- **cairocffi:** a set of Python bindings and object-oriented API for cairo
- **coverage:** code coverage measurement for Python
- **cython:** compiling Python modules to C for speed up
- **dde:** Data Driven Estimator for neural network thermochemistry prediction
- **ffmpeg:** (optional) used to encode videos, necessary for generating video flux diagrams
- **gaussian:** (optional) commercial software program for quantum mechanical calculations. Must be installed separately.
- **gcc:** GNU compiler collection for C, C++, and Fortran. (MinGW is used in windows)
- **gprof2dot:** converts Python profiling output to a dot graph
- **graphviz:** generating flux diagrams

- **jinja2**: Python templating language for html rendering
- **jupyter**: (optional) for using IPython notebooks
- **lpsolve**: mixed integer linear programming solver, used for resonance structure generation. Must also install Python extension.
- **markupsafe**: implements XML/HTML/XHTML markup safe strings for Python
- **matplotlib**: library for making plots
- **mock**: for unit-testing
- **mopac**: semi-empirical software package for QM calculations
- **mpmath**: for arbitrary-precision arithmetic used in Arkane
- **muq**: (optional) MIT Uncertainty Quantification library, used for global uncertainty analysis
- **networkx**: (optional) network analysis for reaction-path analysis IPython notebook
- **nose**: advanced unit test controls
- **numpy**: fast matrix operations
- **openbabel**: chemical toolbox for speaking the many languages of chemical data
- **psutil**: system utilization diagnostic tool
- **pydas**: differential algebraic system solver
- **pydot**: interface to Dot graph language
- **pydqed**: constrained nonlinear optimization
- **pyparsing**: a general parsing module for python
- **pyrdl**: RingDecomposerLib for graph ring perception
- **pyyaml**: Python framework for YAML
- **pyzmq**: Python bindings for zeroMQ
- **quantities**: unit conversion
- **rdkit**: open-source cheminformatics toolkit
- **scipy**: fast mathematical toolkit
- **setuptools**: for packaging Python projects
- **sphinx**: documentation generation
- **symmetry**: calculating symmetry numbers of chemical point groups
- **xlwt**: generating Excel output files

## License Restrictions on Dependencies

All of RMG's dependencies except the ones listed below are freely available and compatible with RMG's open source MIT license (though the specific nature of their licenses vary).

- **pydas**: The DAE solvers used in the simulations come from [Linda Petzold's research group](#) at UCSB. For running sensitivity analysis in RMG, the DASPK 3.1 solver is required, which "is subject to copyright restrictions" for non-academic use. Please visit their website for more details. To run RMG without this restriction, one may switch to compiling with the DASSL solver instead in RMG, which is "available in the public domain."

If you wish to do on-the-fly quantum chemistry calculations of thermochemistry (advisable for fused cyclic species in particular, where the ring corrections to group additive estimates are lacking), then you will need the third-party software for the QM calculations:

- **gaussian**: Gaussian03 and Gaussian09 are currently supported and commercially available. See <https://gaussian.com> for more details.
- **mopac** MOPAC can be found at <http://openmopac.net/>. Though it is not free for industrial use, it is free for non-profit and academic research use.

## 1.4 Creating Input Files

The syntax and parameters within an RMG input file are explained below. We recommend trying to build your first input file while referencing one of the *Example Input Files*.

### 1.4.1 Syntax

The format of RMG-Py `input.py` is based on Python syntax.

Each section is made up of one or more function calls, where parameters are specified as text strings, numbers, or objects. Text strings must be wrapped in either single or double quotes.

### 1.4.2 Datasources

This section explains how to specify various reaction and thermo data sources in the input file.

#### Thermo Libraries

By default, RMG will calculate the thermodynamic properties of the species from Benson additivity formulas. In general, the group-additivity results are suitably accurate. However, if you would like to override the default settings, you may specify the thermodynamic properties of species in the ThermoLibrary. When a species is specified in the ThermoLibrary, RMG will automatically use those thermodynamic properties instead of generating them from Benson's formulas. Multiple libraries may be created, if so desired. The order in which the thermo libraries are specified is important: If a species appears in multiple thermo libraries, the first instance will be used.

Now in RMG, you have two types of thermo libraries: gas and liquid thermo libraries. As species thermo in liquid phase depends on the solvent, those libraries can only be used in liquid phase simulation with the corresponding solvent. Gas phase thermo library can be used either in gas phase simulation or in liquid phase simulation. (see more details on the two *thermo library types* and *how to use thermo libraries in liquid phase simulation*)

Please see Section *editing thermo database* for more details. In general, it is best to leave the ThermoLibrary set to its default value. In particular, the thermodynamic properties for H and H2 must be specified in one of the primary thermo libraries as they cannot be estimated by Benson's method.

For example, if you wish to use the GRI-Mech 3.0 mechanism [GRIMech3.0] as a ThermoLibrary in your model, the syntax will be:

```
thermoLibraries = ['primaryThermoLibrary', 'GRI-Mech3.0']
```

This library is located in the \$RMG/RMG-database/input/thermo/libraries directory. All “Locations” for the ThermoLibrary field must be with respect to the \$RMG/RMG-database/input/thermo/libraries directory.

---

**Note:** Checks during the initialization are made to avoid users to use “liquid thermo libraries” in gas phase simulations or to use “liquid phase libraries” obtained in another solvent than the one defined in the input file in liquid phase simulations.

---

## Reaction Libraries

The next section of the `input.py` file specifies which, if any, Reaction Libraries should be used. When a reaction library is specified, RMG will first use the reaction library to generate all the relevant reactions for the species in the core before going through the reaction templates. Unlike the Seed Mechanism, reactions present in a Reaction Library will not be included in the core automatically from the start.

You can specify your own reaction library in the location section. In the following example, the user has created a reaction library with a few additional reactions specific to n-butane, and these reactions are to be used in addition to the Glarborg C3 library:

```
reactionLibraries = [('Glarborg/C3', False)],
```

The keyword `False/True` permits user to append all unused reactions (= kept in the edge) from this library to the chemkin file. `True` means those reactions will be appended. Using just the string inputs would lead to a default value of `False`. In the previous example, this would look like:

```
reactionLibraries = ['Glarborg/C3'],
```

The reaction libraries are stored in \$RMG-database/input/kinetics/libraries/ and the *Location*: should be specified relative to this path.

Because the units for the Arrhenius parameters are given in each mechanism, the different mechanisms can have different units.

---

**Note:** While using a Reaction Library the user must be careful enough to provide all instances of a particular reaction in the library file, as RMG will ignore all reactions generated by its templates. For example, suppose you supply the Reaction Library with `butyl_1 -> butyl_2`. Although RMG would find two unique instances of this reaction (via a three- and four-member cyclic Transition State), RMG would only use the rate coefficient supplied by you in generating the mechanism.

RMG will not handle irreversible reactions correctly, if supplied in a Reaction Library.

---

## Seed Mechanisms

The next section of the `input.py` file specifies which, if any, Seed Mechanisms should be used. If a seed mechanism is passed to RMG, every species and reaction present in the seed mechanism will be placed into the core, in addition to the species that are listed in the *List of species* section.

For details of the kinetics libraries included with RMG that can be used as a seed mechanism, see *Reaction Libraries*.

You can specify your own seed mechanism in the location section. Please note that the oxidation library should not be used for pyrolysis models. The syntax for the seed mechanisms is similar to that of the primary reaction libraries.

```
seedMechanisms = ['GRI-Mech3.0']
```

The seed mechanisms are stored in `RMG-database/input/kinetics/libraries/`

As the units for the Arrhenius parameters are given in each mechanism, different mechanisms can have different units. Additionally, if the same reaction occurs more than once in the combined mechanism, the instance of it from the first mechanism in which it appears is the one that gets used.

## Kinetics Depositories

Kinetics depositories store reactions which can be used for rate estimation. Depositories are divided by the sources of the data. Currently, RMG database has two depositories. The main depository is *training* which contains reactions from various sources. This depository is loaded by default and can be disabled by adding `'!training'` to the list of depositories. The *NIST* depository contains reactions taken from NIST's gas kinetics database. The *kineticsDepositories* argument in the input file accepts a list of strings describing which depositories to include.:

```
kineticsDepositories = ['training']
```

## Kinetics Families

In this section users can specify the particular reaction families that they wish to use to generate their model. This can be specified with any combination of specific families and predefined sets from `RMG-database/input/kinetics/families/recommended.py`.

For example, you can use only the `H_Abstraction` family to build the model:

```
kineticsFamilies = 'H_Abstraction'
```

You can also specify multiple families in a list:

```
kineticsFamilies = ['H_Abstraction', 'Disproportionation', 'R_Recombination']
```

To use a predefined set, simply specify its name:

```
kineticsFamilies = 'default'
```

You can use a mix of predefined sets and kinetics families:

```
kineticsFamilies = ['default', 'SubstitutionS']
```

It is also possible to request the inverse of a particular list:

```
kineticsFamilies = ['!default', '!SubstitutionS']
```

This will load all kinetics families except the ones in 'default' and 'SubstitutionS'.

Finally, you can also specify 'all' or 'none', which may be useful in certain cases.

### Kinetics Estimator

The last section is specifying that RMG is estimating kinetics of reactions from rate rules. For more details on how kinetic estimations is working check *Kinetics Estimation*:

```
kineticsEstimator = 'rate rules'
```

The following is an example of a database block, based on above chosen libraries and options:

```
database(  
    thermoLibraries = ['primaryThermoLibrary', 'GRI-Mech3.0'],  
    reactionLibraries = [('Glarborg/C3', False)],  
    seedMechanisms = ['GRI-Mech3.0'],  
    kineticsDepositories = ['training'],  
    kineticsFamilies = 'default',  
    kineticsEstimator = 'rate rules',  
)
```

### 1.4.3 List of species

Species to be included in the core at the start of your RMG job are defined in the species block. The label, reactive or inert, and structure of each reactant must be specified.

The label field will be used throughout your mechanism to identify the species. Inert species in the model can be defined by setting reactive to be False. Reaction families will no longer be applied to these species, but reactions of the inert from libraries and seed mechanisms will still be considered. For all other species the reactive status must be set as True. The structure of the species can be defined using either by using SMILES or adjacencyList.

The following is an example of a typical species item, based on methane using SMILE or adjacency list to define the structure:

```
species(  
    label='CH4',  
    reactive=True,  
    structure=SMILES("C"),  
)  
  
species(  
    label='CH4',  
    reactive=True,  
    structure=adjacencyList(  
        """  
        1 C 0  
        """  
)
```

### 1.4.4 Forbidden Structures

RMG explores a wide variety of structures as it builds a mechanism. Sometimes, RMG makes nonsensical, unphysical, or unstable species that make their way into the core.

Luckily, RMG has a remedy to prevent these undesirable structures from making their way into your mechanism. RMG's ForbiddenStructures database contains structures that are forbidden from entering the core (see [Kinetics Database](#) for more information)

While this database forbids many undesirable structures, it may not contain a species or structure you would like to exclude from your model. If you would like to forbid a structure from your model, you can do so by adding it to your input file in the forbidden block.

The label and structure of each forbidden structure must be specified. The structure of the forbidden structure can be defined using either SMILES or adjacencyList.

The following is an example of a forbidden structure item, based on bidentate CO<sub>2</sub> using SMILES or adjacency list to define the structure:

```
forbidden(
    label='CO2_bidentate',
    structure=SMILES("O=C(*)O*"),
)

forbidden(
    label='CO2_bidentate',
    structure=adjacencyList(
        """
        1 O u0 p2 c0 {2,D}
        2 C u0 p0 c0 {1,D} {3,S} {4,S}
        3 X u0 p0 c0 {2,S}
        4 O u0 p2 c0 {2,S} {5,S}
        5 X u0 p0 c0 {4,S}
        """
    )
)
```

If you would like to forbid a functional group from your mechanism, use the `adjacencyListGroup` syntax in the forbidden block.

The following is an example of a forbidden structure using `adjacencyListGroup`. The R-O-Cl forbidden structure forbids any species which contain an “R-O-Cl” group from your mechanism.

```
forbidden(
    label = "R-O-Cl",
    structure=adjacencyListGroup(
        """
        1 R ux {2,S}
        2 O ux {1,S} {3,S}
        3 Cl ux {2,S}
        """
    )
)
```

Note: If you would like to allow Hypochlorous acid (*ClOH*) in your model and forbid any other species with an “R-O-Cl” group, you can do so by changing the *R* atomtype to *R/H* in the R-O-Cl forbidden structure above. Alternatively,

you could explicitly allow *CIOH* by creating a *CIOH* species in your input file (see [List of species](#)) and add “input species” to the *generatedSpeciesConstraints* block discussed here [Miscellaneous Options](#).

### 1.4.5 Reaction System

Every reaction system we want the model to be generated at must be defined individually. Currently, RMG can only model constant temperature and pressure systems. Future versions will allow for variable temperature and pressure. To define a reaction system we need to define the temperature, pressure and initial mole fractions of the reactant species. The initial mole fractions are defined using the label for the species in the species block. Reaction system simulations terminate when one of the specified termination criteria are satisfied. Termination can be specified to occur at a specific time, at a specific conversion of a given initial species or to occur at a given *terminationRateRatio*, which is the characteristic flux in the system at that time divided by the maximum characteristic flux observed so far in the system (measure of how much chemistry is happening at a moment relative to the main chemical process).

The following is an example of a simple reactor system:

```
simpleReactor(  
    temperature=(1350, 'K'),  
    pressure=(1.0, 'bar'),  
    initialMoleFractions={  
        "CH4": 0.104,  
        "H2": 0.0156,  
        "N2": 0.8797,  
    },  
    terminationConversion={  
        'CH4': 0.9,  
    },  
    terminationTime=(1e0, 's'),  
    terminationRateRatio=0.01,  
    sensitivity=['CH4', 'H2'],  
    sensitivityThreshold=0.001,  
)
```

Troubleshooting tip: if you are using a goal conversion rather than time, the reaction systems may reach equilibrium below the goal conversion, leading to a job that cannot converge physically. Therefore it is may be necessary to reduce the goal conversion or set a goal reaction time.

For sensitivity analysis, RMG-Py must be compiled with the DASPK solver, which is done by default but has some dependency restrictions. (See [License Restrictions on Dependencies](#) for more details.) The *sensitivity* and *sensitivityThreshold* are optional arguments for when the user would like to conduct sensitivity analysis with respect to the reaction rate coefficients for the list of species given for *sensitivity*.

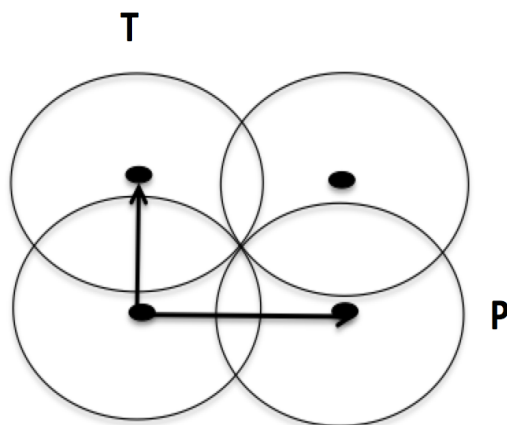
Sensitivity analysis is conducted for the list of species given for *sensitivity* argument in the input file. The normalized concentration sensitivities with respect to the reaction rate coefficients  $\text{dln}(C_i)/\text{dln}(k_j)$  are saved to a csv file with the file name *sensitivity\_1\_SPC\_1.csv* with the first index value indicating the reactor system and the second naming the index of the species the sensitivity analysis is conducted for. Sensitivities to thermo of individual species is also saved as semi normalized sensitivities  $\text{dln}(C_i)/\text{d}(G_j)$  where the units are given in  $1/(\text{kcal mol}^{-1})$ . The *sensitivityThreshold* is set to some value so that only sensitivities for  $\text{dln}(C_i)/\text{dln}(k_j) > \text{sensitivityThreshold}$  or  $\text{dln}C_i/\text{d}(G_j) > \text{sensitivityThreshold}$  are saved to this file.

Note that in the RMG job, after the model has been generated to completion, sensitivity analysis will be conducted in one final simulation (sensitivity is not performed in intermediate iterations of the job).



### Advanced Setting: Range Based Reactors

Under this setting rather than using reactors at fixed points, reaction conditions are sampled from a range of conditions. Conditions are chosen using a weighted stochastic grid sampling algorithm. An implemented objective function measures how desirable it is to sample from a point condition (T, P, concentrations) based on prior run conditions (weighted by how recent they were and how many objects they returned). Each iteration this objective function is evaluated at a grid of points spanning the reactor range (the grid has  $20^N$  points where N is the number of dimensions). The grid values are then normalized to one and a grid point is chosen with probability equal to its normalized objective function value. Then a random step of maximum length  $\sqrt{2}/2$  times the distance between grid points is taken from that grid point to give the chosen condition point. The random numbers are seeded so that this does not make the algorithm non-deterministic.



The T and P range, the grid points and the circle of conditions chosen from at each grid point.

These variable condition reactors run a defined number of times (nSims) each reactor cycle. Use of these reactors tends to improve treatment of reaction conditions that otherwise would be between reactors and reduce the number of simulations needed by focusing on reaction conditions at which the model terminates earlier. An example with sensitivity analysis at a specified reaction condition is available below:

```
simpleReactor(
    temperature=[(1000, 'K'), (1500, 'K')],
    pressure=[(1.0, 'bar'), (10.0, 'bar')],
    nSims=12,
    initialMoleFractions={
        "ethane": [0.05, 0.15],
        "O2": 0.1,
        "N2": 0.9,
    },
    terminationConversion={
        'ethane': 0.1,
    },
    terminationTime=(1e1, 's'),
    sensitivityTemperature = (1000, 'K'),
    sensitivityPressure = (10.0, 'bar'),
    sensitivityMoleFractions = {"ethane": 0.1, "O2": 0.9},
    sensitivity=["ethane", "O2"],
```

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```
sensitivityThreshold=0.001,  
balanceSpecies = "N2",  
)
```

Note that increasing `nSims` improves convergence over the entire range, but convergence is only guaranteed at the last set of `nSims` reaction conditions. Theoretically if `nSims` is set high enough the RMG model converges over the entire interval. Except at very small values for `nSims` the convergence achieved is usually as good or superior to that achieved using the same number of evenly spaced fixed reactors.

If there is a particular reaction condition you expect to converge more slowly than the rest of the range there is virtually no cost to using a single condition reactor (or a ranged reactor at a smaller range) at that condition and a ranged reactor with a smaller value for `nSims`. This is because the fixed reactor simulations will almost always be useful and keep the overall RMG job from terminating while the ranged reactor samples the faster converging conditions.

What you should actually set `nSims` to is very system dependent. The value you choose should be at least  $2 + N$  where  $N$  is the number of dimensions the reactor spans ( $T \Rightarrow N=1$ ,  $T$  and  $P \Rightarrow N=2$ , etc...). There may be benefits to setting it as high as  $2 + 5N$ . The first should give you convergence over most of the interval that is almost always better than the same number of fixed reactors. The second should get you reasonably close to convergence over the entire range for  $N \leq 2$ .

For gas phase reactors if normalization of the ranged mole fractions is undesirable (eg. perhaps a specific species mole fractions needs to be kept constant) one can use a `balanceSpecies`. When a `balanceSpecies` is used instead of normalizing the mole fractions the concentration of the defined `balanceSpecies` is adjusted to maintain an overall mole fraction of one. This ensures that all species except the `balanceSpecies` have mole fractions within the range specified.

### 1.4.6 Simulator Tolerances

The next two lines specify the absolute and relative tolerance for the ODE solver, respectively. Common values for the absolute tolerance are  $1e-15$  to  $1e-25$ . Relative tolerance is usually  $1e-4$  to  $1e-8$ :

```
simulator(  
    atol=1e-16,  
    rtol=1e-8,  
    sens_atol=1e-6,  
    sens_rtol=1e-4,  
)
```

The `sens_atol` and `sens_rtol` are optional arguments for the sensitivity absolute tolerance and sensitivity relative tolerances, respectively. They are set to a default value of  $1e-6$  and  $1e-4$  respectively unless the user specifies otherwise. They do not apply when sensitivity analysis is not conducted.

### 1.4.7 Model Tolerances

Model tolerances dictate how species get included in the model. For more information, see the theory behind how RMG builds models using the *Flux-based Algorithm*. For running an initial job, it is recommended to only change the `toleranceMoveToCore` and `toleranceInterruptSimulation` values to an equivalent desired value. We find that typically a value between  $0.01$  and  $0.05$  is best. If your model cannot converge within a few hours, more advanced settings such as *reaction filtering* or *pruning* can be turned on to speed up your simulation at a slight risk of omitting chemistry.

```
model(
    toleranceMoveToCore=0.1,
    toleranceInterruptSimulation=0.1,
)
```

- `toleranceMoveToCore` indicates how high the edge flux ratio for a species must get to enter the core model. This tolerance is designed for controlling the accuracy of final model.
- `toleranceInterruptSimulation` indicates how high the edge flux ratio must get to interrupt the simulation (before reaching the `terminationConversion` or `terminationTime`). This value should be set to be equal to `toleranceMoveToCore` unless the advanced *pruning* feature is desired.

### Advanced Setting: Speed Up by Filtering Reactions

For generating models for larger molecules, RMG-Py may have trouble converging because it must find reactions on the order of  $(n_{\text{reaction sites}})^{n_{\text{species}}}$ . Thus it can be further sped up by pre-filtering reactions that are added to the model. This modification to the algorithm does not react core species together until their concentrations are deemed high enough. It is recommended to turn on this flag when the model does not converge with normal parameter settings. See *Filtering Reactions within the Flux-based Algorithm*. for more details.

```
model(
    toleranceMoveToCore=0.1,
    toleranceInterruptSimulation=0.1,
    filterReactions=True,
    filterThreshold=5e8,
)
```

#### Additional parameters:

- `filterReactions`: set to True if reaction filtering is turned on. By default it is set to False.
- `filterThreshold`: click [here](#) for more description about its effect. Default: 5e8

### Advanced Setting: Speed Up by Pruning

For further speed-up, it is also possible to perform mechanism generation with pruning of “unimportant” edge species to reduce memory usage.

A typical set of parameters for pruning is:

```
model(
    toleranceMoveToCore=0.5,
    toleranceInterruptSimulation=1e8,
    toleranceKeepInEdge=0.05,
    maximumEdgeSpecies=200000,
    minCoreSizeForPrune=50,
    minSpeciesExistIterationsForPrune=2,
)
```

#### Additional parameters:

- `toleranceKeepInEdge` indicates how low the edge flux ratio for a species must be to keep on the edge. This should be set to zero, which is its default.

- `maximumEdgeSpecies` indicates the upper limit for the size of the edge. The default value is set to 1000000 species.
- `minCoreSizeForPrune` ensures that a minimum number of species are in the core before pruning occurs, in order to avoid pruning the model when it is far away from completeness. The default value is set to 50 species.
- `minSpeciesExistIterationsForPrune` is set so that the edge species stays in the job for at least that many iterations before it can be pruned. The default value is 2 iterations.

### Recommendations:

We recommend setting `toleranceKeepInEdge` to not be larger than 10% of `toleranceMoveToCore`, based on a pruning case study. In order to always enable pruning, `toleranceInterruptSimulation` should be set as a high value, e.g.  $1e8$ . `maximumEdgeSpecies` can be adjusted based on user's RAM size. Usually 200000 edge species would cause memory shortage of 8GB computer, setting `maximumEdgeSpecies` = 200000 (or lower values) could effectively prevent memory crash.

### Additional Notes:

Note that when using pruning, RMG will not prune unless all reaction systems reach the goal reaction time or conversion without exceeding the `toleranceInterruptSimulation`. Therefore, you may find that RMG is not pruning even though the model edge size exceeds `maximumEdgeSpecies`, or an edge species has flux below the `toleranceKeepInEdge`. This is a safety check within RMG to ensure that species are not pruned too early, resulting in inaccurate chemistry. In order to increase the likelihood of pruning you can try increasing `toleranceInterruptSimulation` to an arbitrarily high value.

As a contrast, a typical set of parameters for non-pruning is:

```
model(  
    toleranceKeepInEdge=0,  
    toleranceMoveToCore=0.5,  
    toleranceInterruptSimulation=0.5,  
)
```

where `toleranceKeepInEdge` is always 0, meaning all the edge species will be kept in edge since all the edge species have positive flux. `toleranceInterruptSimulation` equals to `toleranceMoveToCore` so that ODE simulation get interrupted once discovering a new core species. Because the ODE simulation is always interrupted, no pruning is performed.

Please find more details about the theory behind pruning at [Pruning Theory](#).

## Advanced Setting: Thermodynamic Pruning

Thermodynamic pruning is an alternative to flux pruning that does not require a given simulation to complete to remove excess species. The thermodynamic criteria is calculated by determining the minimum and maximum Gibbs energies of formation ( $G_{min}$  and  $G_{max}$ ) among species in the core. If the Gibbs energy of formation of a given species is  $G$  the value of the criteria is  $(G - G_{max}) / (G_{max} - G_{min})$ . All of the Gibbs energies are evaluated at the highest temperature used in all of the reactor systems. This means that a value of 0.2 for the criterion implies that it will not add species that have Gibbs energies of formation greater than 20% of the core Gibbs energy range greater than the maximum Gibbs energy of formation within the core.

For example

```
model(  
    toleranceMoveToCore=0.5,  
    toleranceInterruptSimulation=0.5,  
    toleranceThermoKeepSpeciesInEdge=0.5,
```

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```

maximumEdgeSpecies=200000,
minCoreSizeForPrune=50,
)

```

**Advantages over flux pruning:**

Species are removed immediately if they violate tolerance. Completing a simulation is unnecessary for this pruning so there is no need to waste time setting the interrupt tolerance higher than the movement tolerance. Will always maintain the correct `maximumEdgeSpecies`.

**Primary disadvantage:**

Since we determine whether to add species primarily based on flux, at tight tolerances this is more likely to kick out species RMG might otherwise have added to core.

**Advanced Setting: Taking Multiple Species At A Time**

Taking multiple objects (species, reactions or `pdepNetworks`) during a given simulation can often decrease your overall model generation time over only taking one. For this purpose there is a `maxNumObjsPerIter` parameter that allows RMG to take that many species, reactions or `pdepNetworks` from a given simulation. This is done in the order they trigger their respective criteria.

You can also set `terminateAtMaxObjects=True` to cause it to terminate when it has the maximum number of objects allowed rather than waiting around until it hits an interrupt tolerance. This avoids additional simulation time, but will also make it less likely to finish simulations, which can affect flux pruning.

For example

```

model(
    toleranceKeepInEdge=0.0,
    toleranceMoveToCore=0.1,
    toleranceInterruptSimulation=0.3,
    maxNumObjsPerIter=2,
    terminateAtMaxObjects=True,
)

```

Note that this can also result in larger models, however, sometimes these larger models (from taking more than one object at a time) pick up chemistry that would otherwise have been missed.

**Advanced Setting: Dynamics Criterion**

While the flux criterion works very well for identifying new species that have high flux and therefore will likely be high throughput or high concentration species, it provides few automatic guarantees about how well a given model will accurately represent the concentrations of the involved species. The dynamics criterion is more complex than the flux criterion, but in general it is a measure of how much impact a given reaction will have on the concentrations of core species. A more detailed explanation is available in the theory section: [Dynamics Criterion](#).

Reasonable values for the dynamics criterion range typically between 2-30.

For example

```

model(
    toleranceMoveToCore=0.1,
    toleranceInterruptSimulation=0.1,

```

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```
toleranceMoveEdgeReactionToCore=10.0,  
toleranceMoveEdgeReactionToCoreInterrupt=5.0,  
)
```

Note that it is highly recommended to use the dynamics criterion only alongside the flux criterion and not by itself.

### Advanced Setting: Surface Algorithm

One common issue with the dynamics criterion is that it treats all core species equally as discussed in our theory section: *Dynamics Criterion*. Because of this, if the dynamics criterion is set too low it enters a feedback loop where it adds species and then since it can't get those species' concentrations right it adds more species and so on. In order to avoid this feedback loop the surface algorithm was developed. It creates a new partition called the *surface* that is considered part of the core. We will refer to the part of the core that is not part of the surface as the *bulk core*. When operating without the dynamics criterion everything moves from edge to the bulk core as usual; however the dynamics criterion is managed differently. When using the surface algorithm most reactions pulled in by the dynamics criterion enter the surface instead of the bulk core. However, unlike movement to bulk core a constraint is placed on movement to the surface. Any reaction moved to the surface must have either both reactants or both products in the bulk core. This prevents the dynamics criterion from pulling in reactions to get the concentrations of species in the surface right avoiding the feedback loop. To avoid important species being trapped in the surface we also add criteria for movement from surface to bulk core based on flux or dynamics criterion.

For example

```
model(  
    toleranceMoveToCore=0.1,  
    toleranceInterruptSimulation=0.1,  
    toleranceMoveEdgeReactionToCore=30.0,  
    toleranceMoveEdgeReactionToCoreInterrupt=5.0,  
    toleranceMoveEdgeReactionToSurface=10.0,  
    toleranceMoveSurfaceSpeciesToCore=.01,  
    toleranceMoveSurfaceReactionToCore=5.0,  
)
```

### 1.4.8 On the fly Quantum Calculations

This block is used when quantum mechanical calculations are desired to determine thermodynamic parameters. These calculations are only run if the molecule is not included in a specified thermo library. The `onlyCyclics` option, if `True`, only runs these calculations for cyclic species. In this case, group additive estimates are used for all other species.

Molecular geometries are estimated via RDKit [RDKit]. Either MOPAC (2009 and 2012) or GAUSSIAN (2003 and 2009) can be used with the semi-empirical pm3, pm6, and pm7 (pm7 only available in MOPAC2012), specified in the software and method blocks. A folder can be specified to store the files used in these calculations, however if not specified this defaults to a *QMfiles* folder in the output folder.

The calculations are also only run on species with a maximum radical number set by the user. If a molecule has a higher radical number, the molecule is saturated with hydrogen atoms, then quantum mechanical calculations with subsequent hydrogen bond incrementation is used to determine the thermodynamic parameters.

The following is an example of the quantum mechanics options

```
quantumMechanics(  
    software='mopac',
```

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```

method='pm3',
fileStore='QMfiles',
scratchDirectory = None,
onlyCyclics = True,
maxRadicalNumber = 0,
)

```

## 1.4.9 Machine Learning-based Thermo Estimation

This block is used to turn on the machine learning module to estimate thermodynamic parameters. These calculations are only run if the molecule is not included in a specified thermo library. There are a number of different settings that can be specified to tune the estimator so that it only tries to estimate some species. This is useful because the machine learning model may perform poorly for some molecules and group additivity may be more suitable. Using the machine learning estimator for fused cyclic species of moderate size or any species with significant proportions of oxygen and/or nitrogen atoms will most likely yield better estimates than group additivity.

The available options with their default values are

```

mlEstimator(
    thermo=True,
    name='main',
    minHeavyAtoms=1,
    maxHeavyAtoms=None,
    minCarbonAtoms=0,
    maxCarbonAtoms=None,
    minOxygenAtoms=0,
    maxOxygenAtoms=None,
    minNitrogenAtoms=0,
    maxNitrogenAtoms=None,
    onlyCyclics=False,
    onlyHeterocyclics=False,
    minCycleOverlap=0,
    H298UncertaintyCutoff=(3.0, 'kcal/mol'),
    S298UncertaintyCutoff=(2.0, 'cal/(mol*K)'),
    CpUncertaintyCutoff=(2.0, 'cal/(mol*K)')
)

```

name is the name of the folder containing the machine learning model architecture and parameters in the RMG database. The next several options allow setting limits on the numbers of atoms. onlyCyclics means that only cyclic species will be estimated. onlyHeterocyclics means that only heterocyclic species will be estimated. Note that if onlyHeterocyclics setting is set to True, the machine learning estimator will be restricted to heterocyclic species regardless of the onlyCyclics setting. If onlyCyclics is False and onlyHeterocyclics is True, RMG will log a warning that onlyCyclics should also be True and the machine learning estimator will be restricted to heterocyclic species because they are a subset of cyclics. minCycleOverlap specifies the minimum number of atoms that must be shared between any two cycles. For example, if there are only disparate monocycles or no cycles in a species, the overlap is zero; “spiro” cycles have an overlap of one; “fused” cycles have an overlap of two; and “bridged” cycles have an overlap of at least three. Note that specifying any value greater than zero will automatically restrict the machine learning estimator to only consider cyclic species regardless of the onlyCyclics setting. If onlyCyclics is False and minCycleOverlap is greater than zero, RMG will log a warning that onlyCyclics should also be True and the machine learning estimator will be restricted to only cyclic species with the specified minimum cycle overlap.

Note that the current machine learning model is not yet capable of estimating uncertainty so the UncertaintyCutoff values do not yet have any effect.

### 1.4.10 Pressure Dependence

This block is used when the model should account for pressure dependent rate coefficients. RMG can estimate pressure dependence kinetics based on `Modified Strong Collision` and `Reservoir State` methods. The former utilizes the modified strong collision approach of Chang, Bozzelli, and Dean [Chang2000], and works reasonably well while running more rapidly. The latter utilizes the steady-state/reservoir-state approach of Green and Bhatti [Green2007], and is more theoretically sound but more expensive.

The following is an example of pressure dependence options

```
pressureDependence(  
    method='modified strong collision',  
    maximumGrainSize=(0.5,'kcal/mol'),  
    minimumNumberOfGrains=250,  
    temperatures=(300,2000,'K',8),  
    pressures=(0.01,100,'bar',5),  
    interpolation=('Chebyshev', 6, 4),  
    maximumAtoms=16,  
)
```

The various options are as follows:

#### Method used for estimating pressure dependent kinetics

To specify the modified strong collision approach, this item should read

```
method='Modified Strong Collision'
```

To specify the reservoir state approach, this item should read

```
method='Reservoir State'
```

For more information on the two methods, consult the following resources :

#### Grain size and minimum number of grains

Since the  $k(E)$  requires discretization in the energy space, we need to specify the number of energy grains to use when solving the Master Equation. The default value for the minimum number of grains is 250; this was selected to balance the speed and accuracy of the Master Equation solver method. However, for some pressure-dependent networks, this number of energy grains will result in the pressure-dependent  $k(T, P)$  being greater than the high-P limit

```
maximumGrainSize=(0.5,'kcal/mol')  
minimumNumberOfGrains=250
```



## Temperature and pressure for the interpolation scheme

To generate the  $k(T, P)$  interpolation model, a set of temperatures and pressures must be used. RMG can do this automatically, but it must be told a few parameters. We need to specify the limits of the temperature and pressure for the fitting of the interpolation scheme and the number of points to be considered in between this limit. For typical combustion model temperatures of the experiments range from 300 - 2000 K and pressure 1E-2 to 100 bar

```
temperatures=(300,2000,'K',8)
pressures=(0.01,100,'bar',5)
```

## Interpolation scheme

To use logarithmic interpolation of pressure and Arrhenius interpolation for temperature, use the line

```
interpolation=('PDepArrhenius',)
```

The auxillary information printed to the Chemkin chem.inp file will have the “PLOG” format. Refer to Section 3.5.3 of the `CHEMKIN_Input.pdf` document and/or Section 3.6.3 of the `CHEMKIN_Theory.pdf` document. These files are part of the CHEMKIN manual.

To fit a set of Chebyshev polynomials on inverse temperature and logarithmic pressure axes mapped to [-1,1], specify “*Chebyshev*” interpolation. You should also specify the number of temperature and pressure basis functions by adding the appropriate integers. For example, the following specifies that six basis functions in temperature and four in pressure should be used

```
interpolation=('Chebyshev', 6, 4)
```

The auxillary information printed to the Chemkin chem.inp file will have the “CHEB” format. Refer to Section 3.5.3 of the `CHEMKIN_Input.pdf` document and/or Section 3.6.4 of the `CHEMKIN_Theory.pdf` document.

Regarding the number of polynomial coefficients for Chebyshev interpolated rates, please refer to the `rmgpy.kinetics.Chebyshev` documentation. The number of pressures and temperature coefficients should always be smaller than the respective number of user-specified temperatures and pressures.

## Maximum size of adduct for which pressure dependence kinetics be generated

By default pressure dependence is run for every system that might show pressure dependence, i.e. every isomerization, dissociation, and association reaction. In reality, larger molecules are less likely to exhibit pressure-dependent behavior than smaller molecules due to the presence of more modes for randomization of the internal energy. In certain cases involving very large molecules, it makes sense to only consider pressure dependence for molecules smaller than some user-defined number of atoms. This is specified e.g. using the line

```
maximumAtoms=16
```

to turn off pressure dependence for all molecules larger than the given number of atoms (16 in the above example).

### 1.4.11 Uncertainty Analysis

It is possible to request automatic uncertainty analysis following the convergence of an RMG simulation by including an uncertainty options block in the input file:

```
uncertainty(
    localAnalysis=False,
    globalAnalysis=False,
    uncorrelated=True,
    correlated=True,
    localNumber=10,
    globalNumber=5,
    terminationTime=None,
    pceRunTime=1800,
    pceErrorTol=None,
    pceMaxEvals=None,
    logx=True
)
```

RMG can perform local uncertainty analysis using first-order sensitivity coefficients output by the native RMG solver. This is enabled by setting `localAnalysis=True`. Performing local uncertainty analysis requires suitable settings in the reactor block (see [Reaction System](#)). At minimum, the output species to perform sensitivity analysis on must be specified, via the `sensitivity` argument. RMG will then perform local uncertainty analysis on the same species. Species and reactions with the largest sensitivity indices will be reported in the log file and output figures. The number of parameters reported can be adjusted using `localNumber`.

RMG can also perform global uncertainty analysis, implemented using Cantera [[Cantera](#)] and the MIT Uncertainty Quantification (MUQ) [[MUQ](#)] library. This is enabled by setting `globalAnalysis=True`. Note that local analysis is a required prerequisite of running the global analysis (at least for this semi-automatic approach), so `localAnalysis` will be enabled regardless of the input file setting. The analysis is performed by allowing the input parameters with the largest sensitivity indices (as determined from the local uncertainty analysis) to vary while performing reactor simulations using Cantera. MUQ is used to fit a Polynomial Chaos Expansion (PCE) to the resulting output surface. The number of input parameters chosen can be adjusted using `globalNumber`. Note that this number applies independently to thermo and rate parameters and output species. For example `globalNumber=5` for analysis on a single output species will result in 10 parameters being varied, while having two output species could result in up to 20 parameters being varied, assuming no overlap in the sensitive input parameters for each output.

The `uncorrelated` and `correlated` options refer to two approaches for uncertainty analysis. Uncorrelated means that all input parameters are considered to be independent, each with their own uncertainty bounds. Thus, the output uncertainty distribution is determined on the basis that every input parameter could vary within the full range of its uncertainty bounds. Correlated means that inherent relationships between parameters (such as rate rules for kinetics or group additivity values for thermochemistry) are accounted for, which reduces the uncertainty space of the input parameters.

Finally, there are a few miscellaneous options for global uncertainty analysis. The `terminationTime` applies for the reactor simulation. It is only necessary if termination time is not specified in the reactor settings (i.e. only other termination criteria are used). For PCE generation, there are three termination options: `pceRunTime` sets a time limit for adapting the PCE to the output, `pceErrorTol` sets the target L2 error between the PCE model and the true output, and `pceMaxEvals` sets a limit on the total number of model evaluations used to adapt the PCE. Longer run time, smaller error tolerance, and more model evaluations all contribute to more accurate results at the expense of computation time. The `logx` option toggles the output parameter space between mole fractions and log mole fractions. Results in mole fraction space are more physically meaningful, while results in log mole fraction space can be directly compared against local uncertainty results.

**Important Note:** The current implementation of uncertainty analysis assigns values for input parameter uncertainties based on the estimation method used by RMG. Actual uncertainties associated with the original data sources are not

used. Thus, the output uncertainties reported by these analyses should be viewed with this in mind.

### 1.4.12 Miscellaneous Options

Miscellaneous options:

```
options(
    name='Seed',
    generateSeedEachIteration=True,
    saveSeedToDatabase=True,
    units='si',
    generateOutputHTML=True,
    generatePlots=False,
    saveSimulationProfiles=True,
    verboseComments=False,
    saveEdgeSpecies=True,
    keepIrreversible=True,
    trimolecularProductReversible=False,
    saveSeedModulus=-1
)
```

The name field is the name of any generated seed mechanisms

Setting `generateSeedEachIteration` to `True` (default) tells RMG to save and update a seed mechanism and thermo library during the current run

Setting `saveSeedToDatabase` to `True` tells RMG (if generating a seed) to also save that seed mechanism and thermo library directly into the database

The units field is set to `si`. Currently there are no other unit options.

Setting `generateOutputHTML` to `True` will let RMG know that you want to save 2-D images (png files in the local species folder) of all species in the generated core model. It will save a visualized HTML file for your model containing all the species and reactions. Turning this feature off by setting it to `False` may save memory if running large jobs.

Setting `generatePlots` to `True` will generate a number of plots describing the statistics of the RMG job, including the reaction model core and edge size and memory use versus execution time. These will be placed in the output directory in the `plot/` folder.

Setting `saveSimulationProfiles` to `True` will make RMG save csv files of the simulation in `.csv` files in the `solver/` folder. The filename will be `simulation_1_26.csv` where the first number corresponds to the reaction system, and the second number corresponds to the total number of species at the point of the simulation. Therefore, the highest second number will indicate the latest simulation that RMG has complete while enlarging the core model. The information inside the csv file will provide the time, reactor volume in  $\text{m}^3$ , as well as mole fractions of the individual species.

Setting `verboseComments` to `True` will make RMG generate chemkin files with complete verbose commentary for the kinetic and thermo parameters. This will be helpful in debugging what values are being averaged for the kinetics. Note that this may produce very large files.

Setting `saveEdgeSpecies` to `True` will make RMG generate chemkin files of the edge reactions in addition to the core model in files such as `chem_edge.inp` and `chem_edge_annotated.inp` files located inside the `chemkin` folder. These files will be helpful in viewing RMG's estimate for edge reactions and seeing if certain reactions one expects are actually in the edge or not.

Setting `keepIrreversible` to `True` will make RMG import library reactions as is, whether they are reversible or irreversible in the library. Otherwise, if `False` (default value), RMG will force all library reactions to be reversible, and will assign the forward rate from the relevant library.

Setting `trimolecularProductReversible` to `False` will not allow families with three products to react in the reverse direction. Default is `True`.

Setting `saveSeedModulus` to `-1` will only save the seed from the last iteration at the end of an RMG job. Alternatively, the seed can be saved every `n` iterations by setting `saveSeedModulus` to `n`.

### 1.4.13 Species Constraints

RMG can generate mechanisms with a number of optional species constraints, such as total number of carbon atoms or electrons per species. These are applied to all of RMG's reaction families.

```
generatedSpeciesConstraints(  
    allowed=['input species', 'seed mechanisms', 'reaction libraries'],  
    maximumCarbonAtoms=10,  
    maximumOxygenAtoms=2,  
    maximumNitrogenAtoms=2,  
    maximumSiliconAtoms=2,  
    maximumSulfurAtoms=2,  
    maximumHeavyAtoms=10,  
    maximumSurfaceSites=2,  
    maximumRadicalElectrons=2,  
    maximumSingletCarbenes=1,  
    maximumCarbeneRadicals=0,  
    maximumIsotopicAtoms=2,  
    allowSingletO2 = False,  
)
```

An additional flag `allowed` can be set to allow species from either the input file, seed mechanisms, or reaction libraries to bypass these constraints. Note that this should be done with caution, since the constraints will still apply to subsequent products that form.

By default, the `allowSingletO2` flag is set to `False`. See [Representing Oxygen](#) for more information.

### 1.4.14 Staging

It is now possible to concatenate different model and simulator blocks into the same run in stages. Any given stage will terminate when the RMG run terminates and then the current group of model and simulator parameters will be switched out with the next group and the run will continue until that stage terminates. Once the last stage terminates the run ends normally. This is currently enabled only for the model and simulator blocks.

There must be the same number of each of these blocks (although only having one simulator block and many model blocks is enabled as well) and RMG will enter each stage these define in the order they were put in the input file.

To enable easier manipulation of staging a new parameter in the model block was developed `maxNumSpecies` that is the number of core species at which that stage (or if it is the last stage the entire model generation process) will terminate.

For example

```
model(  
    toleranceKeepInEdge=0.0,  
    toleranceMoveToCore=0.1,
```

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```

toleranceInterruptSimulation=0.1,
maximumEdgeSpecies=100000,
maxNumSpecies=100
)

```

### 1.4.15 Restarting from a Seed Mechanism

The only method for restarting an RMG-Py job is to restart the job from a seed mechanism. There are many scenarios when the user might want to do this, including continuing on a job that ran out of time or crashed as the result of a now fixed bug. To restart from a seed mechanism, the block below must be added on to the input file.

```
restartFromSeed(path='seed')
```

The `path` flag is the path to the seed mechanism folder, which contains three subfolders that must be titled as follows: `filters`, `seed`, `seed_edge`. The path can be a relative path from the input.py file or an absolute path on disk

Alternatively, you may also specify the paths to each of the following files/directories: `coreSeed` (path to seed mechanism folder containing files named `reactions.py` and `dictionary.txt` that will go into the model core), `edgeSeed` (path to edge seed mechanism folder containing files named `reactions.py` and `dictionary.txt` that will go into the model edge), `filters` (an h5 binary file storing the uni-, bi-, and optionally tri-molecular thresholds generated by RMG from previous run (must be RMG version > 2.4.1)), `speciesMap` (a YAML file specifying what species are at each index in the filters).

```

restartFromSeed(coreSeed='seed/seed' # Path to core seed folder. Must contain
↳ `reactions.py` and `dictionary.txt`
                edgeSeed='seed/seed_edge' # Path to edge seed folder containing
↳ `reactions.py` and `dictionary.txt`
                filters='seed/filters/filters.h5',
                speciesMap='seed/filters/species_map.yml')

```

Then, to restart from the seed mechanism the input file is submitted as normal.

```
python rmg.py input.py
```

Once the restart job has begun, RMG will move the seed mechanism files to a new subfolder in the output directory entitled `previous_restart`. This is to back-up the seed mechanism used for restarting, as everything in the `seed` subfolder of the output directory is overwritten by RMG during the course of mechanism generation.

RMG also outputs a file entitled `restart_from_seed.py` the first time a seed mechanism is generated during the course of an RMG job (so long as the RMG job was not itself a restarted job). This file is an exact duplicate of the original input file with the exception that the restart block has been added on automatically for convenience. In this way this file is treated in the exact way as a normal input file.

Finally, **note that it is advised to turn on generating the seed each iteration so that you can restart an RMG job right where it left off**. This can be done by setting `generateSeedEachIteration=True` in the options block of the input file.

## 1.5 Example Input Files

Perhaps the best way to learn the input file syntax is by example. To that end, a number of example input files and their corresponding output have been given in the `examples` directory. Two of the RMG jobs are shown below.

### 1.5.1 Ethane pyrolysis (Minimal)

This is the minimal example file characterizing a very basic system for ethane pyrolysis and should run quickly if RMG is set up properly. It does not include any calculation of pressure-dependent reaction rates.

```
# Data sources
database(
    thermoLibraries = ['primaryThermoLibrary'],
    reactionLibraries = [],
    seedMechanisms = [],
    kineticsDepositories = ['training'],
    kineticsFamilies = 'default',
    kineticsEstimator = 'rate rules',
)

# List of species
species(
    label='ethane',
    reactive=True,
    structure=SMILES("CC"),
)

# Reaction systems
simpleReactor(
    temperature=(1350, 'K'),
    pressure=(1.0, 'bar'),
    initialMoleFractions={
        "ethane": 1.0,
    },
    terminationConversion={
        'ethane': 0.9,
    },
    terminationTime=(1e6, 's'),
)

simulator(
    atol=1e-16,
    rtol=1e-8,
)

model(
    toleranceKeepInEdge=0.0,
    toleranceMoveToCore=0.1,
    toleranceInterruptSimulation=0.1,
    maximumEdgeSpecies=100000,
    filterReactions=True,
)
```

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```
options(
    units='si',
    generateOutputHTML=True,
    generatePlots=False,
    saveEdgeSpecies=True,
    saveSimulationProfiles=True,
)
```

### 1.5.2 1,3-hexadiene pyrolysis

This example models the pyrolysis of 1,3-hexadiene and demonstrates the effect of turning on the pressure-dependence module within RMG.

```
# Data sources
database(
    thermoLibraries = ['primaryThermoLibrary', 'GRI-Mech3.0'],
    reactionLibraries = [],
    seedMechanisms = [],
    kineticsDepositories = ['training'],
    kineticsFamilies = 'default',
    kineticsEstimator = 'rate rules',
)

# Constraints on generated species
generatedSpeciesConstraints(
    maximumRadicalElectrons = 2,
)

# List of species
species(
    label='HxD13',
    reactive=True,
    structure=SMILES("C=CC=CCC"),
)
species(
    label='CH4',
    reactive=True,
    structure=SMILES("C"),
)
species(
    label='H2',
    reactive=True,
    structure=adjacencyList(
        """
        1 H u0 p0 {2,S}
        2 H u0 p0 {1,S}
        """,
    ),
)
species(
    label='N2',
```

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```

    reactive=False,
    structure=InChI("InChI=1/N2/c1-2"),
)

# Reaction systems
simpleReactor(
    temperature=(1350, 'K'),
    pressure=(1.0, 'bar'),
    initialMoleFractions={
        "HxD13": 6.829e-4,
        "CH4": 0.104,
        "H2": 0.0156,
        "N2": 0.8797,
    },
    terminationConversion={
        'HxD13': 0.9,
    },
    terminationTime=(1e0, 's'),
)

simulator(
    atol=1e-16,
    rtol=1e-8,
)

model(
    toleranceKeepInEdge=0.0,
    toleranceMoveToCore=0.5,
    toleranceInterruptSimulation=0.5,
    maximumEdgeSpecies=100000
)

quantumMechanics(
    software='mopac',
    method='pm3',
    # fileStore='QMfiles', # relative to where it is run. Defaults within the output_
    ↪ folder.
    scratchDirectory = None, # not currently used
    onlyCyclics = True,
    maxRadicalNumber = 0,
)

pressureDependence(
    method='modified strong collision',
    maximumGrainSize=(0.5, 'kcal/mol'),
    minimumNumberOfGrains=250,
    temperatures=(300, 2000, 'K', 8),
    pressures=(0.01, 100, 'bar', 5),
    interpolation=('Chebyshev', 6, 4),
)

options(

```

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```

units='si',
generateOutputHTML=False,
generatePlots=False,
)

```

### 1.5.3 Commented input file

This is a fully commented input file with all optional blocks for new users to better understand the options of rmg input files

```

# Uncomment either of the blocks below to restart from a seed mechanism
#
# # Option 1: Specify the path to an RMG (version > 2.4.1) generated seed mechanism
# ↪ folder, which contains all of the
# # required files (core and edge seed, filters and mappings) in their default
# ↪ locations and names in the seed folder.
# restartFromSeed(path='seed') # Location of the seed mechanism (with `filters`
# ↪ subfolder) to load for restarting
#
# # Option 2: Specify the paths of each of the required files individually.
# restartFromSeed(coreSeed='seed/seed' # Path to core seed folder. Must contain
# ↪ `reactions.py` and `dictionary.txt`
#                 edgeSeed='seed/seed_edge' # Path to edge seed folder containing
# ↪ `reactions.py` and `dictionary.txt`
#                 filters='seed/filters/filters.h5',
#                 speciesMap='seed/filters/species_map.yml')

# Data sources
database(
    # overrides RMG thermo calculation of RMG with these values.
    # libraries found at http://rmg.mit.edu/database/thermo/libraries/
    # if species exist in multiple libraries, the earlier libraries overwrite the
    # previous values
    thermoLibraries=['BurkeH202', 'primaryThermoLibrary', 'DFT-QCI-thermo', 'CBS-QB3-
    ↪ 1dHR'],
    # overrides RMG transport calculations with these values.
    # if species exist in multiple libraries, the earlier libraries overwrite the
    ↪ previous values
    transportLibraries=['PrimaryTransportLibrary.py'],
    # overrides RMG kinetics estimation if needed in the core of RMG.
    # list of libraries found at http://rmg.mit.edu/database/kinetics/libraries/
    # libraries can be input as either a string or tuple of form ('library_name', True/
    ↪ False)
    # where a `True` indicates that all unused reactions will be automatically added
    # to the chemkin file at the end of the simulation. Placing just string values
    # defaults the tuple to `False`. The string input is sufficient in almost
    # all situations
    reactionLibraries=[('C3', False)],
    # seed mechanisms are reactionLibraries that are forced into the initial mechanism
    # in addition to species listed in this input file.
    # This is helpful for reducing run time for species you know will appear in

```

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```

# the mechanism.
seedMechanisms=['primaryH2O2', 'ERC-FoundationFuelv0.9'],
# lists specific families used to generate the model. 'default' uses a list of
# families from RMG-Database/input/kinetics/families/recommended.py
# a visual list of families is available in PDF form at RMG-database/families
kineticsFamilies='default',
# this is normally not changed in general RMG runs. Usually used for testing with
# outside kinetics databases
kineticsDepositories='default',
# specifies how RMG calculates rates. currently, the only option is 'rate rules'
kineticsEstimator='rate rules',
)

# List of species
# list initial and expected species below to automatically put them into the core_
↪mechanism.
# 'structure' can utilize method of SMILES("put_SMILES_here"),
# adjacencyList("""put_adj_list_here"""), or InChI("put_InChI_here")
# for molecular oxygen, use the smiles string [O][O] so the triplet form is used
species(
    label='butane',
    reactive=True, # this parameter is optional if true
    structure=SMILES("CCCC"),
)
species(
    label='O2',
    structure=SMILES("[O][O]"),
)
species(
    label='N2',
    reactive=False,
    structure=adjacencyList("""
1 N u0 p1 c0 {2,T}
2 N u0 p1 c0 {1,T}
"""),
)
# You can list species not initially in reactor to make sure RMG includes them in the_
↪mechanism
species(
    label='QOOH',
    reactive=True,
    structure=SMILES("O0CC[CH]C")
)
species(
    label='CO2',
    reactive=True,
    structure=SMILES("O=C=O")
)

# You can also list forbidden structures to forbid a certain molecule or set of_
↪molecules from your model
# To prevent a single molecule from your model, use SMILES or adjacencyList to define_
↪the structure

```

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```

# For example, if you do not want cyclopropyne in your model, you can forbid it using
→ SMILES
# forbidden(
#     label='cyclopropyne',
#     structure=SMILES("C1#CC1")
# )
# or adjacencyList
# forbidden(
#     label='cyclopropyne',
#     structure=adjacencyList("""
# 1 C u0 p0 c0 {2,S} {3,S} {4,S} {5,S}
# 2 C u0 p0 c0 {1,S} {3,T}
# 3 C u0 p0 c0 {1,S} {2,T}
# 4 H u0 p0 c0 {1,S}
# 5 H u0 p0 c0 {1,S}
# """),
# )
# If you want to exclude not just cyclopropyne but all three member rings, use
→ `adjacencyListGroup`
# to define the forbidden group structure
# forbidden(
#     label='Three-member Ring',
#     structure=adjacencyListGroup("""
# 1 R ux {2,[S,D,T]} {3,[S,D,T]}
# 2 R ux {1,[S,D,T]} {3,[S,D,T]}
# 3 R ux {1,[S,D,T]} {2,[S,D,T]}
# """),
# )

# Reaction systems
# currently RMG models only constant temperature and pressure as homogeneous batch
→ reactors.
# two options are: simpleReactor for gas phase or liquidReactor for liquid phase
# use can use multiple reactors in an input file for each condition you want to test.
simpleReactor(
    # specifies reaction temperature with units
    temperature=(700, 'K'),
    # specifies reaction pressure with units
    pressure=(10.0, 'bar'),
    # list initial mole fractions of compounds using the label from the 'species'
→ label.
    # RMG will normalize if sum/=1
    initialMoleFractions={
        "N2": 4,
        "O2": 1,
        "butane": 1. / 6.5,
    },
    # number of simulations used to explore variable temperature and pressure reactors
    nSims=6,
    # the following two values specify when to determine the final output model
    # only one must be specified
    # the first condition to be satisfied will terminate the process

```

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```

    terminationConversion={
        'butane': .99,
    },
    terminationTime=(40, 's'),
    # the next two optional values specify how RMG computes sensitivities of
    # rate coefficients with respect to species concentrations.
    # sensitivity contains a list of species' labels to conduct sensitivity analysis.
    → on.
    # sensitivityThreshold is the required sensitivity to be recorded in the csv output.
    → file
    # sensitivity=['CH4'],
    # sensitivityThreshold=0.0001,
)

# liquidReactor(
#     temperature=(500, 'K'),
#     initialConcentrations={
#         "N2": 4,
#         "O2": 1,
#         "CO": 1,
#     },
#     terminationConversion=None,
#     terminationTime=(3600, 's'),
#     sensitivity=None,
#     sensitivityThreshold=1e-3
# )
# liquid reactors also have solvents, you can specify one solvent
# list of solvents available at : http://rmg.mit.edu/database/solvation/libraries/
→ solvent/
# solvation('water')

# determines absolute and relative tolerances for ODE solver and sensitivities.
# normally this doesn't cause many issues and is modified after other issues are
# ruled out
simulator(
    atol=1e-16,
    rtol=1e-8,
    # sens_atol=1e-6,
    # sens_rtol=1e-4,
)

# used to add species to the model and to reduce memory usage by removing unimportant.
→ additional species.
# all relative values are normalized by a characteristic flux at that time point
model(
    # determines the relative flux to put a species into the core.
    # A smaller value will result in a larger, more complex model
    # when running a new model, it is recommended to start with higher values and
    → then decrease to converge on the model
    toleranceMoveToCore=0.1,
    # comment out the next three terms to disable pruning
    # determines the relative flux needed to not remove species from the model.

```

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```

# Lower values will keep more species and utilize more memory
toleranceKeepInEdge=0.01,
# determines when to stop a ODE run to add a species.
# Lower values will improve speed.
# if it is too low, may never get to the end simulation to prune species.
toleranceInterruptSimulation=1,
# number of edge species needed to accumulate before pruning occurs
# larger values require more memory and will prune less often
maximumEdgeSpecies=100000,
# minimum number of core species needed before pruning occurs.
# this prevents pruning when kinetic model is far away from completeness
minCoreSizeForPrune=50,
# make sure that the pruned edge species have existed for a set number of RMG
iterations.
# the user can specify to increase it from the default value of 2
minSpeciesExistIterationsForPrune=2,
# filter the reactions during the enlarge step to omit species from reacting if
their
# concentration are deemed to be too low
filterReactions=False,
# for bimolecular reactions, will only allow them to react if
# filterThreshold*C_A*C_B > toleranceMoveToCore*characteristic_rate
# and if filterReactions=True
filterThreshold=1e8,
)

options(
# provides a name for the seed mechanism produced at the end of an rmg run
default is 'Seed'
name='SeedName',
# if True (default) every iteration it saves the current model as libraries/seeds
# (and deletes the old one)
# Unlike HTML this is inexpensive time-wise
# note a seed mechanism will be generated at the end of a completed run and some
incomplete
# runs even if this is set as False
generateSeedEachIteration=True,
# If True the mechanism will also be saved directly as kinetics and thermo
libraries in the database
saveSeedToDatabase=False,
# only option is 'si'
units='si',
# Draws images of species and reactions and saves the model output to HTML.
# May consume extra memory when running large models.
generateOutputHTML=True,
# generates plots of the RMG's performance statistics. Not helpful if you just
want a model.
generatePlots=False,
# saves mole fraction of species in 'solver/' to help you create plots
saveSimulationProfiles=False,
# gets RMG to output comments on where kinetics were obtained in the chemkin file.
# useful for debugging kinetics but increases memory usage of the chemkin output
file
    
```

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```

    verboseComments=False,
    # gets RMG to generate edge species chemkin files. Uses lots of memory in output.
    # Helpful for seeing why some reaction are not appearing in core model.
    saveEdgeSpecies=False,
    # Sets a time limit in the form DD:HH:MM:SS after which the RMG job will stop.
    ↪ Useful for profiling on jobs that
    # do not converge.
    # wallTime = '00:00:00',
    # Forces RMG to import library reactions as reversible (default). Otherwise, if
    ↪ set to True, RMG will import library
    # reactions while keeping the reversibility as as.
    keepIrreversible=False,
    # Allows families with three products to react in the diverse direction (default).
    trimolecularProductReversible=True,
    # Allows a seed to be saved every n iterations.
    # The default of -1 causes the iteration to only be saved at the end of the RMG
    ↪ job
    saveSeedModulus=-1
)

# optional module allows for correction to unimolecular reaction rates at low
↪ pressures and/or temperatures.
pressureDependence(
    # two methods available: 'modified strong collision' is faster and less accurate
    ↪ than 'reservoir state'
    method='modified strong collision',
    # these two categories determine how fine energy is discretized.
    # more grains increases accuracy but takes longer
    maximumGrainSize=(0.5, 'kcal/mol'),
    minimumNumberOfGrains=250,
    # the conditions for the rate to be output over
    # parameter order is: low_value, high_value, units, internal points
    temperatures=(300, 2200, 'K', 2),
    pressures=(0.01, 100, 'bar', 3),
    # The two options for interpolation are 'PDepArrhenius' (no extra arguments) and
    # 'Chebyshev' which is followed by the number of basis sets in
    # Temperature and Pressure. These values must be less than the number of
    # internal points specified above
    interpolation=('Chebyshev', 6, 4),
    # turns off pressure dependence for molecules with number of atoms greater than
    ↪ the number specified below
    # this is due to faster internal rate of energy transfer for larger molecules
    maximumAtoms=15,
)

# optional block adds constraints on what RMG can output.
# This is helpful for improving the efficiency of RMG, but wrong inputs can lead to
↪ many errors.
generatedSpeciesConstraints(
    # allows exceptions to the following restrictions
    allowed=['input species', 'seed mechanisms', 'reaction libraries'],
    # maximum number of each atom in a molecule

```

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```

maximumCarbonAtoms=4,
maximumOxygenAtoms=7,
maximumNitrogenAtoms=0,
maximumSiliconAtoms=0,
maximumSulfurAtoms=0,
# max number of non-hydrogen atoms
# maximumHeavyAtoms=20,
# maximum radicals on a molecule
maximumRadicalElectrons=1,
# maximum number of singlet carbenes (lone pair on a carbon atom) in a molecule
maximumSingletCarbenes=1,
# maximum number of radicals on a molecule with a singlet carbene
# should be lower than maximumRadicalElectrons in order to have an effect
maximumCarbeneRadicals=0,
# If this is false or missing, RMG will throw an error if the more less-stable
→ form of O2 is entered
# which doesn't react in the RMG system. normally input O2 as triplet with SMILES
→ [O][O]
# allowSingletO2=False,
# maximum allowed number of non-normal isotope atoms:
# maximumIsotopicAtoms=2,
)

# optional block allows thermo to be estimated through quantum calculations
# quantumMechanics(
#     # the software package for calculations...can use 'mopac' or 'gaussian' if
→ installed
#     software='mopac',
#     # methods available for calculations. 'pm2' 'pm3' or 'pm7' (last for mopac only)
#     method='pm3',
#     # where to store calculations
#     fileStore='QMfiles',
#     # where to store temporary run files
#     scratchDirectory=None,
#     # onlyCyclics allows linear molecules to be calculated using bensen group
→ additivity....need to verify
#     onlyCyclics=True,
#     # how many radicals should be utilized in the calculation.
#     # If the amount of radicals is more than this, RMG will use hydrogen bond
→ incrementation method
#     maxRadicalNumber=0,
# )

# optional block allows thermo to be estimated through ML estimator
# mlEstimator(
#     thermo=True,
#     # Name of folder containing ML architecture and parameters in database
#     name='main',
#     # Limits on atom numbers
#     minHeavyAtoms=1,
#     maxHeavyAtoms=None,
#     minCarbonAtoms=0,

```

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```

#     maxCarbonAtoms=None,
#     minOxygenAtoms=0,
#     maxOxygenAtoms=None,
#     minNitrogenAtoms=0,
#     maxNitrogenAtoms=None,
#     # Limits on cycles
#     onlyCyclics=False,
#     onlyHeterocyclics=False, # If onlyHeterocyclics is True, the machine learning
    ↳ estimator is restricted to only
#                               heterocyclics species regardless of onlyCyclics
    ↳ setting.
#                               But onlyCyclics should also be True if
    ↳ onlyHeterocyclics is True.
#     minCycleOverlap=0, # specifies the minimum number of atoms that must be shared
    ↳ between any two cycles.
#                               If minCycleOverlap is greater than zero, the machine
    ↳ learning estimator is restricted to
#                               only cyclic species with the specified minimum cyclic
    ↳ overlap regardless of onlyCyclics
#                               setting.
#     # If the estimated uncertainty of the thermo prediction is greater than
#     # any of these values, then don't use the ML estimate
#     H298UncertaintyCutoff=(3.0, 'kcal/mol'),
#     S298UncertaintyCutoff=(2.0, 'cal/(mol*K)'),
#     CpUncertaintyCutoff=(2.0, 'cal/(mol*K)')
# )

```

## 1.6 Running a Job

**Note:** In all these examples `rmg.py` should be the path to your installed RMG (eg. yours might be `/Users/joeblogs/Code/RMG-Py/rmg.py`) and `input.py` is the path to the input file you wish to run (eg. yours might be `RMG-runs/hexadiene/input.py`). If you get an error like `python: can't open file 'rmg.py': [Errno 2] No such file or directory` then probably the first of these is wrong. If you get an error like `IOError: [Errno 2] No such file or directory: '/some/path/to/input.py'` then probably the second of these is wrong.

Running a basic RMG job is straightforward, as shown in the example below. However, depending on your case you might want to add the flags outlined in the following section. We recommend you make a job-specific directory for each RMG simulation. Some jobs can take quite a while to complete, so we also recommend using a job scheduler if working in a linux environment.

Basic run:

```
python rmg.py input.py
```



### 1.6.1 Input flags

The options for input flags can be found in `/RMG-Py/rmgpy/util.py`. Running

```
python rmg.py -h
```

at the command line will print the documentation from `util.py`, which is reproduced below for convenience:

```
usage: rmg.py [-h] [-q | -v | -d] [-o DIR] [-r path/to/seed/] [-p] [-P]
            [-t DD:HH:MM:SS] [-i MAXITER] [-n MAXPROC] [-k]
            FILE

Reaction Mechanism Generator (RMG) is an automatic chemical reaction mechanism
generator that constructs kinetic models composed of elementary chemical
reaction steps using a general understanding of how molecules react.

positional arguments:
  FILE                  a file describing the job to execute

optional arguments:
  -h, --help            show this help message and exit
  -q, --quiet           only print warnings and errors
  -v, --verbose         print more verbose output
  -d, --debug           print debug information
  -o DIR, --output-directory DIR
                        use DIR as output directory
  -r path/to/seed/, --restart path/to/seed/
                        restart RMG from a seed
  -p, --profile         run under cProfile to gather profiling statistics, and
                        postprocess them if job completes
  -P, --postprocess     postprocess profiling statistics from previous
                        [failed] run; does not run the simulation
  -t DD:HH:MM:SS, --walltime DD:HH:MM:SS
                        set the maximum execution time
  -i MAXITER, --maxiter MAXITER
                        set the maximum number of RMG iterations
  -n MAXPROC, --maxproc MAXPROC
                        max number of processes used during reaction
                        generation
  -k, --kineticsdatastore
                        output a folder, kinetics_database, that contains a
                        .txt file for each reaction family listing the
                        source(s) for each entry
```

Some representative example usages are shown below.

Run by restarting from a seed mechanism:

```
python rmg.py -r path/to/seed/ input.py
```

Run with CPU time profiling:

```
python rmg.py -p input.py
```

Run with multiprocessing for reaction generation and QMTP:

```
python rmg.py -n <Max number of processes allowed> input.py
```

Run with setting a limit on the maximum execution time:

```
python rmg.py -t <DD:HH:MM:SS> input.py
```

Run with setting a limit on the maximum number of iterations:

```
python rmg.py -i <Max number of desired iterations> input.py
```

## 1.6.2 Details on the multiprocessing implementation

Currently, multiprocessing is implemented for reaction generation and the generation of QMfiles when using the QMTP option to compute thermodynamic properties of species. The processes are spawned and closed within each function. The number of processes is determined based on the ratio of currently available RAM and currently used RAM. The user can input the maximum number of allowed processes from the command line. For each reaction generation or QMTP call the number of processes will be the minimum value of either the number of allowed processes due to user input or the value obtained by the RAM ratio. The RAM limitation is employed, because multiprocessing is forking the base process and the memory limit (SWAP + RAM) might be exceeded when using too many processors for a base process large in memory.

## 1.6.3 Details on profiling RMG jobs

Here, we explain how to profile an RMG job. For starters, use the `saveSeedModulus` option in the input file, as described in the Section [Miscellaneous Options](#), to save the seed mechanism at regular intervals, perhaps every 50 or 100 iterations depending on the size of the mechanism. This option is particularly important for saving intermediate steps when working with large mechanisms; it may be prudent to save and examine how the chemistry changes over mechanism development rather than just obtaining the final seed mechanism.

These seeds can then be restarted with use of the `-r` flag, as described in the Section [Input Flags](#) above. Additionally, restarting these seeds with the `-i` flag allows examination of how computational effort, time spent in each module, individual processor memory consumption if using the `-n` flag, and overall memory consumption change over the course of mechanism development. To time profile, one could use:

```
rmg.py -r <path_to_seed>/seed -p -i 15 restart_from_seed.py
```

such that 15 iterations was arbitrarily chosen as a representative sample size to obtain profiling information. To run memory profiling, one option is to install a [python memory profiler](#) as an additional dependency. As detailed in their linked GitHub, there are options for line-by-line memory usage of small functions and for time-based memory usage. An example of memory profiling is:

```
mprof run --multiprocess rmg.py -r <path_to_seed>/seed -i 15 -n 3 restart_from_seed.py
```

such that this example demonstrates how to obtain memory consumption for each of three specified processes and again use 15 iterations to obtain representative profiling information. Please see the linked GitHub to learn more about how the memory profiler tool can help characterize your process.

## 1.7 Analyzing the Output Files

You will see that a successfully executed RMG job will create multiple output files and folders: `output.html` (if `generateOutputHTML=True` is specified) `/chemkin /pdep /plot /solver /species` `RMG.log`

### 1.7.1 The Chemkin Folder

The `/chemkin` folder will likely have a large number of chemkin formatted files. In general, these can be disregarded, as you will be mainly interested in `chem.inp`, the chemkin formatted input file with a species list, thermochemical database, and a list of elementary reactions. All of `inp` files appended with numbers are those that have been generated by RMG as it runs and the mechanism is still in progress of enlarging. `chem_annotated.inp` is provided as a means to help make sense of species syntax and information sources (i.e., how RMG estimated individual kinetic and thermodynamic parameters). In addition, a species dictionary, `species_dictionary.txt`, is generated containing all the species in your mechanism in the format of an adjacency list. Either chemkin file, in addition to the dictionary, may be used as inputs in the [tools](#) section of this website to better [visualize](#) the species and reactions. Alternatively, if the input option `generateOutputHTML=` is set to `True`, you will be able to visualize 2D images of all species and reactions in your mechanism as image files and in an html file, `output.html`. Once you are able to visualize the mechanism, several useful tools exist. For example, in the *Reaction Details* section, you'll see the following with check-box fields beside them:

- Kinetics
- Comments
- Chemkin strings

If you check the last box, chemkin strings, you can then search for strings corresponding to seemingly nonsensical named species (e.g. `S(1234)`) that may show up in any analyses/simulations you perform (e.g., with Cantera or Chemkin). Further, under *Reaction Families*, you can selectively view the reactions that been generated based on a particular RMG reaction family or library.

### 1.7.2 The Species Folder

If `generateOutputHTML=True` is specified as an RMG input *option*, the species folder will be populated with png files with 2D pictures of each species in your final mechanism. Otherwise, it will contain no files, or files generated from pressure dependent jobs.

### 1.7.3 The Pdep Folder

The `/pdep` folder will contain files associated with the pressure-dependent reactions that RMG has generated, if you requested such a job. These files are formatted as input files for *Arkane*, which can be run independently. This can be useful if one wants to visualize the potential energy surface corresponding to any particular network.

### 1.7.4 The Solver Folder

RMG currently includes a solver for isothermal batch reactors. This is in fact a critical part of the model enlargement algorithm. If you have included simulations in your input file, the solutions will be located in `/solver`. You will probably only be interested in the files with the largest number tags. Please note that up to and including RMG-Py version 2.3.0 these files showed mole fraction of each species at each step, but they now show amount (number of moles) of each species; you must divide by the sum if you wish to get a mole fraction.

## 1.8 Guidelines for Building a Model

RMG has been designed to build kinetic models for gas phase pyrolysis and combustion of organic molecules made of C, H, O and S. By kinetic model, we mean a set of reactions and associated kinetics that represent the chemical transformations occurring in the system of interest. These systems could be the combustion of fuels, pyrolysis of hydrocarbon feedstocks, etc. The total number of reactions and species typically required to describe some of these processes can run into the thousands making these models difficult and error-prone to build manually. This is the main motivation behind using software like RMG that build such models automatically in a systematic reproducible manner.

In RMG, the user is expected to provide an input file specifying the conditions (temperature, pressure, etc.) under which one desires to develop kinetic models. The following are some tips for setting up your input/condition file.

### 1.8.1 Start with a good seed mechanism

RMG is a useful tool in elucidating important pathways in a given process but may not capture certain special reaction types which may be specific to the system you are interested in. However, if you already have a good idea of these reactions that are important and are not available in the standard RMG library, you can create a ‘seed mechanism’ and include it in the input file to RMG. This will directly include these in the model core and add other reactions from the RMG library on top of it using our rate based algorithm. (Similarly, you can specify your own thermodynamic parameters for species using thermochemistry libraries which are similar in concept to seed mechanisms. In order to build these libraries, you will need to specify all species in the RMG adjacency list format.) In a combustion system, RMG tends to do a decent job filling in the termination and propagation steps of a mechanism if it is guided with the initiation and chain branching steps using a seed mechanism. Ideally, RMG should be able to find all the right chemistry through our kinetics database but holes in current kinetic databases can make this task difficult. A good seed mechanism can address this issue for the system of interest and also reduce the size, cost and time taken to arrive at a converged model.

### 1.8.2 Setting up the right termination criterion

Start with a relatively large tolerance (such as 0.1) when building your first model to make sure that RMG can converge the model to completion without any hiccups, then begin tightening the tolerance if you are able to converge the initial model. For large molecules such as tetradecane (C<sub>14</sub>), even a tolerance of 0.1 may be too tight for RMG to work with and lead to convergence problems. Note that a good seed mechanism allows for faster convergence.

### 1.8.3 Restricting the number of carbon atoms, oxygen atoms, and radical sites per species

Options to tune the maximum number of carbon or oxygen atoms, or number of radical sites per species can be specified at the beginning of the condition file. In most systems, we do not expect large contributions from species with more than 1 radical center (i.e. biradicals, etc.) to affect the overall chemistry, thus it may be useful to limit the maximum number of radicals to 2 (to allow for O<sub>2</sub>). The same applies for the maximum number of oxygens you want to allow per species. Restricting the number of carbon atoms in each species may also be worthwhile to prevent very large molecules from being generated if many such species appear in your model. Using any of these options requires some prior knowledge of the chemistry in your system. It is recommended that an initial model be generated without turning these options on. If many unlikely species show up in your model (or if your model has trouble converging and is generating many unlikely species on the edge), you can begin tuning these options to produce a better model.

### 1.8.4 Adding key species into the initial condition file

Sometimes, chain branching reactions like dissociation of ROOH species do not make it to the core directly because if their fluxes are very small and the tolerance is not tight enough. In these cases, seeding the condition file with these species (with zero concentration) is helpful. By adding these species to the initial set of species in the condition file, the reactions involving those species will be automatically added to the core. (Putting these reactions in the seed mechanism has the same effect.) Thus, if a species is known to be a part of your system and RMG is having trouble incorporating it within your model, it should be added to the condition file with 0.0 set as the concentration.

### 1.8.5 Starting with a single molecule when generating a model for a mixture

For modeling the combustion of fuel mixtures, you may want to start with determining their composition and starting with a kinetic study of the dominant compound. It is possible to model the combustion of fuel mixtures but they are more challenging as well as harder to converge in RMG because RMG will automatically generate all cross reactions between the reacting species and intermediates. Starting with single species is always a good idea and is also useful when thinking about fuel mixtures. In order to build a better background in chemical kinetic model development and validation, please look at a recent paper from our group on butanol combustion available [here](#). This should give you some idea about how RMG can be put to use for the species of interest to you.

## 1.9 Standalone Modules

There are several standalone modules that can be run separately from RMG. These scripts can be found in the RMG-Py/`scripts` folder, unless mentioned otherwise.

### 1.9.1 HTML Chemkin Output

The script, `generateChemkinHTML.py`, will create a formatted HTML page displaying all of the species and reactions in a given Chemkin file. Thermo and kinetics parameters are also displayed, along with any comments if the Chemkin file was generated by RMG.

This script gives the same output as turning on `generateOutputHTML` in the *options* section of the RMG input file. However, having using that setting can increase the memory usage and computation time for large jobs, so this script provides an option for generating the HTML file after job completion.

To use this script, you need a Chemkin input file and an RMG species dictionary. The syntax is as follows:

```
python generateChemkinHTML.py [-h, -f] CHEMKIN DICTIONARY [OUTPUT]
```

Positional arguments:

CHEMKIN	The path to the Chemkin file
DICTIONARY	The path to the RMG dictionary file
OUTPUT	Location to save the output files, defaults to the current directory

Optional arguments:

-h, --help	Show help message <b>and</b> exit
-f, --foreign	Not an RMG generated Chemkin file

This method is also available to use with a web browser from the RMG website: [Convert Chemkin File](#).

## 1.9.2 Model Comparison

The script `diffModels` compares two RMG generated models to determine their differences. To use this method you will need the chemkin and species dictionary outputs from RMG. These can be found in the `chemkin` folder from the directory of the `input.py` file used for the RMG run. The syntax is as follows:

```
python diffModels.py CHEMKIN1 SPECIESDICT1 --thermo1 THERMO1 CHEMKIN2 SPECIESDICT2 --
↳ thermo2 THERMO2 --web
```

where CHEMKIN represents the chemkin input file (`chem00XX.inp`), SPECIESDICT is the species dictionary from RMG (`species_dictionary.txt`) and the optional `--thermo` flag can be used to add separate thermo CHEMKIN files THERMO. The numbers (1 and 2) represent which model to each file is from. The optional `--web` flag is used for running this script through the RMG-website.

Running the script without any optional flags looks like:

```
python diffModels.py CHEMKIN1 SPECIESDICT1 CHEMKIN2 SPECIESDICT2
```

Output of each comparison is printed, and the method then produces a html file (`diff.html`) for easy viewing of the comparison.

This method is also available to use with a web browser from the RMG website: [Model Comparison Tool](#).

## 1.9.3 Merging Models

This script combines up to 5 RMG models together. The thermo and kinetics from common species and reactions is taken from the first model with the commonality. To better understand the difference in two models, use `diffModels.py`. To use this method type:

```
python mergeModels.py --model1 chemkin1 speciesdict1 --model2 chemkin2 speciesdict2
```

where chemkin specifies the chemkin input file from the RMG run and speciesdict represents the species dictionary from the RMG run. These can be found in the `chemkin` folder from the directory of the `input.py` file used for the RMG run. The numbers are for different models that you want to merge. To merge more than two files, you can add `--model3 chemkin3 speciesdict3`. Up to 5 models can be merged together this way

Running this method will create a new species dictionary (`species_dictionary.txt`) and chemkin input file (`chem.inp`) in the parent directory of the terminal.

This method is also available to use with a web browser from the RMG website: [Model Merge Tool](#).

### 1.9.4 Generate Reactions

The script `generateReactions.py` generates reactions between all species mentioned in an input file. To call this method type:

```
python generateReactions.py Input_File
```

where `Input_File` is a file similar to a general RMG input file which contains all the species for RMG to generate reactions between. An example file is placed in `$RMGPy/examples/scripts/generateReactions/input.py`

```
# Data sources for kinetics
database(
    thermoLibraries = ['BurkeH202', 'primaryThermoLibrary', 'DFT_QCI_thermo', 'CBS-QB3_
↳ 1dHR'],
    reactionLibraries = [],
    seedMechanisms = [],
    kineticsDepositories = 'default',
    #this section lists possible reaction families to find reactions with
    kineticsFamilies = ['default'],
    kineticsEstimator = 'rate rules',
)

# List all species you want reactions between
species(
    label='ethane',
    reactive=True,
    structure=SMILES("CC"),
)

species(
    label='H',
    reactive=True,
    structure=SMILES("[H]"),
)

species(
    label='butane',
    reactive=True,
    structure=SMILES("CCCC"),
)

# you must list reactor conditions (though this may not effect the output)
simpleReactor(
    temperature=(650, 'K'),
    pressure=(10.0, 'bar'),
    initialMoleFractions={
        "ethane": 1,
    },
    terminationConversion={
        'butane': .99,
    },
    terminationTime=(40, 's'),
)
```

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```
#optional module if you want to get pressure dependent kinetics.

#pressureDependence(
#    method='modified strong collision',
#    maximumGrainSize=(0.5,'kcal/mol'),
#    minimumNumberOfGrains=250,
#    temperatures=(300,2200,'K',2),
#    pressures=(0.01,100,'bar',3),
#    interpolation=('Chebyshev', 6, 4),
#    maximumAtoms=15,
#)

#optional module if you want to limit species produced in reactions.

#generatedSpeciesConstraints(
#    allowed=['input species','seed mechanisms','reaction libraries'],
#    maximumCarbonAtoms=4,
#    maximumOxygenAtoms=7,
#    maximumNitrogenAtoms=0,
#    maximumSiliconAtoms=0,
#    maximumSulfurAtoms=0,
#    maximumHeavyAtoms=20,
#    maximumRadicalElectrons=1,
#)
```

This method will produce an output.html file in the directory of input.py which contains the all the reactions produced between the species.

This method is also available to use with a web browser from the RMG website: [Populate Reactions](#).

### 1.9.5 Simulation and Sensitivity/Uncertainty Analysis

For sensitivity analysis, RMG-Py must be compiled with the DASPK solver, which is done by default but has some dependency restrictions. (See [License Restrictions on Dependencies](#) for more details.) Sensitivity analysis or a simulation (without sensitivity) can be conducted in a standalone system for an existing kinetics model in Chemkin format.

To run a simulation and/or sensitivity analysis, use the simulate module in RMG-Py/scripts:

```
python simulate.py input.py chem.inp species_dictionary.txt
```

where chem.inp is the CHEMKIN file and the species\_dictionary.txt contains the dictionary of species associated with the CHEMKIN file. input.py is an input file similar to one used for an RMG job but does not generate a RMG job. See the following input.py example file found under the \$RMGPy/examples/sensitivity/input.py folder

```
# Data sources
database(
    thermoLibraries = ['primaryThermoLibrary'],
    reactionLibraries = [],
    seedMechanisms = [],
    kineticsDepositories = ['training'],
```

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```

    kineticsFamilies = ['!Intra_Disproportionation', '!Substitution_0'],
    kineticsEstimator = 'rate rules',
)

# Constraints on generated species
generatedSpeciesConstraints(
    maximumRadicalElectrons = 2,
)

# List of species
species(
    label='ethane',
    reactive=True,
    structure=SMILES("CC"),
)

# Reaction systems
simpleReactor(
    temperature=(1350, 'K'),
    pressure=(1.0, 'bar'),
    initialMoleFractions={
        "ethane": 1.0,
    },
    terminationConversion={
        'ethane': 0.9,
    },
    terminationTime=(1e6, 's'),
    sensitivity=['ethane'],
    sensitivityThreshold=0.01,
)

simulator(
    atol=1e-16,
    rtol=1e-8,
    sens_atol=1e-6,
    sens_rtol=1e-4,
)

model(
    toleranceKeepInEdge=0.0,
    toleranceMoveToCore=0.1,
    toleranceInterruptSimulation=0.1,
    maximumEdgeSpecies=100000
)

options(
    units='si',
    saveSimulationProfiles=False,
    generateOutputHTML=False,
    generatePlots=False,
)

```

The names of species named in the input file must coincide with the names specified in the CHEMKIN file.

Other options that can be specified for the `simulate.py` scripts are:

```
--no-dlim      Turn off diffusion-limited rates for LiquidReactor
-f, --foreign  Not an RMG generated Chemkin file (will be checked for duplicates)
```

Sensitivity analysis is conducted for the list of species given for the `sensitivity` argument in the input file. The normalized concentration sensitivities with respect to the reaction rate coefficients  $\text{dln}(C_i)/\text{dln}(k_j)$  are saved to a csv file with the file name `sensitivity_1_SPC_1.csv` with the first index value indicating the reactor system and the second naming the index of the species the sensitivity analysis is conducted for. Sensitivities to thermo of individual species is also saved as semi normalized sensitivities  $\text{dln}(C_i)/\text{d}(G_j)$  where the units are given in  $1/(\text{kcal mol}^{-1})$ . The `sensitivityThreshold` is set to some value so that only sensitivities for  $\text{dln}(C_i)/\text{dln}(k_j) > \text{sensitivityThreshold}$  or  $\text{dln}C_i/\text{d}(G_j) > \text{sensitivityThreshold}$  are saved to this file.

Uncertainty analysis can also be requested via input file options. For more details, see [Uncertainty Analysis](#). The results of the analysis will be printed in the `simulate.log` file which is generated.

### 1.9.6 Generating Flux Diagrams

The script, `generateFluxDiagrams.py`, will create a movie out of a completed RMG model that shows interconnected arrows between species that represent fluxes.

To use this method, you just need a Chemkin input file and an RMG species dictionary. The syntax is as follows:

```
python generateFluxDiagram.py [-h] [--java] [--no-dlim] [-s SPECIES] [-f]
                             [-n N] [-e N] [-c TOL] [-r TOL] [-t S]
                             INPUT CHEMKIN DICTIONARY [CHEMKIN_OUTPUT]
```

Positional arguments:

INPUT	RMG <b>input</b> file
CHEMKIN	Chemkin file
DICTIONARY	RMG dictionary file
CHEMKIN_OUTPUT	Chemkin output file

Optional arguments:

-h, --help	show this help message <b>and</b> exit
--java	process RMG-Java model
--no-dlim	Turn off diffusion-limited rates
-s DIR, --species DIR	Path to folder containing species images
-f, --foreign	Not an RMG generated Chemkin file (will be checked <b>for</b> <b>↪</b> duplicates)
-n N, --maxnode N	Maximum number of nodes to show <b>in</b> diagram
-e N, --maxedge N	Maximum number of edges to show <b>in</b> diagram
-c TOL, --conctol TOL	Lowest fractional concentration to show
-r TOL, --ratetol TOL	Lowest fractional species rate to show
-t S, --tstep S	Multiplicative factor to use between consecutive time points

This method is also available to use with a web browser from the RMG website: [Generate Flux Diagram](#).

### 1.9.7 Thermo Estimation Module

The thermo estimation module can be run stand-alone. An example input file for this module is shown below:

```
database(
    thermoLibraries = ['primaryThermoLibrary', 'GRI-Mech3.0']
)

species(
    label='Cineole',
    structure=SMILES('CC12CCC(CC1)C(C)(C)O2'),
)

quantumMechanics(
    software='mopac', #mopac or gaussian
    method='pm3', #pm3, pm6, pm7
    fileStore='QMfiles', # defaults to inside the output folder.
    onlyCyclics = True, #True, False
    maxRadicalNumber = 0, # 0, 1
)
```

The `database` block is used to specify species thermochemistry libraries. Multiple libraries may be created, if so desired. The order in which the thermo libraries are specified is important: If a species appears in multiple thermo libraries, the first instance will be used.

Please see Section [Thermo Database](#) for details on editing the thermo library. In general, it is best to leave the `ThermoLibrary` set to its default value. In particular, the thermodynamic properties for H and H2 must be specified in one of the primary thermo libraries as they cannot be estimated by Benson's method.

For example, if you wish to use the GRI-Mech 3.0 mechanism [[GRIMech3.0](#)] as a `ThermoLibrary` in your model, the syntax will be:

```
thermoLibraries = ['primaryThermoLibrary', 'GRI-Mech3.0']
```

This library is located in the `RMG-database/input/thermo/libraries` directory. All "Locations" for the `ThermoLibrary` field must be with respect to the `RMG-database/input/thermo/libraries` directory.

The optional `quantumMechanics` block is used when quantum mechanical calculations are desired to determine thermodynamic parameters. These calculations are only run if the molecule is not included in a specified thermo library. The `software` option accepts either the `mopac` or `gaussian` string. The `method` option refers to the level-of-theory, which can either be `pm3`, `pm6`, or `pm7`. A folder can be specified to store the files used in these calculations, however if not specified this defaults to a `QMfiles` folder in the output folder. The `onlyCyclics` option, if `True`, only runs these calculations for cyclic species. In this case, group contribution estimates are used for all other species. The calculations are also only run on species with a maximum radical number set by the user. If a molecule has a higher radical number, the molecule is saturated with hydrogen atoms, then quantum mechanical calculations with subsequent hydrogen bond incrementation is used to determine the thermodynamic parameters.

Submitting a job is easy:

```
python thermoEstimator.py input.py
```

We recommend you make a job-specific directory for each `thermoEstimator` simulation.

You can also specify that an RMG-style thermo library be saved upon completion:

```
python thermoEstimator.py -l input.py
```

Note that the RMG website also provides thermo estimation through the [Molecule Search](#).

### 1.9.8 Convert FAME to Arkane Input File

This module is utilized to convert FAME file types (used in RMG-Java) to Arkane (formerly called CanTherm) objects (used in RMG-Py) for pressure dependent calculations.

FAME is an early version of the pdep code in Arkane, and it is written in Fortran and used by RMG-Java. This script enables importing FAME input files into Arkane. Note that it is mostly designed to load the FAME input files generated automatically by RMG-Java, and may not load hand-crafted FAME input files. If you specify a *moleculeDict*, then this script will use it to associate the species with their structures.

```
python convertFAME.py fame_object
```

where `fame_object` is the FAME file used to be converted into the Arkane object.

Some additional options involve adding an RMG dictionary to process with the file. The syntax for this is

```
python convertFAME.py -d RMG_dictionary.txt fame_object
```

where `RMG_dictionary.txt` is the dictionary to process with the file.

A max energy cutoff is also possible when converting the file formats.

```
python convertFAME.py -d RMG_dictionary.txt -x value units value units fame_object
```

where `value` represents the max energy amount and `units` represents its units

### 1.9.9 Database Scripts

This section details usage for scripts available in `RMG-database/scripts` folder.

#### **evansPolanyi.py**

This script will generate an Evans-Polanyi plot for a single kinetics depository.

Usage:

```
python evansPolanyi.py [-h] <family> <kinetics_depository> [<kinetics_depository> ...]
```

#### **Positional arguments::**

<family> the family to use <kinetics\_depository> the kineticsDepository to use, e.g., training, NIST

Optional arguments:

```
-h, --help    show help message and exit
```

### exportKineticsLibraryToChemkin.py

This script exports an individual RMG-Py kinetics library to a chemkin and dictionary file. Thermo is taken from RMG's estimates and libraries. In order to use more specific thermo, you must tweak the thermoLibraries and estimators in use when loading the database. The script will save the chem.inp and species\_dictionary.txt files in the local directory.

Usage:

```
python exportKineticsLibrarytoChemkin.py [-h] LIBRARYNAME
```

Positional arguments:

```
LIBRARYNAME    the libraryname of the RMG-Py format kinetics library
```

Optional arguments:

```
-h, --help      show help message and exit
```

### importChemkinLibrary.py

This script imports a chemkin file (along with RMG dictionary) from a local directory and saves a set of RMG-Py kinetics library and thermo library files. These py files are automatically added to the input/kinetics/libraries and input/thermo/libraries folder under the user-specified *name* for the chemkin library.

Usage:

```
python importChemkinLibrary.py [-h] CHEMKIN DICTIONARY NAME
```

Positional arguments:

```
CHEMKIN        The path of the chemkin file
DICTIONARY     The path of the RMG dictionary file
NAME           Name of the chemkin library to be saved
```

Optional arguments:

```
-h, --help      show help message and exit
```

### process\_family\_images.py

This script processes reaction family template images (saved as eps files) into user friendly files (pdf and pngs). This should typically be run whenever a new family is added or an existing family is updated.

**Notes:**

- Make sure you have a working LaTeX installation with pdflatex
- Make sure you have a working GhostScript installation for epstopdf
- Make sure you have ImageMagick installed for png generation
- ImageMagick may have security limitations in place which prevent reading eps files. To circumvent these, edit the /etc/ImageMagick-6/policy.xml file by changing `<policy domain="coder" rights="none" pattern="EPS" />` to `<policy domain="coder" rights="read|write" pattern="EPS" />`

Usage:

```
python process_family_images.py
```

### 1.9.10 Standardize Model Species Names

This script enables the automatic renaming of species names of two or more Chemkin files (and associated species dictionaries) so that they use consistent, matching names. Simply pass the paths of the Chemkin files and species dictionaries on the command-line, e.g.:

```
python standardizeModelSpeciesNames.py --model1 /path/to/chem1.inp /path/to/species_
dictionary1.txt --model2 /path/to/chem2.inp /path/to/species_dictionary2.txt
```

The resulting files are saved as chem1.inp and species\_dictionary1.txt, chem2.inp, species\_dictionary2.txt and so forth (depending on how many models you want to standardize) and will be saved in the execution directory.

### 1.9.11 Isotopes

#### Describing isotopes in adjacency lists

Isotopic enrichment can be indicated in a molecular structure's adjacency list. The example below is methane with an isotopically labeled carbon of isotope number 13, which is indicated with i13:

```
1 C u0 p0 c0 i13 {2,S} {3,S} {4,S} {5,S}
2 H u0 p0 c0 {1,S}
3 H u0 p0 c0 {1,S}
4 H u0 p0 c0 {1,S}
5 H u0 p0 c0 {1,S}
```

#### Running the RMG isotopes algorithm

The isotopes script is located in the folder scripts. To run the algorithm, ensure the RMG packages are loaded and type:

```
python /path/to/rmg/scripts/isotopes.py /path/to/input/file.py
```

The input file is identical to a standard RMG input file and should contain the conditions you want to run (unless you are inputting an already completed RMG model). Without any options, the script will run the original RMG input file to generate a model. Once the RMG job is finished, it will create new species for all isotopologues of previously generated species and then generate all reactions between the isotopologues.

Some arguments can be used to alter the behavior of the script. If you already have a model (which includes atom mapping in RMG's format) which you would like to add isotope labels to, you can use the option `--original path/to/model/directory` with the desired model files stored within with structure chemkin/chem\_annotated.inp and chemkin/species\_dictionary.txt. With this option, the isotope script will use the specified model instead of re-running an RMG job.

If you only desire the reactions contained in the specific RMG job, you can add `--useOriginalReactions` in addition to `--original`. This will create a full set of isotopically labeled versions of the reactions you input and avoid a time-consuming generate reactions procedure. Note that without `--useOriginalReactions`, labeled and unlabeled reactions may not match the same depository reactions, leading to inconsistent kinetics. If degeneracy errors arise when generating reactions from scratch, try using this option to see if it reduces errors in degeneracy.

The argument `--maximumIsotopicAtoms [integer]` limits the number of enriched atoms in any isotopologue in the model. This is beneficial for decreasing model size, runtime of model creation and runtime necessary for analysis.

Adding kinetic isotope effects which are described in this paper can be obtained through the argument `--kineticIsotopeEffect simple`. Currently this is the only supported method, though this can be extended to other effects.

If you have a desired output folder, `--output output_folder_name` can direct all output files to the specified folder. The default is to create a folder named 'iso'.

There are some limitations in what can be used in isotope models. In general, RMG Reaction libraries and other methods of kinetic estimation that do not involve atom mapping to reaction recipes are not compatible (though they can be functional if all isotopologues are included in the reaction library). The algorithm also does not function with pressure dependent mechanisms generated by RMG, and has only been tested for gas phase kinetics. This algorithm currently only works for Carbon-13 enrichments.

Following the generation, a number of diagnostics check model accuracy. Isotopologues are checked to ensure their symmetries are consistent. Then, the reaction path degeneracy among reactions differing only in isotope labeling is checked to ensure it is consistent with the symmetry values of reactions. If one of these checks throws a warning, the model will likely exhibit non-natural fluctuations in enrichment ten to one hundred times larger than from non-hydrogen kinetic isotope effects.

## Output from script

The isotope generation script will output two files inside the nested folders `iso/chemkin`, unless `--output` is specified. The file `species_dictionary.txt` lists the structure of all isotopologue using the RMG adjacency list structure. The other file of importance `chem_annotated.inp` is a chemkin input file containing elements, species, thermo, and reactions of the entire system.

## Further reading & resources

A description of mechanisms generated using this module and its application to obtaining intramolecular isotopic enrichment information is described in [Chemical Geology, Volume 514, page 1](#).

Code to replicate that work, as well as convert between experimental enrichments and the isotopologues used in RMG is deposited at [Zenodo](#).

## 1.10 Species Representation

Species objects in RMG contain a variety of attributes, including user given names, thermochemistry, as well as structural isomers. See the `rmgpy.species.Species` class documentation for more information.

RMG considers each species to be unique, and comprised of a set of molecular structural isomers, including resonance isomers. RMG uses the list of resonance isomers to compare whether two species are the same. Each molecular structure is stored in RMG using graph representations, using vertices and edges, where the vertices are the atoms and the edges are the bonds. This form of representation is known as an adjacency list. For more information on adjacency lists, see the `rmgpy.molecule.adjlist` page.

Species objects in the input file can also be constructed using other common representations such as SMILES, SMARTS, and InChIs. The following can all be used to represent the methane species:

```
species(
    label='CH4',
    reactive=True,
```

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```
structure=SMILES("C"),
)
```

Replacing the structure with any of the following representations will also produce the same species:

```
structure=adjacencyList("
1 C u0 p0 c0 {2,S} {3,S} {4,S} {5,S}
2 H u0 p0 c0 {1,S}
3 H u0 p0 c0 {1,S}
4 H u0 p0 c0 {1,S}
5 H u0 p0 c0 {1,S}
"),

structure=SMARTS("[CH4]"),

structure=SMILES("C"),

structure=InChI("InChI=1S/CH4/h1H4"),
```

Be careful using the SMILES shorthand with lowercase letters for aromatics, radicals, or double bonds, because these can be ambiguous and the resulting molecule may depend on the version of OpenBabel, RDKit, and RMG in use. To quickly generate any adjacency list, or to generate an adjacency list from other types of molecular representations such as SMILES, InChI, or even common species names, use the Molecule Search tool found here: [https://rmg.mit.edu/molecule\\_search](https://rmg.mit.edu/molecule_search)

### 1.10.1 Representing Oxygen

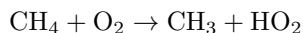
Special care should be taken when constructing a mechanism that involves molecular oxygen. The ground electronic state of molecular oxygen,  $^3\Sigma_g^-$ , does *not* contain a double bond, but instead a single bond and two lone electrons. In RMG's adjacency list notation the ground state of oxygen is represented as

```
1 0 u1 p2 {2,S}
2 0 u1 p2 {1,S}
```

You should use the above adjacency list to represent molecular oxygen in your condition files, seed mechanisms, etc. The triplet form is 22 kcal/mol more stable than the first singlet excited state,  $^1\Delta_g$ , which does contain a double bond. The adjacency list for singlet oxygen is

```
1 0 u0 p2 {2,D}
2 0 u0 p2 {1,D}
```

Selecting the correct structure for oxygen is important, as the reactions generated from a double bond are significantly different than those generated from a radical or diradical. For example, the reaction



would occur for both triplet and singlet oxygen, but in entirely different families. For triplet oxygen the above represents a hydrogen abstraction, while for singlet oxygen it represents the reverse of a disproportionation reaction.

The RMG databases have been modified to make all of the oxygen-related chemistry that was present in RMG databases consistent with the single-bonded biradical representation.

Conversion between triplet and singlet forms is possible through the primary reaction library `OxygenSingTrip`; the reactions involved are very slow, however, and are likely to be absent from any mechanisms generated. At this point, no other reactions of singlet oxygen have been included in RMG.



In order to allow the singlet form of O2 to be used in RMG, please allow it explicitly by setting `allowSingletO2` to `True` in the `generateSpeciesConstraints` section of the RMG input file.

```
generatedSpeciesConstraints(  
    allowSingletO2 = True,  
)
```

## 1.11 Group Representation

Group representations are used to represent molecular substructures within RMG. These are commonly used for identifying functional groups for use in both the thermo and kinetic databases.

For syntax of how to define groups, see `rmgpy.molecule.adjlist`.

## 1.12 Databases

RMG has databases storing thermochemistry and kinetics data. These databases can be visualized on the RMG website here: <https://rmg.mit.edu/database/>

### 1.12.1 Introduction

This section describes some of the general characteristics of RMG's databases.

#### Group Definitions

The main section in many of RMG's databases are the 'group' definitions. Groups are adjacency lists that describe structures around the reacting atoms. Between the adjacency list's index number and atom type, a starred number is inserted if the atom is a reacting atom.

Because groups typically do not describe entire molecules, atoms may appear to be lacking full valency. When this occurs, the omitted bonds are allowed to be anything. An example of a primary carbon group from H-Abstraction is shown below. The adjacency list defined on the left matches any of the three drawn structures on the right (the numbers correspond to the index from the adjacency list).

```
label = "C/H3/C",
```

```
group =
```

```
""
```

```
1 *1 Cs 0 {2,S} {3,S} {4,S} {5,S}
```

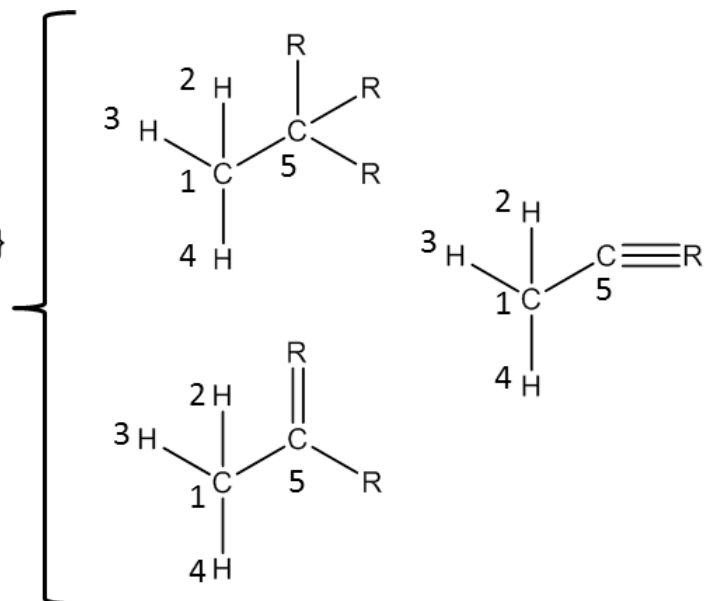
```
2 *2 H 0 {1,S}
```

```
3 H 0 {1,S}
```

```
4 H 0 {1,S}
```

```
5 {Cs, Cd, Ct} 0 {1,S}
```

```
""
```



**Atom types** describe atoms in group definitions. The table below shows all atoms types in RMG.

Atom Type	Chemical Element	Localized electronic structure
R	Any	No requirements
R!H	Any except hydrogen	No requirements
H	Hydrogen	No requirements
C	Carbon	No requirements
Ca	Carbon	Atomic carbon with two lone pairs and no bonds
Cs	Carbon	Up to four single bonds
Csc	Carbon	Up to three single bonds, charged +1
Cd	Carbon	One double bond (to any atom other than O or S), up to two single bonds
Cdc	Carbon	One double bond, up to one single bond, charged +1
CO	Carbon	One double bond to an oxygen atom, up to two single bonds
CS	Carbon	One double bond to an sulfur atom, up to two single bonds
Cdd	Carbon	Two double bonds
Ct	Carbon	One triple bond, up to one single bond
Cb	Carbon	Two benzene bonds, up tp one single bond
Cbf	Carbon	Three benzene bonds (fused aromatics)
C2s	Carbon	One lone pair, up to two single bonds
C2sc	Carbon	One lone pair, up to three single bonds, charged -1
C2d	Carbon	One lone pair, one double bond
C2dc	Carbon	One lone pair, one double bond, up to one single bond, charge -1
C2tc	Carbon	One lone pair, one triple bond, charged -1
N	Nitrogen	No requirements
N0sc	Nitrogen	Three lone pairs, up to one single bond, charged -2
N1s	Nitrogen	Two lone pairs, up to one single bond
N1sc	Nitrogen	Two lone pairs, up to two single bonds, charged -1
N1dc	Nitrogen	Two lone pairs, one double bond, charged -1
N3s	Nitrogen	One lone pair, up to three single bonds
N3d	Nitrogen	One lone pair, one double bond, up to one single bond
N3t	Nitrogen	One lone pair, one triple bond
N3b	Nitrogen	One lone pair, two aromatic bonds

continues on next

Table 1 – continued from previous page

Atom Type	Chemical Element	Localized electronic structure
N5sc	Nitrogen	No lone pairs, up to four single bonds, charged +1
N5dc	Nitrogen	No lone pairs, one double bond, up to two single bonds, charged +1
N5ddc	Nitrogen	No lone pairs, two double bonds, charged +1
N5dddc	Nitrogen	No lone pairs, three double bonds, charged -1
N5tc	Nitrogen	No lone pairs, one triple bond, up to one single bond, charged +1
N5b	Nitrogen	No lone pairs, two aromatic bonds, up to one single bond
O	Oxygen	No requirements
Oa	Oxygen	Atomic oxygen with three lone pairs and no bonds
O0sc	Oxygen	Three lone pairs, up to one single bond, charged -1
O0dc	Oxygen	Three lone pairs, one double bond, charged -2
O2s	Oxygen	Two lone pairs, up to two single bonds
O2sc	Oxygen	Two lone pairs, up to one single bond, charged +1
O2d	Oxygen	Two lone pairs, one double bond
O4sc	Oxygen	One lone pair, up to three single bonds, charged +1
O4dc	Oxygen	One lone pair, one double bond, up to one single bond, charged +1
O4tc	Oxygen	One lone pair, one triple bond, charged +1
Si	Silicon	No requirements
Sis	Silicon	Up to four single bonds
Sid	Silicon	One double bond (not to O), up to two single bonds
SiO	Silicon	One double bond to an oxygen atom, up to two single bonds
Sidd	Silicon	Two double bonds
Sit	Silicon	One triple bond, up to one single bond
Sib	Silicon	Two benzene bonds, up to one single bond
Sibf	Silicon	Three benzene bonds (fused aromatics)
P	Phosphorus	No requirements
P0sc	Phosphorus	Three lone pairs, up to one single bond, charged -2
P1s	Phosphorus	Two lone pairs, up to one single bond
P1sc	Phosphorus	Two lone pairs, up to two single bonds, charged -1
P1dc	Phosphorus	Two lone pairs, one double bond, charged -1
P3s	Phosphorus	One lone pair, up to three single bonds
P3d	Phosphorus	One lone pair, one double bond, up to one single bond
P3t	Phosphorus	One lone pair, one triple bond
P3b	Phosphorus	One lone pair, two aromatic bonds
P5s	Phosphorus	No lone pairs, up to five single bonds
P5sc	Phosphorus	No lone pairs, up to six single bonds, charged -1/+1/+2
P5d	Phosphorus	No lone pairs, one double bond, up to three single bonds
P5dd	Phosphorus	No lone pairs, two double bonds, up to one single bond
P5dc	Phosphorus	No lone pairs, one double bond, up to two single bonds, charged +1
P5ddc	Phosphorus	No lone pairs, two double bonds, charged +1
P5t	Phosphorus	No lone pairs, one triple bond, up to two single bonds
P5td	Phosphorus	No lone pairs, one triple bond, one double bond
P5tc	Phosphorus	No lone pairs, one triple bond, up to one single bond, charged +1
P5b	Phosphorus	No lone pairs, two aromatic bonds, up to one single bond, charged 0/+1
P5bd	Phosphorus	No lone pairs, two aromatic bonds, one double bond
S	Sulfur	No requirements
Sa	Sulfur	Atomic sulfur with three lone pairs and no bonds
S0sc	Sulfur	Three lone pairs, up to one single bond, charged -1
S2s	Sulfur	Two lone pairs, up to two single bonds
S2sc	Sulfur	Two lone pairs, up to three single bonds, charged -1/+1

continues on next

Table 1 – continued from previous page

Atom Type	Chemical Element	Localized electronic structure
S2d	Sulfur	Two lone pairs, one double bond
S2dc	Sulfur	Two lone pairs, one to two double bonds, up to one single bond, charged -1
S2tc	Sulfur	Two lone pairs, one triple bond, charged -1
S4s	Sulfur	One lone pair, up to four single bonds
S4sc	Sulfur	One lone pair, up to five single bonds, charged -1/+1
S4d	Sulfur	One lone pair, one double bond, up to two single bonds
S4dd	Sulfur	One lone pair, two double bonds
S4dc	Sulfur	One lone pair, one to three double bonds, up to three single bonds, charged -1/+1
S4b	Sulfur	One lone pair, two aromatic bonds
S4t	Sulfur	One lone pair, one triple bond, up to one single bond
S4tdc	Sulfur	One lone pair, one to two triple bonds, up to two double bonds, up to two single bonds, charged -1/+1
S6s	Sulfur	No lone pairs, up to six single bonds
S6sc	Sulfur	No lone pairs, up to seven single bonds, charged -1/+1/+2
S6d	Sulfur	No lone pairs, one double bond, up to four single bonds
S6dd	Sulfur	No lone pairs, two double bonds, up to two single bonds
S6ddd	Sulfur	No lone pairs, up to three double bonds
S6dc	Sulfur	No lone pairs, one to three double bonds, up to five single bonds, charged -1/-1/+2
S6t	Sulfur	No lone pairs, one triple bond, up to three single bonds
S6td	Sulfur	No lone pairs, one triple bond, one double bond, up to one single bond
S6tt	Sulfur	No lone pairs, two triple bonds
S6tdc	Sulfur	No lone pairs, one to two triple bonds, up to two double bonds, up to four single bonds, charged -1/+1/+2
Cl	Chlorine	No requirements
Cl1s	Chlorine	Three lone pairs, zero to one single bonds
Br	Bromine	No requirements
Br1s	Bromine	Three lone pairs, zero to one single bonds
I	Iodine	No requirements
I1s	Iodine	Three lone pairs, zero to one single bonds
F	Fluorine	No requirements
F1s	Fluorine	Three lone pairs, zero to one single bonds
He	Helium	No requirements, nonreactive
Ne	Neon	No requirements, nonreactive
Ar	Argon	No requirements, nonreactive

Additionally, groups can also be defined as unions of other groups. For example,:

```
label="X_H_or_Xrad_H",
group=OR{X_H, Xrad_H},
```

## Forbidden Groups

Forbidden groups can be defined to ban structures globally in RMG or to ban pathways in a specific kinetic family.

Globally forbidden structures will ban all reactions containing either reactants or products that are forbidden. These groups are stored in the file located at `RMG-database/input/forbiddenStructures.py`.

To ban certain specific pathways in the kinetics families, a *forbidden* group must be created, like the following group in the `intra_H_migration` family:

```
forbidden(
    label = "bridged56_1254",
```

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```

    group =
    """
    1 *1 C 1 {2,S} {6,S}
    2 *4 C 0 {1,S} {3,S} {7,S}
    3   C 0 {2,S} {4,S}
    4 *2 C 0 {3,S} {5,S} {8,S}
    5 *5 C 0 {4,S} {6,S} {7,S}
    6   C 0 {1,S} {5,S}
    7   C 0 {2,S} {5,S}
    8 *3 H 0 {4,S}
    """,
    shortDesc = u"",
    longDesc =
    u""

    """,
)
    
```

Forbidden groups should be placed inside the groups.py file located inside the specific kinetics family's folder RMG-database/input/kinetics/family\_name/ alongside normal group entries. The starred atoms in the forbidden group ban the specified reaction recipe from occurring in matched products and reactants.

In addition for forbidding groups, there is the option of forbidding specific molecules or species. Forbidding a molecule will prevent that exact structure from being generated, while forbidding a species will prevent any of its resonance structures from being generated. To specify a forbidden molecule or species, simply replace the group keyword with molecule or species:

```

# This forbids a molecule
forbidden(
    label = "C_quintet",
    molecule =
    """
multiplicity 5
1 C u4 p0
""",
    shortDesc = u"",
    longDesc =
    u""

    """,
)

# This forbids a species
forbidden(
    label = "C_quintet",
    species =
    """
multiplicity 5
1 C u4 p0
""",
    shortDesc = u"",
    longDesc =
    u""
    
```

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```

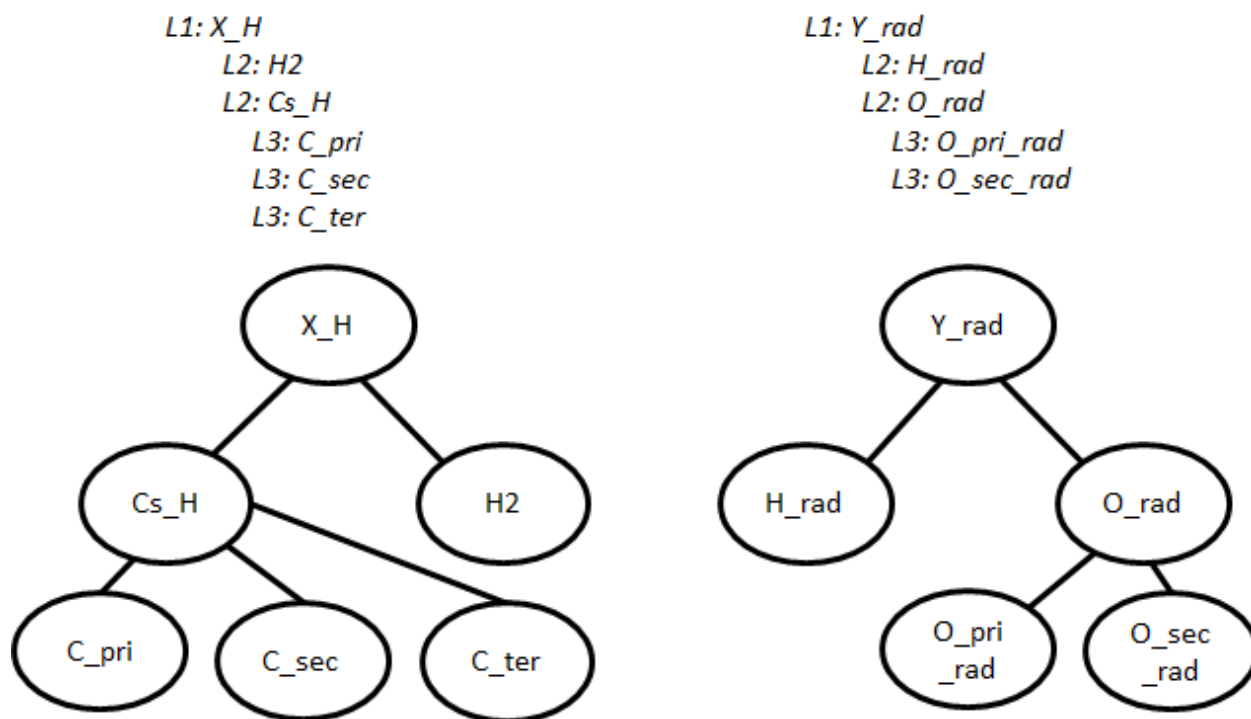
"""
)

```

## Hierarchical Trees

Groups are ordered into the nodes of a hierarchical trees which is written at the end of groups.py. The root node of each tree is the most general group with the reacting atoms required for the family. Descending from the root node are more specific groups. Each child node is a subset of the parent node above it.

A simplified example of the trees for H-abstraction is shown below. The indented text shows the syntax in groups.py and a schematic is given underneath.



Individual groups only describe part of the reaction. To describe an entire reaction we need one group from each tree, which we call **node templates** or simply templates. (C\_pri, O\_pri\_rad), (H2, O\_sec\_rad), and (X\_H, Y\_rad) are all valid examples of templates. Templates can be filled in with kinetic parameters from the training set or rules.

### 1.12.2 Thermo Database

This section describes the general usage of RMG's thermochemistry databases. Thermochemical data in RMG is reported using three different quantities:

1. Standard heat capacity data  $C_p^o(T)$  as a function of temperature  $T$
2. Standard enthalpy of formation at 298K  $\Delta_f H^o(298K)$
3. Standard entropy at 298K  $S^o(298K)$

A heat capacity model based on the Wilhoit equation is used for inter- and extrapolation of the heat capacity data as a function of temperature.

## Libraries

### Library types

Two types of thermo libraries are available in RMG: “gas phase” and “liquid thermo” libraries respectively identified thanks to the absence or presence of the keyword *solvent* = “*solvent\_name*” in the header of a thermo library. Here is an example of a liquid thermo library header:

```
name = "example_liquid_thermo_library"
solvent = "octane"
shortDesc = u"test"
longDesc = u""
```

In this example the library name is “example\_liquid\_thermo\_library” and thermo data provided was obtained in *octane* solvent. The only difference between gas phase and liquid phase thermo libraries is made through this keyword, the rest of the library is similar to gas phase.

**Note:** You can only provide one solvent per library and users should pay attention to not mix thermo of species obtained in different solvent in a same library. RMG will raise an error if users try to load a liquid thermo library obtained in another solvent than the one provided in input file. (in the example provided here, this liquid thermo library can only be used in liquid phase simulation with octane as solvent. RMG will also raise an error if user try to use liquid phase thermo library in gas phase simulations.

### Species thermochemistry libraries

The folder RMG-database/input/thermo/libraries/ in RMG-database is the location to store species thermochemistry libraries. Each particular library is stored in a file with the extension .py, e.g. ‘DFT\_QCI\_thermo.py’.

An example of a species thermochemistry entry is shown here below:

```
entry(
    index = 1,
    label = "H2",
    molecule =
    """
1 H 0 0 {2,S}
2 H 0 0 {1,S}
    """,
    thermo = ThermoData(
        Tdata = ([300,400,500,600,800,1000,1500], 'K'),
        Cpdata = ([6.948,6.948,6.949,6.954,6.995,7.095,7.493], 'cal/(mol*K)'),
        H298 = (0, 'kcal/mol'),
        S298 = (31.095, 'cal/(mol*K)'),
    ),
    shortDesc = u" ",
    longDesc =
    u" "
    """
)
```

The text above describes the first entry in the library (index = 1), labeled 'H2', through the adjacency list representation. Heat capacity data ('Cpdata') is described at 7 different temperatures, along with the standard enthalpy of formation at 298K ('H298'), and the standard entropy at 298K ('S298').

According to the *thermo classes* available in RMG, you can provide different thermo data: NASA, thermodata (as shown above), wilhoit or NASAPolynomial.

## Groups

The folder RMG-database/input/thermo/groups/ in RMG-database is the location to store group contribution databases. Each particularly type of group contribution is stored in a file with the extension .py, e.g. 'groups.py':

file	Type of group contribution
gauche.py	1,4-gauche non-nearest neighbor interactions (NNIs)
group.py	group additive values (GAVs)
int15.py	1,5-repulsion non-nearest neighbor interactions (NNIs)
other.py	other non-nearest neighbor interactions (NNIs)
polycyclic.py	polycyclic ring corrections (RSCs)
radical.py	hydrogen bond increments (HBIs)
ring.py	monocyclic ring corrections (RSCs)

Like many other entities in RMG, the database of each type of group contribution is organized in a hierarchical tree, and is defined at the bottom of the database file. E.g.:

```
tree(
    """
    L1: R
        L2: C
            L3: Cbf
                L4: Cbf-CbCbCb
                L4: Cbf-CbCbCbCb
                L4: Cbf-CbfCbCbCb
            L3: Cb
                L4: Cb-H
                L4: Cb-0s
                L4: Cb-S2s
                L4: Cb-C
                    L5: Cb-Cs
                    L5: Cb-Cds
                        L6: Cb-(Cds-0d)
                    ...
    """
)
```

More information on hierarchical tree structures in RMG can be found here: [Introduction](#).



## Group additive values (GAV)

An example of a GAV entry in group.py is shown here below:

```
entry(
    index = 3,
    label = "Cbf-CbCbCbf",
    group =
    """
1 * Cbf 0 {2,B} {3,B} {4,B}
2 Cb 0 {1,B}
3 Cb 0 {1,B}
4 Cbf 0 {1,B}
    """,
    thermo = ThermoData(
        Tdata = ([300,400,500,600,800,1000,1500], 'K'),
        Cpdata = ([3.01,3.68,4.2,4.61,5.2,5.7,6.2], 'cal/(mol*K)',
                  '+|-', [0.1,0.1,0.1,0.1,0.1,0.1,0.1]),
        H298 = (4.8, 'kcal/mol', '+|-', 0.17),
        S298 = (-5, 'cal/(mol*K)', '+|-', 0.1),
    ),
    shortDesc = u""Cbf-CbCbCb STEIN and FAHR; J. PHYS. CHEM. 1985, 89, 17, 3714""",
    longDesc =
    u""
Taken from STEIN and FAHR; J. PHYS. CHEM. 1985, 89, 17, 3714
    """,
)
```

The text above describes a GAV “Cb<sub>f</sub>-CbCbCb<sub>f</sub>”, with the central atom denoted by the asterisk in the adjacency list representation. Uncertainty margins are added in the data, after the unit specification. A short description ‘shortDesc’ specifies the origin of the data.

## Ring Strain Corrections (RSC)

RMG distinguishes between monocyclic and polycyclic ring correction databases.

Monocyclic RSCs are used for molecules that contain one single ring. An example of a monocyclic RSC entry in ring.py is shown here below:

```
entry(
    index = 1,
    label = "Cyclopropane",
    group =
    """
1 * Cs 0 {2,S} {3,S}
2 Cs 0 {1,S} {3,S}
3 Cs 0 {1,S} {2,S}
    """,
    thermo = ThermoData(
        Tdata = ([300,400,500,600,800,1000,1500], 'K'),
        Cpdata = ([-3.227,-2.849,-2.536,-2.35,-2.191,-2.111,-1.76], 'cal/(mol*K)'),
        H298 = (27.53, 'kcal/mol'),
        S298 = (32.0088, 'cal/(mol*K)'),
    ),
)
```

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```

    ),
    shortDesc = u""Cyclopropane ring BENSON"",
    longDesc =
u""
""",
)

```

A molecule may have two or more fused rings that mutually interact. In that case, a polycyclic ring strain correction may be more adequate. RMG identifies molecules with fused ring systems and subsequently searches through polycyclic.py to identify an adequate RSC.

An example of a polycyclic RSC entry in polycyclic.py is shown here below:

```

entry(
    index = 2,
    label = "norbornane",
    group =
    """
1 * Cs 0 {3,S} {4,S} {7,S}
2 * Cs 0 {3,S} {5,S} {6,S}
3 * Cs 0 {1,S} {2,S}
4 * Cs 0 {1,S} {5,S}
5 * Cs 0 {2,S} {4,S}
6 * Cs 0 {2,S} {7,S}
7 * Cs 0 {1,S} {6,S}
    """,
    thermo = ThermoData(
        Tdata = ([300,400,500,600,800,1000,1500], 'K'),
        Cpdata = ([-4.5, -3.942, -3.291, -2.759, -2.08, -1.628, -0.898], 'cal/(mol*K)'),
        H298 = (16.14, 'kcal/mol'),
        S298 = (53.47, 'cal/(mol*K)'),
    ),
    shortDesc = u"""",
    longDesc =
u""
""",
)

```

## Hydrogen Bond Increments (HBI)

An example of a HBI entry in radical.py is shown here below:

```

entry(
    index = 4,
    label = "CH3",
    group =
    """
1 * C 1 {2,S} {3,S} {4,S}
2 * H 0 {1,S}
    """
)

```

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```

3  H 0 {1,S}
4  H 0 {1,S}
"""
    thermo = ThermoData(
        Tdata = ([300,400,500,600,800,1000,1500], 'K'),
        Cpdata = ([0.71,0.34,-0.33,-1.07,-2.43,-3.54,-5.43], 'cal/(mol*K)'),
        H298 = (104.81, 'kcal/mol', '+|-', 0.1),
        S298 = (0.52, 'cal/(mol*K)'),
    ),
    shortDesc = u""""Calculated in relation to methane from NIST values""",
    longDesc =
u""""
"""
)

```

## Non-nearest neighbor interactions

The majority of the NNIs groups pertain to small enthalpy of formation corrections. Only a very limited number include entropy or heat capacity corrections. The database other.py contains cis-, ortho- and ketene-corrections.

An example of a NNI entry in gauche.py is shown here below:

```

entry(
    index = 11,
    label = "Cs(Cs(CsCsR)Cs(CsCsR)RR)",
    group =
    """
1  * Cs                      0 {2,S} {3,S} {4,S} {5,S}
2  Cs                      0 {1,S} {6,S} {7,S} {8,S}
3  Cs                      0 {1,S} {9,S} {10,S} {11,S}
4  {Cd,Cdd,Ct,Cb,Cbf,Os,CO,H} 0 {1,S}
5  {Cd,Cdd,Ct,Cb,Cbf,Os,CO,H} 0 {1,S}
6  Cs                      0 {2,S}
7  Cs                      0 {2,S}
8  {Cd,Cdd,Ct,Cb,Cbf,Os,CO,H} 0 {2,S}
9  Cs                      0 {3,S}
10 Cs                      0 {3,S}
11 {Cd,Cdd,Ct,Cb,Cbf,Os,CO,H} 0 {3,S}
    """,
    thermo = ThermoData(
        Tdata = ([300,400,500,600,800,1000,1500], 'K'),
        Cpdata = ([0,0,0,0,0,0,0], 'cal/(mol*K)'),
        H298 = (0.8, 'kcal/mol'),
        S298 = (0, 'cal/(mol*K)'),
    ),
    shortDesc = u""""""",
    longDesc =
u""""
"""
)

```

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)

### 1.12.3 Kinetics Database

This section describes the general usage of RMG's kinetic database. See [Modifying the Kinetics Database](#) for instructions on modifying the database.

Pressure independent reaction rates in RMG are calculated using a modified Arrhenius equation, designating the reaction coefficient as  $k(T)$  at temperature  $T$ .

$$k(T) = A \left( \frac{T}{T_0} \right)^n e^{-(E_0 + \alpha \Delta H_{rxn})/(RT)}$$

$R$  is the universal gas constant. The **kinetic parameters** determining the rate coefficient are:

- $A$ : the pre-exponential A-factor
- $T_0$ : the reference temperature
- $n$ : the temperature exponent
- $E_0$ : the activation energy for a thermoneutral reaction (a barrier height intrinsic to the kinetics family)
- $\alpha$ : the Evans-Polanyi coefficient (characterizes the position of the transition state along the reaction coordinate,  $0 \leq \alpha \leq 1$ )
- $\Delta H_{rxn}$ : the enthalpy of reaction

When Evans-Polanyi corrections are used,  $\Delta H_{rxn}$  is calculated using RMG's thermo database, instead of being specified in the kinetic database. When Evans-Polanyi corrections are not used,  $\Delta H_{rxn}$  and  $\alpha$  are set to zero, and  $E_0$  is the activation energy of the reaction.

### Libraries

Kinetic libraries delineate kinetic parameters for specific reactions. RMG always chooses to use kinetics from libraries over families. If multiple libraries contain the same reaction, then precedence is given to whichever library is listed first in the input.py file.

For combustion mechanisms, you should always use at least one small-molecule combustion library, such as the pre-packaged *BurkeH2O2* and/or *FFCM1* for natural gas. The reactions contained in these libraries are poorly estimated by kinetic families and are universally important to combustion systems.

Kinetic libraries should also be used in the cases where:

- A set of reaction rates were optimized together
- You know the reaction rate is not generalizable to similar species (perhaps due to catalysis or aromatic structures)
- No family exists for the class of reaction
- You are not confident about the accuracy of kinetic parameters

Below is a list of pre-packaged kinetics library reactions in RMG:

Library	Description
1989_Stewart_2CH3_to_C2H5_H	Chemically Activated Methyl Recombination to Ethyl (2)
2001_Tokmakov_H_Toluene_to_CH3_Benzene	H + Toluene = CH3 + Benzene

Table 2 – continued from previous page

Library	Description
2005_Senosiain_OH_C2H2	pathways on the OH + acetylene surface
2006_Joshi_OH_CO	pathways on OH + CO = HOCO = H + CO <sub>2</sub> surface
2009_Sharma_C5H5_CH3_highP	Cyclopentadienyl + CH <sub>3</sub> in high-P limit
2015_Buras_C2H3_C4H6_highP	Vinyl + 1,3-Butadiene and other C <sub>6</sub> H <sub>9</sub> reactions in high-P
biCPD_H_shift	Sigmatropic 1,5-H shifts on biCPD PES
BurkeH2O2inArHe	Comprehensive H <sub>2</sub> /O <sub>2</sub> kinetic model in Ar or He atmospheres
BurkeH2O2inN2	Comprehensive H <sub>2</sub> /O <sub>2</sub> kinetic model in N <sub>2</sub> atmosphere
C2H4+O_Klipp2017	C <sub>2</sub> H <sub>4</sub> + O intersystem crossing reactions, probably important
C10H11	Cyclopentadiene pyrolysis in the presence of ethene
C3	Cyclopentadiene pyrolysis in the presence of ethene
C6H5_C4H4_Mebel	Formation Mechanism of Naphthalene and Indene
Chernov	Soot Formation with C1 and C2 Fuels (aromatic reactions)
CurranPentane	Ignition of pentane isomers
Dooley	Methyl formate (contains several mechanisms)
ERC-FoundationFuelv0.9	Small molecule combustion (natural gas)
Ethylamine	Ethylamine pyrolysis and oxidation
FFCM1(-)	Foundational Fuel Chemistry Model Version 1.0 (excited species)
First_to_Second_Aromatic_Ring/2005_Ismail_C6H5_C4H6_highP	Phenyl + 1,3-Butadiene and other C <sub>10</sub> H <sub>11</sub> reactions in high-P
First_to_Second_Aromatic_Ring/2012_Matsugi_C3H3_C7H7_highP	Propargyl + Benzyl and other C <sub>10</sub> H <sub>10</sub> reactions in high-P
First_to_Second_Aromatic_Ring/2016_Mebel_C9H9_highP	C <sub>9</sub> H <sub>9</sub> reactions in high-P limit
First_to_Second_Aromatic_Ring/2016_Mebel_C10H9_highP	C <sub>10</sub> H <sub>9</sub> reactions in high-P limit
First_to_Second_Aromatic_Ring/2016_Mebel_Indene_CH3_highP	CH <sub>3</sub> + Indene in high-P limit
First_to_Second_Aromatic_Ring/2017_Buras_C6H5_C3H6_highP	Phenyl + Propene and other C <sub>9</sub> H <sub>11</sub> reactions in high-P limit
First_to_Second_Aromatic_Ring/2017_Mebel_C6H4C2H_C2H2_highP	C <sub>10</sub> H <sub>7</sub> HACA reactions in high-P limit
First_to_Second_Aromatic_Ring/2017_Mebel_C6H5_C2H2_highP	C <sub>8</sub> H <sub>7</sub> HACA reactions in high-P limit
First_to_Second_Aromatic_Ring/2017_Mebel_C6H5_C4H4_highP	Phenyl + Vinylacetylene and other C <sub>10</sub> H <sub>9</sub> reactions in high-P
First_to_Second_Aromatic_Ring/2017_Mebel_C6H5C2H2_C2H2_highP	C <sub>10</sub> H <sub>9</sub> HACA reactions in high-P limit
First_to_Second_Aromatic_Ring/phenyl_diacetylene_effective	Effective Phenyl + Diacetylene rates to Benzofulvenyl and other
Fulvene_H	Cyclopentadiene pyrolysis in the presence of ethene
GRI-HCO	The $HCO \rightleftharpoons H + CO$ reaction
GRI-Mech3.0	Gas Research Institute natural gas mechanism optimized
GRI-Mech3.0-N	GRI-Mech3.0 including nitrogen chemistry (NO <sub>x</sub> from N <sub>2</sub> )
Glarborg	Mechanisms by P. Glarborg, assorted by carbon number
JetSurF2.0	Jet Surrogate Fuel model up to C <sub>12</sub> (excited species removed)
Klippenstein_Glarborg2016	Methane oxidation at high pressures and intermediate temperatures
Lai_Hexylbenzene	Alkylaromatic reactions for hexylbenzene
Mebel_C6H5_C2H2	Pathways from benzene to naphthalene
Mebel_Naphthyl	Reactions of naphthyl-1 and naphthyl-2
Methylformate	Methyl formate
Narayanaswamy	Oxidation of substituted aromatic species (aromatic reactions)
Nitrogen_Dean_and_Bozzelli	Combustion Chemistry of Nitrogen
Nitrogen_Glarborg_Gimenez_et_al	High pressure C <sub>2</sub> H <sub>4</sub> oxidation with nitrogen chemistry
Nitrogen_Glarborg_Lucassen_et_al	Fuel-nitrogen conversion in the combustion of small amines
Nitrogen_Glarborg_Zhang_et_al	Premixed nitroethane flames at low pressure
NOx	important NO <sub>x</sub> related reactions, e.g., thermal & prompt
NOx/LowT	Low temperature kinetics (~<1000K) for selected reactions
OxygenSingTrip	Reactions of singlet and triplet oxygen
SOx	important SO <sub>x</sub> related reactions, e.g., H-S, C-S, SO <sub>x</sub>
Sulfur/DMDS	Dimethyl disulfide (CH <sub>3</sub> SSCH <sub>3</sub> )

Table 2 – continued from previous page

Library	Description
Sulfur/DMS	Dimethyl disulfide (CH <sub>3</sub> SSCH <sub>3</sub> )
Sulfur/DTBS	Di-tert-butyl Sulfide (C <sub>4</sub> H <sub>9</sub> SSC <sub>4</sub> H <sub>9</sub> )
Sulfur/GlarborgBozzelli	SO <sub>2</sub> effect on moist CO oxidation with and without NO
Sulfur/GlarborgH <sub>2</sub> S	H <sub>2</sub> S oxidation at high pressures
Sulfur/GlarborgMarshall	OCS chemistry
Sulfur/GlarborgNS	Interactions between nitrogen and sulfur species in comb
Sulfur/Hexanethial_nr	Hexyl sulfide (C <sub>6</sub> H <sub>13</sub> SC <sub>6</sub> H <sub>13</sub> ) + hexadecane (C <sub>16</sub> H <sub>34</sub> )
Sulfur/Sendt	Small sulfur molecule
Sulfur/TP_Song	Thiophene (C <sub>4</sub> H <sub>4</sub> S, aromatic)
Sulfur/Thial_Hydrolysis	Thioformaldehyde (CH <sub>2</sub> S) and thioacetaldehyde (C <sub>2</sub> H <sub>4</sub> S)
TEOS	Organic oxidized silicone
c-C <sub>5</sub> H <sub>5</sub> _CH <sub>3</sub> _Sharma	Cyclopentadienyl + CH <sub>3</sub>
combustion_core	Leeds University natural gas mechanism (contains version 1.0)
fascella	Cyclopentadienyl + acetyl
kislovB	Formation of indene in combustion
naphthalene_H	Cyclopentadiene pyrolysis in the presence of ethene Part 1
vinylCPD_H	Cyclopentadiene pyrolysis in the presence of ethene Part 2
PrimaryH <sub>2</sub> O <sub>2</sub>	Updated rate parameters for the H <sub>2</sub> O <sub>2</sub> system that include

## Families

Allowable reactions in RMG are divided up into classes called **reaction families**. All reactions not listed in a kinetic library have their kinetic parameters estimated from the reaction families.

Each reaction family contains the files:

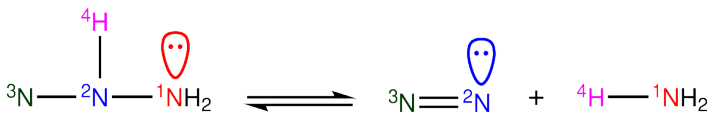
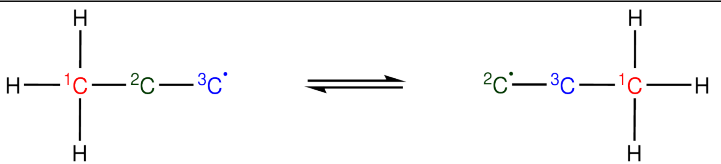
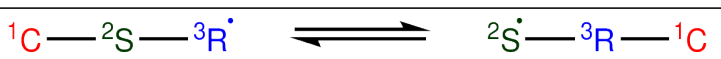
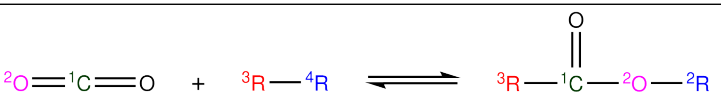
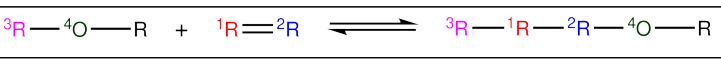
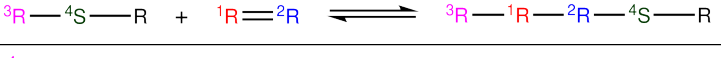
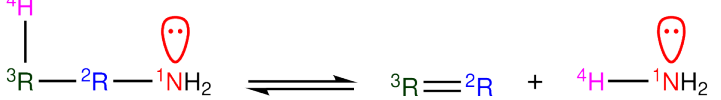
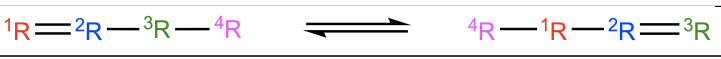
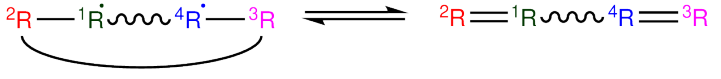
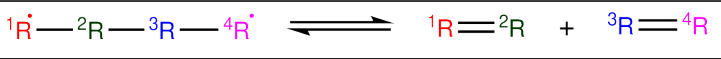
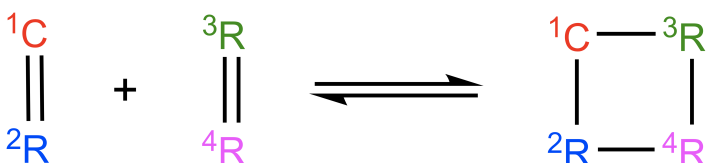
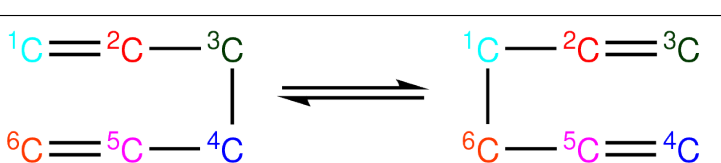
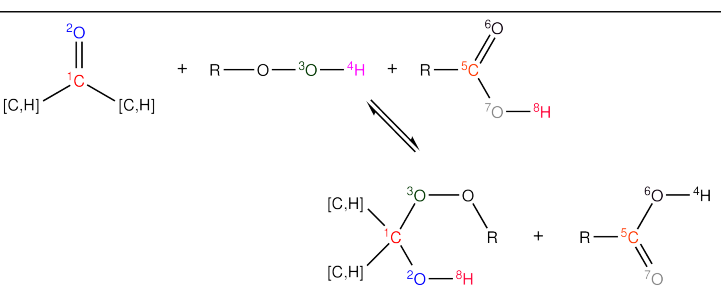
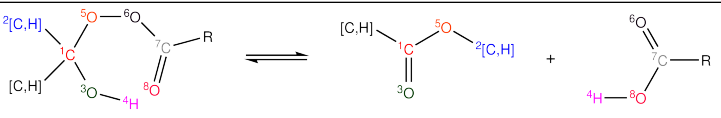
- groups.py containing the recipe, group definitions, and hierarchical trees
- training.py containing a training set for the family
- rules.py containing kinetic parameters for rules

There are currently 74 reaction families in RMG:

<b>1+2_Cycloaddition</b>	${}^1\text{R}=\text{}^2\text{R} + {}^3\text{R} \begin{array}{c} \diagup \\ \diagdown \end{array} \rightleftharpoons \begin{array}{c} {}^1\text{R}-\text{}^2\text{R} \\ \diagup \quad \diagdown \\ {}^3\text{R} \end{array}$
<b>1,2-Birad_to_alkene</b>	${}^1\text{R}\cdot-\text{}^2\text{R}\cdot \rightleftharpoons {}^1\text{R}=\text{}^2\text{R}$
<b>1,2_Insertion_CO</b>	${}^1\text{C}\equiv\text{}^4\text{O}^+ + {}^2\text{R}-\text{}^3\text{R} \rightleftharpoons \begin{array}{c} {}^4\text{O} \\    \\ {}^2\text{R}-\text{}^1\text{C}-\text{}^3\text{R} \end{array}$
<b>1,2_Insertion_carbene</b>	$\begin{array}{c} \text{O} \\ \diagup \quad \diagdown \\ {}^1\text{CH}_2 \end{array} + {}^2\text{R}-\text{}^3\text{R} \rightleftharpoons \begin{array}{c} {}^2\text{R}-\text{}^1\text{C}-\text{}^3\text{R} \\   \quad   \\ \text{H} \quad \text{H} \end{array}$

continues on next page

Table 3 – continued from previous page

1,2_NH3_elimination	
1,2_shiftC	
1,2_shiftS	
1,3_Insertion_CO2	
1,3_Insertion_ROR	
1,3_Insertion_RSR	
1,3_NH3_elimination	
1,3_sigmatropic_rearrangement	
1,4_Cyclic_birad_scission	
1,4_Linear_birad_scission	
2+2_cycloaddition	
6_membered_central_C-C_shift	
Baeyer-Villiger_step1_cat	
Baeyer-Villiger_step2	

continues on next page

Table 3 – continued from previous page

Baeyer-Villiger_step2_cat	
Bimolec_Hydroperoxide_Decomposition	$R-\overset{1}{O}-\overset{2}{O}-H + R-O-\overset{4}{O}-\overset{3}{H} \rightleftharpoons R-\overset{1}{O}\cdot + H-\overset{2}{O}-\overset{3}{H} + R-O-\overset{4}{O}\cdot$
Birad_R_Recombination	$^1R\cdot + ^2R\cdot \rightleftharpoons ^1R-^2R$
Birad_recombination	
CO_Disproportionation	$^1R\cdot + ^2O=\overset{3}{C}-\overset{4}{H} \rightleftharpoons ^1R-\overset{4}{H} + ^2O\equiv\overset{3}{C}$
Concerted_Intra_Diels_alder_monocyclic_1,2_shiftH	
Cyclic_Ether_Formation	$^1R\cdot \sim \sim \sim ^2O-\overset{3}{OR} \rightleftharpoons ^1R \sim \sim \sim ^2O + ^3OR\cdot$
Cyclic_Thioether_Formation	$^1R\cdot \sim \sim \sim ^2S-\overset{3}{(O/S)R} \rightleftharpoons ^1R \sim \sim \sim ^2S + ^3(O'S)R\cdot$
Cyclopentadiene_scission	
Diels_alder_addition	
Disproportionation	$^1R\cdot + ^3R-\overset{2}{R}-\overset{4}{H} \rightleftharpoons ^1R-\overset{4}{H} + ^3R=\overset{2}{R}$
HO2_Elimination_from_PeroxyRadical	$^5H-\overset{1}{R}-\overset{2}{R}-\overset{3}{O}-\overset{4}{O}\cdot \rightleftharpoons ^3O-\overset{4}{O}-\overset{5}{H} + ^1R=\overset{2}{R}$
H_Abstraction	$^1R-\overset{2}{H} + ^3R\cdot \rightleftharpoons ^1R\cdot + ^2H-\overset{3}{R}$

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Table 3 – continued from previous page

Intra_2+2_cycloaddition_Cd	
Intra_5_membered_conjugated_C=C_C=C_addition	
Intra_Diels_alder_monocyclic	
Intra_Disproportionation	
Intra_RH_Add_Endocyclic	
Intra_RH_Add_Exocyclic	
Intra_R_Add_Endocyclic	
Intra_R_Add_ExoTetCyclic	
Intra_R_Add_Exo_scission	
Intra_R_Add_Exocyclic	
Intra_Retro_Diels_alder_bicyclic	
Intra_ene_reaction	

continues on next page

Table 3 – continued from previous page

Korcek_step1	
Korcek_step1_cat	
Korcek_step2	
Peroxyl_Disproportionation	$R-\overset{1}{O}-\overset{2}{O}\cdot + R-\overset{3}{O}-\overset{4}{O}\cdot \rightleftharpoons R-\overset{1}{O}\cdot + R-\overset{3}{O}\cdot + \overset{2}{O}=\overset{4}{O}$
Peroxyl_Termination	$\overset{4}{H}-\overset{1}{R}-\overset{2}{O}-\overset{3}{O}\cdot + R-\overset{5}{O}-\overset{6}{O}\cdot \rightleftharpoons \overset{1}{R}=\overset{2}{O} + R-\overset{5}{O}-\overset{4}{H} + \overset{3}{O}=\overset{6}{O}$
R_Addition_COM	
R_Addition_CSm	
R_Addition_MultipleBond	
R_Recombination	
Singlet_Carbene_Intra_Disproportionation	
Singlet_Val6_to_triplet	
SubstitutionS	
Substitution_O	
Surface_Abstraction	

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Table 3 – continued from previous page

Surface_Adsorption_Bidentate	$  \begin{array}{c}  {}^1\text{R}=\text{}^2\text{R} \\  + \\  {}^3\text{X} + {}^4\text{X}  \end{array}  \rightleftharpoons  \begin{array}{c}  {}^1\text{R}-\text{}^2\text{R} \\    \quad   \\  {}^3\text{X} \quad {}^4\text{X}  \end{array}  $
Surface_Adsorption_Dissociative	$  \begin{array}{c}  {}^1\text{R}-\text{}^2\text{R} \\  + \\  {}^3\text{X} + {}^4\text{X}  \end{array}  \rightleftharpoons  \begin{array}{c}  {}^1\text{R} \\    \\  {}^3\text{X}  \end{array}  +  \begin{array}{c}  {}^2\text{R} \\    \\  {}^4\text{X}  \end{array}  $
Surface_Adsorption_Double	$  \begin{array}{c}  {}^1\text{R}: \\  + \\  {}^2\text{X}  \end{array}  \rightleftharpoons  \begin{array}{c}  {}^1\text{R} \\     \\  {}^2\text{X}  \end{array}  $
Surface_Adsorption_Single	$  \begin{array}{c}  {}^1\text{R}\cdot \\  + \\  {}^2\text{X}  \end{array}  \rightleftharpoons  \begin{array}{c}  {}^1\text{R} \\    \\  {}^2\text{X}  \end{array}  $
Surface_Adsorption_vdW	$  \begin{array}{c}  {}^1\text{R} \\  + \\  {}^2\text{X}  \end{array}  \rightleftharpoons  \begin{array}{c}  {}^1\text{R} \\  \cdots \\  {}^2\text{X}  \end{array}  $
Surface_Bidentate_Dissociation	$  \begin{array}{c}  {}^1\text{R}=\text{}^2\text{R}-\text{}^3\text{R} \\    \quad   \quad   \\  {}^4\text{X} + {}^5\text{X} + {}^6\text{X}  \end{array}  \rightleftharpoons  \begin{array}{c}  {}^1\text{R}-\text{}^2\text{R} \\    \quad   \\  {}^4\text{X} \quad {}^5\text{X}  \end{array}  +  \begin{array}{c}  {}^3\text{R} \\    \\  {}^6\text{X}  \end{array}  $
Surface_Dissociation	$  \begin{array}{c}  {}^1\text{R}-\text{}^2\text{R} \\    \\  {}^3\text{X}  \end{array}  +  {}^4\text{X}  \rightleftharpoons  \begin{array}{c}  {}^1\text{R} \\     \\  {}^3\text{X}  \end{array}  +  \begin{array}{c}  {}^2\text{R} \\    \\  {}^4\text{X}  \end{array}  $
Surface_Dissociation_vdW	$  \begin{array}{c}  {}^1\text{R}-\text{}^2\text{R} \\  \cdots \\  {}^3\text{X}  \end{array}  +  {}^4\text{X}  \rightleftharpoons  \begin{array}{c}  {}^1\text{R} \\    \\  {}^3\text{X}  \end{array}  +  \begin{array}{c}  {}^2\text{R} \\    \\  {}^4\text{X}  \end{array}  $
Surface_Recombination	$  \begin{array}{c}  {}^1\text{R} \\     \\  {}^2\text{X}  \end{array}  +  \begin{array}{c}  {}^3\text{R} \\    \\  {}^4\text{X}  \end{array}  \rightleftharpoons  \begin{array}{c}  {}^1\text{R}-\text{}^3\text{R} \\    \\  {}^2\text{X}  \end{array}  +  {}^4\text{X}  $
intra_H_migration	$  {}^3\text{H}-\text{}^2\text{R}\text{---}\text{}^1\text{R}\cdot \rightleftharpoons \cdot\text{}^2\text{R}\text{---}\text{}^1\text{R}-\text{}^3\text{H}  $
intra_NO2_ONO_conversion	$  \begin{array}{c}  {}^1\text{R}\cdot-\text{}^2\text{N}^+-\text{}^3\text{O}^- \\     \\  \text{O}  \end{array}  \rightleftharpoons  \begin{array}{c}  \text{:}\text{}^2\text{N}-\text{}^3\text{O}-\text{}^1\text{R} \\     \\  \text{O}  \end{array}  $
intra_OH_migration	$  {}^1\text{R}\cdot\text{---}\text{}^2\text{O}-\text{}^3\text{OH} \rightleftharpoons {}^3\text{HO}-\text{}^1\text{R}\text{---}\text{}^2\text{O}\cdot  $

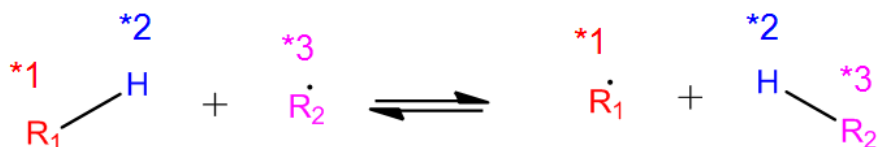
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<b>intra_substitutionCS_cyclization</b>	${}^3\dot{\text{R}}\text{---}{}^1\text{C}\text{---}{}^2\text{S} \rightleftharpoons {}^3\text{R}\text{---}{}^1\text{C} + {}^2\dot{\text{S}}$
<b>intra_substitutionCS_isomerization</b>	${}^3\dot{\text{R}}\text{---}{}^2\text{S}\text{---}{}^1\text{C} \rightleftharpoons {}^1\text{C}\text{---}{}^3\text{R}\text{---}{}^2\dot{\text{S}}$
<b>intra_substitutionS_cyclization</b>	${}^3\dot{\text{R}}\text{---}{}^1\text{S}\text{---}{}^2\text{R} \rightleftharpoons {}^3\text{R}\text{---}{}^1\text{S} + {}^2\dot{\text{R}}$
<b>intra_substitutionS_isomerization</b>	${}^3\dot{\text{R}}\text{---}{}^2\text{R}\text{---}{}^1\text{S} \rightleftharpoons {}^1\text{S}\text{---}{}^3\text{R}\text{---}{}^2\dot{\text{R}}$
<b>lone_electron_pair_bond</b>	$\text{R}-\text{N}(\text{R})-\text{R} + {}^2\ddot{\text{O}} \rightleftharpoons \text{R}-\text{N}^+(\text{R})-\text{R} + {}^2\ddot{\text{O}}^-$

## Recipe

The recipe can be found near the top of groups.py and describes the changes in bond order and radicals that occur during the reaction. Reacting atoms are labelled with a starred number. Shown below is the recipe for the H-abstraction family.



### Recipe

- (1) BREAK\_BOND  $\{\textcolor{red}{*}1, \textcolor{blue}{*}2\}$
- (2) FORM\_BOND  $\{\textcolor{blue}{*}2, \textcolor{violet}{*}3\}$
- (3) GAIN\_RADICAL  $\{\textcolor{red}{*}1, 1\}$
- (4) LOSE\_RADICAL  $\{\textcolor{violet}{*}3, 1\}$

The table below shows the possible actions for recipes. The arguments are given in the curly braces as shown above. For the order of bond change in the Change\_Bond action, a -1 could represent a triple bond changing to a double bond while a +1 could represent a single bond changing to a double bond.

Action	Argument1	Argument2	Argument3
Break_Bond	First bonded atom	Type of bond	Second bonded atom
Form_Bond	First bonded atom	Type of bond	Second bonded atom
Change_Bond	First bonded atom	Order of bond change	Second bonded atom
Gain_Radical	Specified atom	Number of radicals	
Lose_Radical	Specified atom	Number of radicals	

Change\_Bond order cannot be directly used on benzene bonds. During generation, aromatic species are kekulized to alternating double and single bonds such that reaction families can be applied. However, RMG cannot properly handle benzene bonds written in the kinetic group definitions.

## Training Set vs Rules

The training set and rules both contain trusted kinetics that are used to fill in templates in a family. The **training set** contains kinetics for specific reactions, which are then matched to a template. The kinetic **rules** contain kinetic parameters that do not necessarily correspond to a specific reaction, but have been generalized for a template.

When determining the kinetics for a reaction, a match for the template is searched for in the kinetic database. The three cases in order of decreasing reliability are:

1. Reaction match from training set
2. Node template exact match using either training set or rules
3. Node template estimate averaged from children nodes

Both training sets and reaction libraries use the observed rate, but rules must first be divided by the degeneracy of the reaction. For example, the reaction  $\text{CH}_4 + \text{OH} \rightarrow \text{H}_2\text{O} + \text{CH}_3$  has a reaction degeneracy of 4. If one performed an experiment or obtained this reaction rate using Arkane (applying the correct symmetry), the resultant rate parameters would be entered into libraries and training sets unmodified. However a kinetic rule created for this reaction must have its A-factor divided by 4 before being entered into the database.

The reaction match from training set is accurate within the documented uncertainty for that reaction. A template exact match is usually accurate within about one order of magnitude. When there is no kinetics available for the template in either the training set or rules, the kinetics are averaged from the children nodes as an estimate. In these cases, the kinetic parameters are much less reliable. For more information on the estimation algorithm see [Kinetics Estimation](#).

The training set can be modified in `training.py` and the rules can be modified in `rules.py`. For more information on modification see [Adding Training Reactions](#) and [Adding Kinetic Rules](#).

### 1.12.4 Database Modification

Note that the RMG-Py database is written in Python code where line indentations determine the scope. When modifying the database, be sure to preserve all line indentations shown in the examples.

#### Modifying the Thermo Database

##### Creating Thermo Libraries

##### Adding Thermo Groups

##### Adding Thermo to the Depository

#### Modifying the Kinetics Database

For the casual user, it is recommended to use either a kinetic library or add to the training set instead of modifying the kinetic groups.

Put kinetic parameters into a kinetic library when:

- A set of reaction rates were optimized together
- You know the reaction rate is not generalizable to similar species (perhaps due to catalysis or aromatic structures)
- No family exists for the class of reaction
- You are not confident about the accuracy of kinetic parameters

Put kinetic parameters into the training set when:

- You are confident on the accuracy of the kinetic parameter
- You wish for the reaction to be generalized to similar reactions in your mechanism

## Adding Reaction Family

There are several places in the RMG-database and RMG-Py source code where reaction family details are hard-coded. You should check all these when you create a new reaction family. Here are some of the places:

- **RMG-database/input/kinetics/families/[family name]**
  - add folder for your family name
  - create `groups.py`, `rules.py` and a template folder with species dictionary and `reactions.py`.
  - fill the files with rate data that you plan to use.
  - **Many tools exist to help with the conversion process:**
    - \* `convertKineticsLibraryToTrainingReactions.ipynb` in `RMG-database/scripts`
    - \* `importChemkinLibrary.py` in `RMG-database/scripts`
- **rmgpy.data.kinetics.family**
  - `applyRecipe`: swapping the atom labels (eg. \*1 and \*2) around
  - `getReactionPairs`: figuring out which species becomes which for flux analyses
  - `__generateReactions`: correcting degeneracy eg. dividing by 2 for radical recombination
- **rmgpy.data.kinetics.rules**
  - `processOldLibraryEntry`: determining units when importing RMG-Java database
  - `getAllRules`: for radical recombination add reverse templates
- **rmgpy.data.kinetics.groups**
  - `getReactionTemplate`: for radical recombination duplicate the template
- **RMG-database/input/kinetics/families/recommended.py**
  - allows the usage of the database with the recommended families.

## Creating Kinetics Libraries

To add a reaction library, simply create a folder bearing the library's name under `RMG-database/input/kinetics/libraries`. You'll need to create two files: `dictionary.txt` and `reactions.py`. The dictionary file contains the Adjacency lists for all relevant species (can be generated using the [Molecule Search](#) function of the rmg website, while the reactions file specifies the kinetics. To conform to RMG's format, simply copy and modify an existing library.

At the top of the reactions file fill in the name and short (one line) and long descriptions. The name must be identical to the folder's name. Then list the kinetics entries, each with a unique index number.

There are two flags relevant for pressure dependent library reactions that one should consider using:

1. **elementary\_high\_p**: Should be set to `True` for *elementary* unimolecular reactions (with only one reactant and/or product) with a kinetics entry that has information about the high pressure kinetics, i.e., Troe or Lindemann, PDepArrhenius or Chebyshev that are defined up to at least 100 bar, or Arrhenius that represents the high pressure limit (i.e., not the measured rate at some low or medium experimental pressure). If set to `True`, RMG will use the high pressure

limit rate when constructing pressure-dependent networks. The kinetics entry of the original library reaction will only be updated if it is an Arrhenius type (will be replaced with either PDepArrhenius or Chebyshev, as specified in the pressureDependent block of the input file). If set to `False` (the default value), RMG will not use the high pressure limit rate in network exploration, and will not convert Arrhenius kinetics of library reactions that have no template (a corresponding reaction family) into a pressure-dependent form.

2. **allow\_pdep\_route**: If set to `True` and RMG discovers a pressure-dependent reaction with the same reactants and products, the latter *will* be considered in addition to the library reaction. This is useful for cases when more than one pathway connects the same reactants and products, and some of these pathways are well-skipping reactions. If set to `False` (the default value), similar network reactions will not be considered in the model generation.

The following formats are accepted as kinetics entries:

**Arrhenius** of the form  $k(T) = A \left(\frac{T}{T_0}\right)^n \exp\left(-\frac{E_a}{RT}\right)$  (see [Arrhenius Class](#) for details):

```
entry(
index = 1,
label = "H + O2 <=> O + OH",
degeneracy = 1,
kinetics = Arrhenius(A=(9.841e+13, 'cm^3/(mol*s)'), n=0, Ea=(15310, 'cal/mol'), T0=(1,
↪ 'K')),
shortDesc = u"This is a short description limited to one line, e.g. 'CBS-QB3'",
longDesc = u""""This is a long description, unlimited by number of lines.
These descriptions can be added to every kinetics type."""")
```

**MultiArrhenius** is the sum of multiple Arrhenius expressions (all apply to the same temperature range) (see [MultiArrhenius Class](#) for details):

```
entry(
index = 2,
label = "O + H2 <=> H + OH",
degeneracy = 1,
    duplicate = True,
kinetics = MultiArrhenius(
    arrhenius = [Arrhenius(A=(3.848e+12, 'cm^3/(mol*s)'), n=0, Ea=(7950, 'cal/mol
↪ '), T0=(1, 'K')),
    Arrhenius(A=(6.687e+14, 'cm^3/(mol*s)'), n=0, Ea=(19180, 'cal/mol'), T0=(1, 'K
↪ '))]))
```

**ThirdBody** for pressure dependent reactions of the sort  $H_2 + M \rightleftharpoons H + H + M$ . efficiencies are optional and specify the factor by which the rate is multiplies if the mentioned species is the third body collider. Note that for complex efficiency behaviour, an efficiency of 0 can be set, and a separate specific reaction can be defined (see [ThirdBody Class](#) for details):

```
entry(
index = 3,
label = "H2 <=> H + H",
degeneracy = 1,
kinetics = ThirdBody(
    arrheniusLow = Arrhenius(A=(4.58e+19, 'cm^3/(mol*s)'), n=-1.4, Ea=(104390,
↪ 'cal/mol'), T0=(1, 'K')),
    efficiencies = {'[Ar]': 0, '[N#N]': 1.01, '[H][H]': 2.55, '[O]': 12.02, '[C-]#[O+]
↪ ': 1.95, '[O=C=O]': 3.83, '[C]': 2.00, '[C=O]': 2.50, '[CO]': 3.00, '[CC]': 3.00}))
entry(
```

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```

index = 4,
label = "H2 + Ar <=> H + H + Ar",
degeneracy = 1,
kinetics = Arrhenius(A=(5.176e+18, 'cm^3/(mol*s)'), n= 1.1, Ea=(104390, 'cal/mol'),
↳ T0=(1, 'K'))

```

**Troe** for pressure dependent reactions (see [Troe Class](#) for details):

```

entry(
index = 5,
label = "H + O2 <=> H02",
degeneracy = 1,
kinetics = Troe(
    arrheniusHigh = Arrhenius(A=(4.565e+12, 'cm^3/(mol*s)'), n=0.44, Ea=(0, 'cal/
↳ mol'), T0=(1, 'K')),
    arrheniusLow = Arrhenius(A=(6.37e+20, 'cm^6/(mol^2*s)'), n = -1.72, Ea =
↳ (525, 'cal/mol'), T0 = (1, 'K')),
    alpha=0.5, T3=(30, 'K'), T1=(90000, 'K'), T2=(90000, 'K'),
    efficiencies = {'[Ar]': 0.6, '[He]': 0.71, 'N#N': 0.96, '[H][H]': 1.87,
↳ '[O][O]': 0.75, 'O': 15.81, '[C-]#[O+]': 1.90, 'O=C=O': 3.45, 'C': 2.00, 'C=O': 2.
↳ 50, 'CO': 3.00, 'CC': 3.00}))

```

**Lindemann** (see [Lindemann Class](#) for details):

```

entry(
    index = 6,
    label = "CO + O <=> CO2",
    degeneracy = 1,
    kinetics = Lindemann(
        arrheniusHigh = Arrhenius(A=(1.88e+11, 'cm^3/(mol*s)'), n=0, Ea=(2430, 'cal/
↳ mol'), T0=(1, 'K')),
        arrheniusLow = Arrhenius(A = (1.4e+21, 'cm^6/(mol^2*s)'), n = -2.1, Ea =
↳ (5500, 'cal/mol'), T0 = (1, 'K')),
        efficiencies = {'[Ar]': 0.87, '[He]': 2.50, 'O': 12.00, '[C-]#[O+]': 1.90,
↳ 'O=C=O': 3.80, 'C': 2.00, 'C=O': 2.50, 'CO': 3.00, 'CC': 3.00}))

```

**PDepArrhenius** where each Arrhenius expression corresponds to a different pressure, as specified. Allowed pressure units are Pa, bar, atm, torr, psi, mbar (see [PDepArrhenius Class](#) for details):

```

entry(
    index = 7,
    label = "HCO <=> H + CO",
    degeneracy = 1,
    kinetics = PDepArrhenius(
        pressures = ([1, 10, 20, 50, 100], 'atm'),
        arrhenius = [
            Arrhenius(A=(9.9e+11, 's^-1'), n=-0.865, Ea=(16755, 'cal/mol'), T0=(1, 'K
↳ ')),
            Arrhenius(A=(7.2e+12, 's^-1'), n=-0.865, Ea=(16755, 'cal/mol'), T0=(1, 'K
↳ ')),
            Arrhenius(A=(1.3e+13, 's^-1'), n=-0.865, Ea=(16755, 'cal/mol'), T0=(1, 'K
↳ ')),
            Arrhenius(A=(2.9e+13, 's^-1'), n=-0.865, Ea=(16755, 'cal/mol'), T0=(1, 'K
↳ ')),

```

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(continued from previous page)

```
Arrhenius(A=(5.3e+13, 's^-1'), n=-0.865, Ea=(16755, 'cal/mol'), T0=(1, 'K'
↳')))))))
```

**MultiPDepArrhenius** (see [MultiPDepArrhenius Class](#) for details):

```
entry(
    index = 8,
    label = "N2H2 <=> NNH + H",
    degeneracy = 1,
    duplicate = True,
    kinetics = MultiPDepArrhenius(
        arrhenius = [
            PDepArrhenius(
                pressures = ([0.1, 1, 10], 'atm'),
                arrhenius = [
                    Arrhenius(A=(5.6e+36, '1/s'), n=-7.75, Ea=(70250.4, 'cal/mol'),
↳T0=(1, 'K')),
                    Arrhenius(A=(1.8e+40, '1/s'), n=-8.41, Ea=(73390, 'cal/mol'),
↳T0=(1, 'K')),
                    Arrhenius(A=(3.1e+41, '1/s'), n=-8.42, Ea=(76043, 'cal/mol'),
↳T0=(1, 'K'))]),
            PDepArrhenius(
                pressures = ([0.1, 1, 10], 'atm'),
                arrhenius = [
                    Arrhenius(A=(1.6e+37, '1/s'), n=-7.94, Ea=(70757, 'cal/mol'),
↳T0=(1, 'K')),
                    Arrhenius(A=(2.6e+40, '1/s'), n=-8.53, Ea=(72923, 'cal/mol'),
↳T0=(1, 'K')),
                    Arrhenius(A=(1.3e+44, '1/s'), n=-9.22, Ea=(77076, 'cal/mol'),
↳T0=(1, 'K'))])])])
```

**Chebyshev** (see [Chebyshev Class](#) for details):

```
entry(
    index = 9,
    label = "CH3 + OH <=> CH2(S) + H2O",
    degeneracy = 1,
    kinetics = Chebyshev(
        coeffs = [
            [12.4209, -0.799241, -0.299133, -0.0143012],
            [0.236291, 0.856853, 0.246313, -0.0463755],
            [-0.0827561, 0.0457236, 0.105699, 0.057531],
            [-0.049145, -0.0760609, -0.0214574, 0.0247001],
            [-0.00664556, -0.0412733, -0.0308561, -0.00959838],
            [0.0111919, -0.00649914, -0.0106088, -0.0137528],
        ],
        kunits='cm^3/(mol*s)', Tmin=(300, 'K'), Tmax=(3000, 'K'), Pmin=(0.0013156,
↳'atm'), Pmax=(131.56, 'atm'))
```

## Adding a specific collider

Only the Troe and Lindemann pressure dependent formats could be defined with a specific species as a third body collider, if needed. For example:

```
entry(
    index = 10,
    label = "S02 + O <=> S03",
    degeneracy = 1,
    kinetics = Troe(
        arrheniusHigh = Arrhenius(A=(3.7e+11, 'cm^3/(mol*s)'), n=0, Ea=(1689, 'cal/mol'), T0=(1, 'K')),
        arrheniusLow = Arrhenius(A=(2.4e+27, 'cm^6/(mol^2*s)'), n=-3.6, Ea=(5186, 'cal/mol'), T0=(1, 'K')),
        alpha = 0.442, T3=(316, 'K'), T1=(7442, 'K'), efficiencies={'O=S=O': 10, 'O': 10, 'O=C=O': 2.5, 'N#N': 0}))

entry(
    index = 11,
    label = "S02 + O (+N2) <=> S03 (+N2)",
    degeneracy = 1,
    kinetics = Troe(
        arrheniusHigh = Arrhenius(A=(3.7e+11, 'cm^6/(mol^2*s)'), n=0, Ea=(1689, 'cal/mol'), T0=(1, 'K')),
        arrheniusLow = Arrhenius(A=(2.9e+27, 'cm^9/(mol^3*s)'), n=-3.58, Ea=(5206, 'cal/mol'), T0=(1, 'K')),
        alpha=0.43, T3=(371, 'K'), T1=(7442, 'K'), efficiencies={}))
```

## Adding New Kinetic Groups and Rate Rules

### Decide on a Template

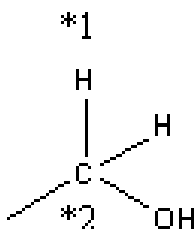
First you need to know the template for your reaction to decide whether or not to create new groups:

1. Type your reaction into the kinetics search at <https://rmg.mit.edu/database/kinetics/search/>
2. Select the correct reaction
3. In the results search for “(RMG-Py rate rules)” and select that link. The kinetic family listed is the family of interest.
4. Scroll to the bottom and look at the end of the long description. There may be very long description of the averaging scheme, but the template for the reaction is the very last one listed:

**Reference:**
**Reference link:** [http://dev.rmg.mit.edu/database/kinetics/families/H\\_Abstraction/rules](http://dev.rmg.mit.edu/database/kinetics/families/H_Abstraction/rules)
**Reference type:**
**Short description:** Estimated by RMG-Py rate rules

**Long description:** Average of (O\_pri,C\_methyl + Average of (O/H/NonDeC,C\_methyl + O/H/OneDe,C\_methyl). + Average of (O\_pri,C\_rad/H2/Cs). + Average of (O/H/NonDeC,C\_rad/H2/Cs + Average of (H2O2,lnChI=1/C4H9O/c1-2-3-4-5/h5H,1-4H2 + H2O2,lnChI=1/C4H9O/c1-3-4(2)5/h4-5H,2-3H2,1H3 + H2O2,lnChI=1/C4H9O/c1-3-4(2)5/h4-5H,1,3H2,2H3 + H2O2,lnChI=1/C4H9O/c1-4(2,3)5/h5H,1H2,2-3H3). + Average of (H2O2,lnChI=1/C3H5/c1-3-2/h3H,1-2H2). + Average of (ROOH\_pri,C\_rad/H2/CO + ROOH\_sec,C\_rad/H2/CO). ). + Average of (O/H/NonDeC,C\_rad/H/NonDeC + Average of (H2O2,lnChI=1/C4H9O/c1-2-3-4-5/h2,5H,3-4H2,1H3 + H2O2,lnChI=1/C4H9O/c1-2-3-4-5/h3,5H,2,4H2,1H3 + H2O2,lnChI=1/C4H9O/c1-3-4(2)5/h3-5H,1-2H3). + Average of (Average of (H2O2,lnChI=1/C4H9O/c1-2-3-4-5/h4-5H,2-3H2,1H3). ). + Average of (Average of (ROOH\_pri,C\_rad/H/CO/Cs). + Average of (ROOH\_sec,C\_rad/H/CO/Cs). ). ). + Average of (Average of (O/H/NonDeC,C\_rad/Cs3). + Average of (Average of (Average of (H2O2,lnChI=1/C4H9O/c1-3-4(2)5/h5H,3H2,1-2H3). ). + Average of (Average of (ROOH\_pri,C\_rad/OOH/Cs/Cs). ). + Average of (Average of (ROOH\_sec,C\_rad/OOH/Cs/Cs). ). ). ). Estimated using template (O\_H,Cs\_rad for rate rule (O\_pri,C\_rad/Cs3)

Now you must determine whether the chosen template is appropriate. A good rule of thumb is to see if the all neighbours of the reacting atoms are as specified as possible. For example, assume your species is ethanol



and RMG suggests the group:

```
label = "C_sec",
group =
"""
1 *1 Cs 0 {2,S} {3,S} {4,S}
2 *2 H 0 {1,S}
3 R!H 0 {1,S}
4 R!H 0 {1,S}
""",
```

If you use the suggested groups you will not capture the effect of the alcohol group. Therefore it is better to make a new group.

```
label = "C/H2/Cs0",
group =
"""
1 *1 Cs  0 {2,S} {3,S} {4,S} {5,S}
2 *2 H   0 {1,S}
3      H  0 {1,S}
4      O  0 {1,S}
5      Cs 0 {1,S}
""",
```

If you have determined the suggested groups is appropriate, skip to [Adding Training Reactions](#) or [Adding Kinetic Rules](#). Otherwise proceed to the next section for instructions on creating the new group.

## Creating a New Group

In the family's `groups.py`, you will need to add an entry of the format:

```
entry(
    index = 61,
    label = "C_sec",
    group =
"""
1 *1 Cs  0 {2,S} {3,S} {4,S} {5,S}
2 *2 H   0 {1,S}
3      C  0 {1,S}
4      H  0 {1,S}
5      R!H 0 {1,S}
""",
    kinetics = None,
    reference = None,
    referenceType = "",
    shortDesc = u"",
    longDesc = u"",
)
```

- The index can be any number not already present in the set
- The label is the name of the group.
- The group is the group adjacency list with the starred reacting atoms.
- The other attributes do not need to be filled for a group

Next, you must enter your new group into the tree. At the bottom of `groups.py` you will find the trees. Place your group in the appropriate position. In the example given in the previous section, the new group would be added under the `C_sec`.

```
L1: X_H
    L2: H2
    L2: Cs_H
        L3: C_pri
        L3: C_sec
            L4: C/H2/Cs0
        L3: C_ter
```

## Adding Kinetic Rules

Rules give generalized kinetic parameters for a specific node template. In most cases, your kinetic parameters describe a specific reaction in which case you will want to add your reaction to the training set.

The rule must be added into `rules.py` in the form:

```
entry(
    index = 150,
    label = "C/H/Cs3;0_rad/NonDe0",
    group1 =
    """
1 *1 Cs 0 {2,S} {3,S} {4,S} {5,S}
2 *2 H 0 {1,S}
3   Cs 0 {1,S}
4   Cs 0 {1,S}
5   Cs 0 {1,S}
    """,
    group2 =
    """
1 *3 0 1 {2,S}
2   0 0 {1,S}
    """,
    kinetics = ArrheniusEP(
        A = (2800000000000.0, 'cm^3/(mol*s)', '*|/', 5),
        n = 0,
        alpha = 0,
        E0 = (16.013, 'kcal/mol', '+|-', 1),
        Tmin = (300, 'K'),
        Tmax = (1500, 'K'),
    ),
    reference = None,
    referenceType = "",
    rank = 5,
    shortDesc = u""Curran et al. [8] Rate expressions for H atom abstraction
    ↪from fuels.""",
    longDesc =
    u""
[8] Curran, H.J.; Gaffuri, P.; Pittz, W.J.; Westbrook, C.K. Combust. Flame 2002, 129,
    ↪253.
Rate expressions for H atom abstraction from fuels.

pg 257 A Comprehensive Modelling Study of iso-Octane Oxidation, Table 1. Radical:H02,
    ↪Site: tertiary (c)

Verified by Karma James
    """,
)
```

- The index can be any number not already used in `rules.py`.
- The label is the name of the rule.
- The groups must have the adjacency list of the respective groups. Between them they should have all starred atoms from the recipe.

- The value and units of kinetic parameters must be given.
  - Multiplicative uncertainty is given as ' $\ast \backslash /$ ', 5 meaning within a factor of 5
  - Additive uncertainty is given as ' $+ \backslash / -$ ', 2 meaning plus or minus 2.
- Rank determines the priority of the rule when compared with other rules.
- The short description will appear in the annotated chemkin file.
- The long description only appears in the database.

## Adding Training Reactions

If you know the kinetics of a specific reaction, rather than a rate rule for a template, you can add the kinetics to the database training set. By default, RMG creates new rate rules from this training set, which in turn benefits the kinetics of similar reactions. The new rate rules are formed by matching the reaction to the most most specific template nodes within the reaction's respective family. If you do not want the training depository reactions to create new rate rules in the database, set the option for `kineticsDepositories` within the database field in your input file to

```
kineticsDepositories = ['!training'],
```

Currently, RMG's rate rule estimates overrides all kinetics depository kinetics, including training reactions. Unless the training reaction's rate rule ranks higher than the existing node, it will not be used. If you want the training reaction to override the rate rule estimates, you should put the reaction into a reaction library or seed mechanism.

The easiest way to add training reactions to the database is via the RMG website. First, search for the reaction using <https://rmg.mit.edu/database/kinetics/search/>. This will automatically search the existing RMG database for the reaction, as well as identify the reaction family template that this reaction matches. If the reaction does not match any family, then it cannot be added to the training reactions. Click the 'Create training rate from average' button underneath the kinetics plot for the reaction and edit the kinetics and reference descriptions for the reaction. The atom labels marking the reaction recipe actions (lose bond, add radical, etc.) will already be automatically labeled for you. After editing the reaction data, write a short message for the reaction added under the 'Summary of changes' field, then click 'Save.' You will need an account for the RMG website to make an entry.

---

**Note:** If you are entering the reaction in the reverse direction of the family, you must still label the reactants and products with the atomLabels of the original reaction template. Otherwise, RMG will not be able to locate the nodes in the group tree to match the reaction.

Entries added in the reverse direction of the original template will use the current RMG job's thermo database to estimate the kinetics in the forward direction. Therefore this value can differ depending on the order of thermo libraries used when running a job.

---

If adding the training reaction manually, first identify the reaction family of the reaction, then go to the family's folder in `RMG-database/input/kinetics/families/`. Create a new kinetics entry in the `training.py` file. Make sure to apply the reaction recipe labels properly for the reactants and products.

## Pitfalls

Be careful with the specificity when naming neighbouring atoms. On upper nodes, you should try to be general so that you do not exclude reactions.

Sibling nodes must be exclusive from one another so that there is no question which group a molecule qualifies as. However, you do not need to be exhaustive and list out every possibility.

Be sure to give errors whenever adding rules. If you don't know the uncertainty, why do you trust the kinetics?

After you are done always check via populate reactions or the website, that your modifications are behaving the way you expect.

Caveat regarding how rate rules are used by RMG and the rate parameters you input: because tunneling is important for many chemical reactions, the rate of a reaction may not be easily represented by a bi-Arrhenius fit. 3-parameter fits are more common. However, the resulting fit may report an 'activation energy' that is much different (possibly by 10+ kcal/mol) than the true barrier height. When RMG is assembling pressure-dependent networks, it will use barrier heights from rate rules. This can lead to very inaccurate rate calculations. To avoid this issue, try to ensure that your fitted arrhenius activation energy truly does reflect the reaction barrier height.

## 1.13 Thermochemistry Estimation

This section gives in-depth descriptions of the methods used for determining thermochemistry of species.

Thermochemistry of species is obtained via three possible ways:

1. Species thermochemistry libraries
2. Group contribution methods
3. On-the-fly Quantum-chemical calculation of Thermochemical Properties (QMTP)

### 1.13.1 Species thermochemistry libraries

These databases contain thermochemical parameters for species. In these databases each entry contains an unambiguous definition of the species (through the adjacency list representation), along with a values for the thermochemistry in a format that allows the evaluation of each thermodynamic variable as a function of temperature.

RMG is shipped with a number of species thermochemistry libraries, located in the 'libraries' folder of RMG-database. More information on these species thermochemistry libraries can be found in *Thermo Database*.

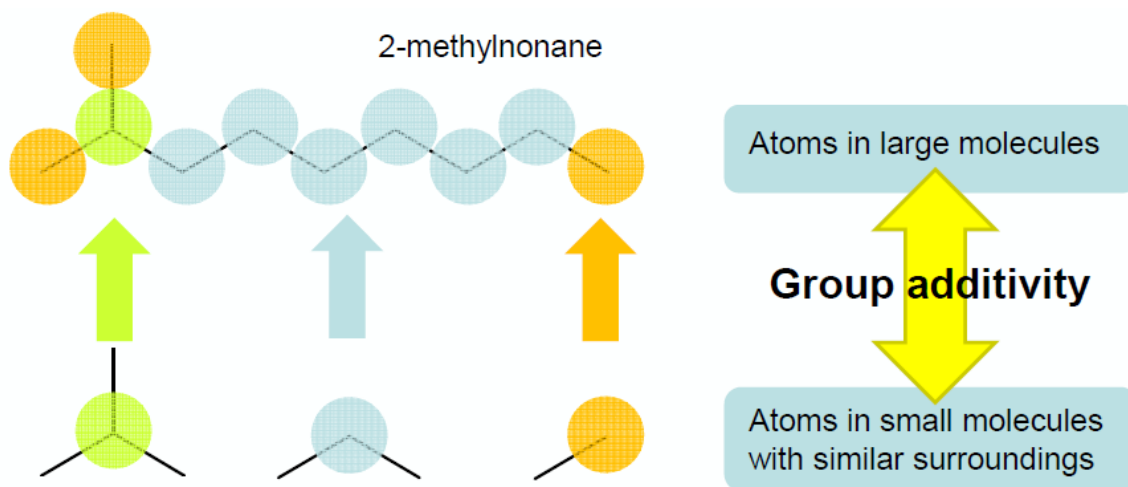
### 1.13.2 Group contribution methods

When the thermochemistry of a species is not present in one of the available species thermochemistry libraries, RMG needs to estimate thermochemistry. One way to do so, is by using group contribution methods that estimate the thermochemistry of a molecule based on the sub-molecular fragments present in the molecule. The Benson group additivity framework is such an example of a group contribution method that has proven to provide accurate estimates of the ideal gas thermochemistry for a large range of molecules.

Benson's Group Additivity approach ([Benson1976]), divides a molecule into functional groups, and the contribution of each functional group to the overall thermochemistry is included. For example, the molecule 2-methylnonane consists of three types of groups:

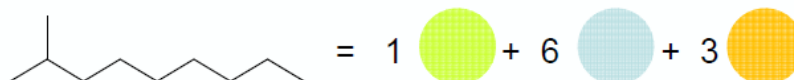
- 1 tertiary carbon atom
- 6 secondary carbon atoms

- 3 primary carbon atoms



**Group definition based on surroundings (ligands)**

**Additivity:**



Thermochemistry for the molecule X is calculated by summing up the values for each of the contributions  $C_i$ . E.g.:

$$\Delta_f H_{298}^\circ(X) = \sum_i GAV(C_i)$$

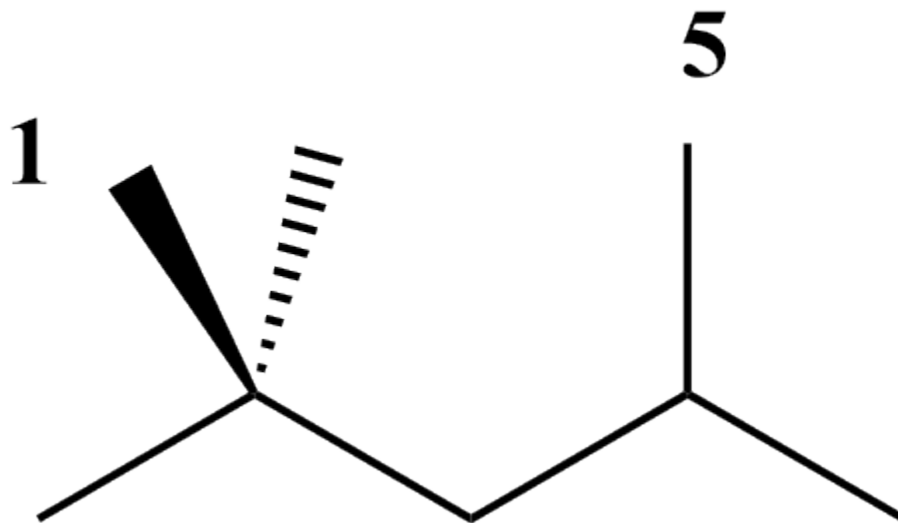
The term ‘group additive value’ (GAV) denotes a polyvalent (ligancy > 1) monoatomic central atom  $C_i$  surrounded by its nearest-neighbor ligands.

Values for each central atomtype (e.g. “tertiary carbon atom”) and its surrounding ligands can be found in the thermo group database, named `group.py`, of RMG. More information can be found here: [Thermo Database](#).

## NNIs

Besides the main group-centered (GAV) contributions, non-next-nearest neighbor interactions (NNI) may also be important to take into account. NNIs are interactions between atoms separated by at least 2 atoms, such as alkane 1,4-gauche, alkane 1,5 (cf. figure), alkene 1,4-gauche, alkene single and double cis, ene-yne cis and ortho interactions.





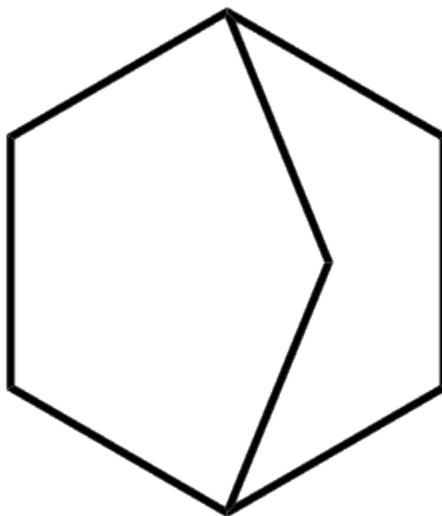
As a result, thermochemistry of the molecule X is determined as :

$$\Delta_f H_{298}^\circ(X) = \sum_i GAV(C_i) + \sum_j NNI_j$$

RMG contains a database with NNIs, named `gauche.py` and `int15.py`. More information on the nature on the available NNIs, and corresponding values can be found here: [Thermo Database](#).

### Ring Strain

To account for ring strain, ring strain corrections (RSC) were introduced. Because there is no obvious relation between the RSC and the ring structure, a specific RSC is required for every type of ring. For example, due to the significant ring strain induced in norbornane (cf. figure), a ring correction (RSC) needs to be added to the sum of the GAVs of the individual carbon atoms:



As a result, thermochemistry of the molecule X is determined as :

$$\Delta_f H_{298}^\circ(X) = \sum_i GAV(C_i) + RSC$$

RMG contains a database with single-ring corrections, ‘ring.py’ and polycyclic ring corrections, ‘polycyclic.py’. More information on the nature on the available NNIs, and corresponding values can be found here: [Thermo Database](#).

### Hydrogen Bond Increment (HBI) method

Lay et al. [Lay] introduced the hydrogen bond increment (HBI) method to predict thermochemical properties of radicals. In contrast to Benson’s method, the HBI method does not use the group-additivity concept. The HBI enthalpy of formation of a radical ( $R^*$ ) is calculated from the enthalpy of formation of the corresponding parent molecule ( $R-H$ ) by adding a HBI to account for the loss of a hydrogen atom. Hence, for standard enthalpies of formation the HBI is defined as

$$HBI = \Delta_f H_{298}^o(R^*) - \Delta_f H_{298}^o(R-H) = BDE(R-H) - \Delta_f H_{298}^o(H^*)$$

with BDE the bond dissociation enthalpy of the  $R-H$  bond at the radical position. Similar expressions are valid for the entropy and heat capacity.

As a result the thermochemistry of the radical is calculated as follows:

$$\begin{aligned}\Delta_f H_{298}^o(R^*) &= HBI(\Delta_f H_{298}^o) + \Delta_f H_{298}^o(R-H) \\ C_p^o(R^*) &= HBI(C_p^o) + C_p^o(R-H) \\ S_{298}^o(R^*) &= HBI(S_{298}^o) + S_{298}^o(R-H)\end{aligned}$$

The HBI method is the default method use to estimate thermochemistry of radicals. Thus, the effect of resonance stabilization on the enthalpy of the radical will be accounted for through the corresponding HBI. For example, the HBI labeled as “C=CC=CCJ” will account for the resonance present in 1,4-pentadien-3-yl radical.

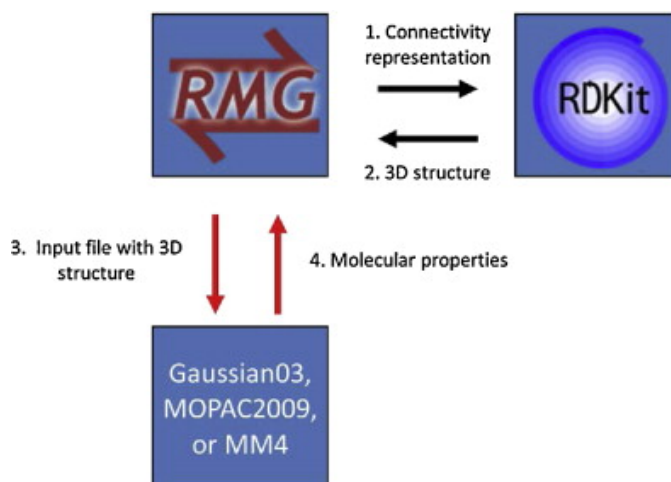
The HBI method can be applied to a variety of saturated compound thermochemistry values. In RMG, library values for saturated compounds are prioritized over group additivity values for saturated compounds. Note that if QMTP is on, the QM saturated value will get priority over group additivity but library value will have priority over QM value. This ensures that there is a systematic HBI correction for values used in the final model: if the saturated molecule thermo uses a library as a source, the radical thermo applies the HBI correction to that same library value.

RMG contains a database for with HBIs, named radical.py. More information on the nature on the available HBIs, and corresponding values can be found here: [Thermo Database](#).

### 1.13.3 On-the-fly Quantum-chemical calculation of Thermochemical Properties (QMTP)

An interface for performing on-the-fly quantum and force field calculations has been developed and integrated into RMG to complement the species thermochemistry databases and group contribution methods [Magoon and Green]\_. This interface is particularly interesting for the estimation of thermochemistry of molecules that are not present in one of the species thermochemistry databases, and which cannot be estimated with sufficient accuracy using the Benson group additivity framework. This pertains specifically to polycyclic fused ring containing species, whose ring strain cannot be modeled using the available ring corrections in RMG’s ring strain correction databases.

The QMTP interface involves a number of steps, summarized in the figure below.



In a first step the connectivity representation is converted into a three-dimensional structure of the molecule through the generation of 3D coordinates for the atoms in the molecule. This is accomplished using a combination of a distance geometry method, followed by a optimization using the UFF force field available in RDKit [RDKit]. Next, an input file is created containing the 3D atomic coordinates along with a number of keywords. This file is sent to a computational chemistry package, either OpenMopac or Gaussian, that calculates the thermochemistry of the given molecule “on-the-fly”. The keywords specify the type of calculation, and the level-of-theory. Finally, the calculated thermochemistry data is sent back to RMG.

The QMTP calculation creates a folder ‘QMfiles’ that contains a number of files that are created during the process. The filename of these files is a combination of the InChI key of the molecule, and a specific filename extension, e.g.

WEEGYLXZBRQIMU-UHFFFAOYSA.out is the output file produced by the QM package for the molecule cineole (SMILES: CC12CCC(CC1)C(C)(C)O2), represented by the InChI key WEEGYLXZBRQIMU-UHFFFAOYSA.

The table belows shows an overview of the used file extensions and their meaning.

File extension	Meaning
.mop	MOPAC input
.out	MOPAC output
.gjf	Gaussian input
.log	Gaussian output
.arc	MOPAC input created by MOPAC
.crude.mol	Mol file using crude, unrefined
.refined.mol	Mol file using UFF refined geometry
.symm	SYMMETRY input
.thermo	thermochemistry output file

For efficiency reasons, RMG minimizes the number of QMTP calculations. As a result, prior to initializing a QMTP routine, RMG checks whether the output files of a specific QMTP calculation are not already present in the QMfiles folder. It does so by comparing the InChI key of the given species to the filenames of the files in the QMfiles folder. If none of the InChI keys of the files correspond to the InChI key of the given species, RMG will initiate a new QMTP calculation.

## Supported QM packages, and levels of theory

The following table shows an overview of the computational chemistry packages and levels of theory that are currently supported in the QMTP interface of RMG.

The MM4 force field software originates from Allinger and Lii. [Allinger].

QM Package	Supported Levels of Theory
OpenMopac	semi-empirical (PM3, PM6, PM7)
Gaussian03	semi-empirical (PM3)
MM4	molecular mechanics (MM4)

### 1.13.4 Symmetry and Chirality

#### Symmetry

The notion of symmetry is an essential part of molecules. Molecular symmetry refers to the indistinguishable orientations of a molecule and can be represented by molecular groups or a symmetry number. RMG uses a symmetry number which is the number of superimposable configurations, which includes external symmetry and internal free rotors, which is described by detail by [Benson]. This is macroscopically quantified as a decrease of the entropy  $S$  by a term  $-R * \ln(\sigma)$  with  $R$  the universal gas constant and  $\sigma$  the global symmetry number, corresponding to the number of indistinguishable orientations of the molecule.

In RMG,  $\sigma$  is calculated as the product of contributions of three symmetry center types : atoms, bonds and axes, cf. below.

$$\sigma = \prod_i \sigma_{atom,i} \cdot \prod_j \sigma_{bond,j} \cdot \prod_k \sigma_{axis,k}$$

More information can be found in the Ph.D Thesis of Joanna Yu [Yu].

For molecules whose thermochemistry is calculated through group contribution techniques, the rotational symmetry number is calculated through graph algorithms of RMG based on the above equation. If the thermochemistry is calculated through the QMTP process, the external, rotational symmetry number is calculated using the open-source software SYMMETRY “Brute Force Symmetry Analyzer” [Patchkovskii]. This program uses the optimized three-dimensional geometry and calculates the corresponding point group.

#### Chirality

RMG does not take stereochemistry into account, effectively assuming a racemic mixture of mirror image enantiomers. As a result, a chirality contribution of  $+R * \ln(2)$  is included in the entropy of the molecule.

Chirality for molecules whose thermochemistry is determined using group contribution techniques is detected using graph algorithms similar to those used for determining the symmetry number. If the thermochemistry is calculated through the QMTP process, chirality is detected using the point group information obtained via the software SYMMETRY.

Chiral molecules belong to point groups that lack a superposable mirror image (i.e. point groups lacking  $\sigma_h$ ,  $\sigma_d$ ,  $\sigma_v$ , and  $S_n$  symmetry elements).

In RMG, chirality is incorporated into the symmetry attribute by dividing the symmetry by two which will increase entropy by  $+R * \ln(2)$ . RMG currently checks for each chiral center, defined by 4 different groups attached to a carbon, and halves the symmetry for each chiral center.

The effect of cis-trans isomers is currently not accounted for in RMG.

### 1.13.5 References

## 1.14 Kinetics Estimation

This section gives in-depth descriptions of algorithms used for determining kinetic parameters. For general usage of the kinetic database see [Kinetics Database](#).

### 1.14.1 Priority of Kinetic Databases

When multiple sources are available for kinetic parameters, the following priority is followed:

1. Seed mechanisms (based on listed order in input.py)
2. Reaction libraries (based on listed order in input.py)
3. Matched training set reactions
4. Exact template matches from rules or matched training groups (based on rank)
5. Estimated averaged rules

In the case where multiple rules or training set reactions fall under the same template node, we use a user-defined rank to determine the priority of kinetic parameters

Rank	Example methods
Rank 1	Experiment/FCI
Rank 2	W4/HEAT with very good (2-d if necessary) rotors
Rank 3	CCSD(T)-F12/cc-PVnZ with n>2 or CCSD(T)-F12/CBS with good (2-d if necessary) rotors
Rank 4	CCSD(T)-F12/DZ, with good (2-d if necessary) rotors
Rank 5	CBS-QB3 with 1-d rotors
Rank 6	Double-hybrid DFT with 1-D rotors
Rank 7	Hybrid DFT (w/ dispersion) (rotors if necessary)
Rank 8	B3LYP & lower DFT (rotors if necessary)
Rank 9	Group Additivity
Rank 10	Direct Estimate/Guess
Rank 11	Average of Rates
Rank 0	General Estimate (Never used in generation)

The rank of 0 is assigned to kinetics that are generally default values for top level nodes that we have little faith in. It is never used in generation and its value will in fact be overridden by averages of its child nodes, which generates an averaged rate rule with rank 11.

Only non-zero rules are used in generation. A rank of 1 is assigned to the most trustworthy kinetics, while a rank of 10 is considered very poor. Thus, a rate rule of rank 3 will be given priority over a rate rule of rank 5.

Short Glossary:

FCI (Full Configuration Interaction): Exact solution to Schrodinger equation within the chosen basis set and Born-Oppenheimer approximation; possible for about 12 electrons with reasonably sized basis set (cost grows factorially with number of electrons).

Wn (Weizmann-n): Composite methods often with sub-kJ/mol accuracies; W1 is possible for about 9 heavy atoms; W1 aims to reproduce CCSD(T)/CBS; W4 aims to reproduce CCSDTQ5/CBS.

HEAT (High Accuracy Extrapolated ab initio thermochemistry): Sub-kJ/mol accuracies; essentially CCSDTQ with various corrections; similar in cost to Wn.

CBS (Complete Basis Set): Typically obtained by extrapolating to the complete basis set limit, i.e., successive cc-pVDZ, cc-pVTZ, cc-pVQZ, etc. calculations with some extrapolation formula.

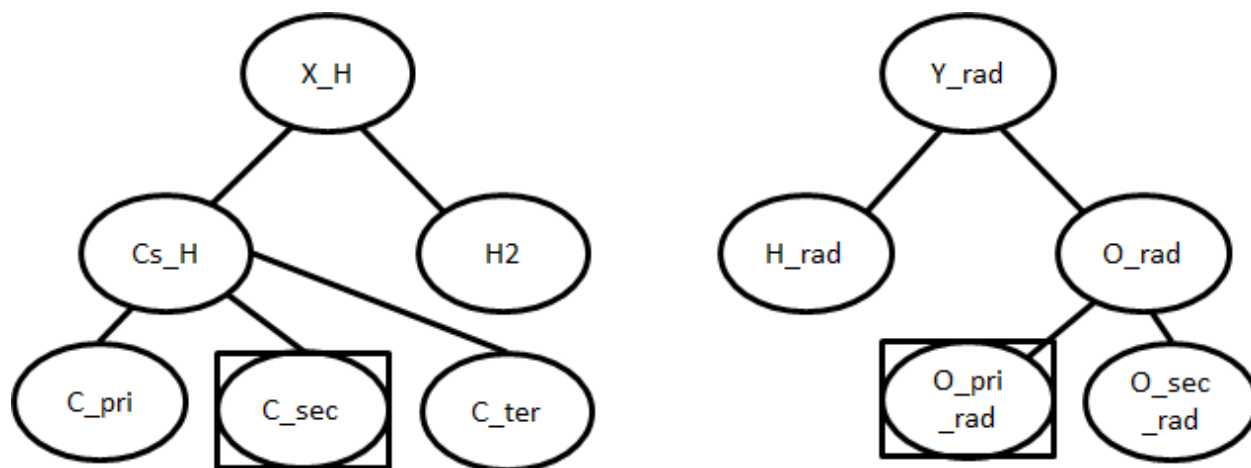
CCSD(T)-F12: Coupled cluster with explicit electron correlation; chemical accuracy (1 kcal/mol) possible with double-zeta basis sets.

### 1.14.2 Kinetic Families

To show the algorithm used by kinetic families, the following H-abstraction will be used as an example

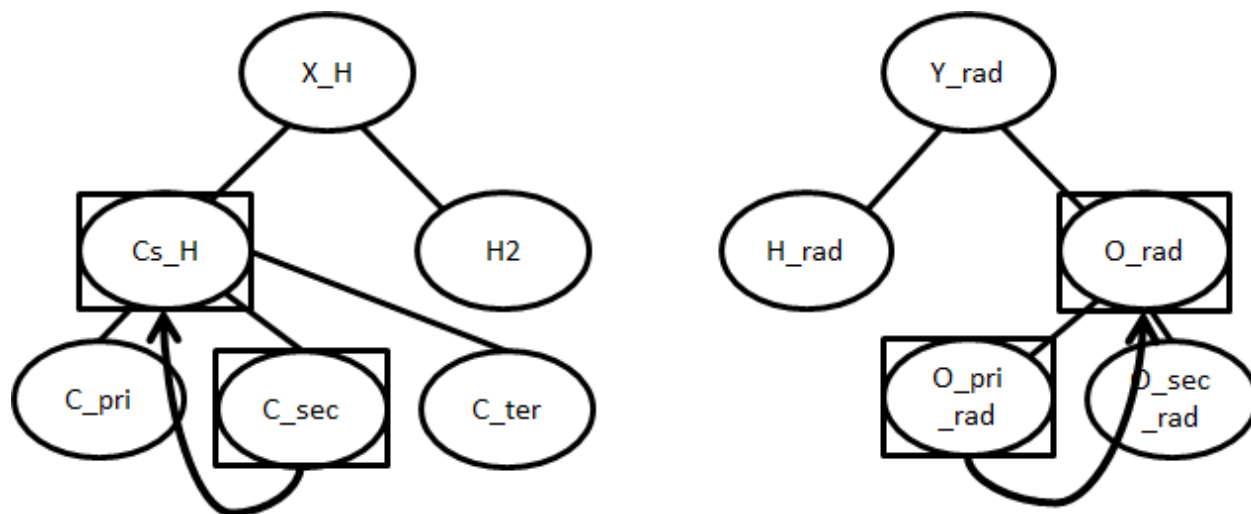


First the reacting atoms will be identified. Then, the family's trees will be descended as far as possible to give the reaction's groups.



Using the sample tree shown above, the desired template is (C\_sec, O\_pri\_rad). The algorithm will then search the database for parameters for the template. If they are present, an exact match will be returned using the kinetics of that template. Note that an exact match refers to the nodes (C\_sec, O\_pri\_rad) and not the molecules (propane, OH).

There may not be an entry for (C\_sec, O\_pri\_rad) in the database. In that case, the rule will attempt to “fall up” to more general nodes:



Now the preferred rule is (Cs\_H, O\_rad). If database contains parameters for this, those will be returned as an estimated match.

If there is still no kinetics for the template, the entire set of children for Cs\_H and O\_rad will be checked. For this example, this set would include every combination of {C\_pri, C\_sec, C\_ter} with {O\_pri\_rad, O\_sec\_rad}. If any these templates have kinetics, an average of their parameters will be returned as an estimated match. The average for  $A$  is a geometric mean, while the average for  $n$ ,  $E_a$ , and  $\alpha$  are arithmetic means.

If there are still no “sibling” kinetics, then the groups will continue to fall up to more and more general nodes. In the worst case, the root nodes may be used.

A *Full List of the Kinetics Families* in RMG is available.

## 1.15 Liquid Phase Systems

To simulate liquids in RMG requires a module in your input file for liquid-phase:

```
solvation(
    solvent='octane'
)
```

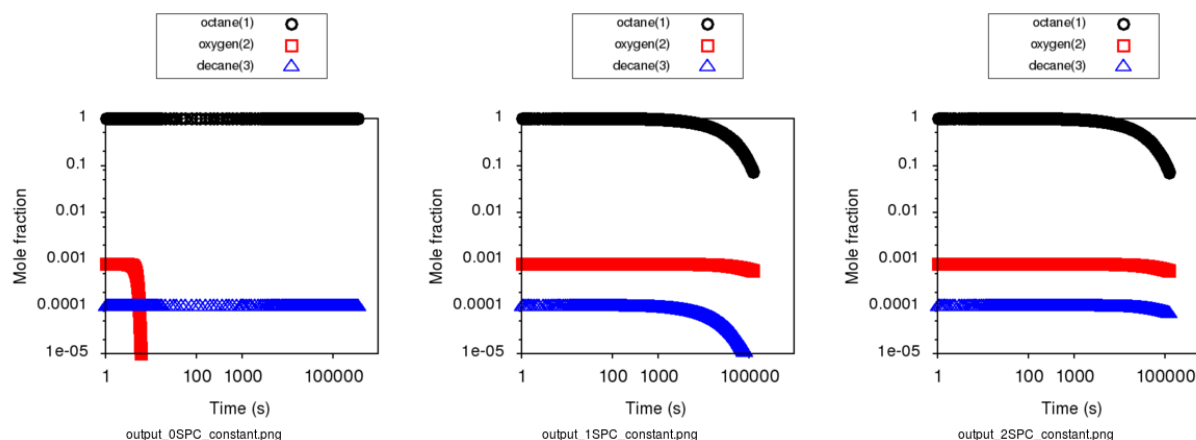
Your reaction system will also be different (liquidReactor rather than simpleReactor):

```
liquidReactor(
    temperature=(500, 'K'),
    initialConcentrations={
        "octane": (6.154e-3, 'mol/cm^3'),
        "oxygen": (4.953e-6, 'mol/cm^3')
    },
    terminationTime=(5, 's'),
    constantSpecies=['oxygen'],
    sensitivity=['octane', 'oxygen'],
    sensitivityThreshold=0.001,
)
```

To simulate the liquidReactor, one of the initial species / concentrations must be the solvent. If the solvent species does not appear as the initial species, RMG run will stop and raise error. The solvent can be either reactive, or nonreactive.

In order for RMG to recognize the species as the solvent, it is important to use the latest version of the RMG-database, whose solvent library contains solvent SMILES. If the latest database is used, RMG can determine whether the species is the solvent by looking at its molecular structure (SMILES or adjacency list). If the old version of RMG-database without the solvent SMILES is used, then RMG can recognize the species as the solvent only by its string name. This means that if the solvent is named “octane” in the solvation block and it is named “n-octane” in the species and initialConcentrations blocks, RMG will not be able to recognize them as the same solvent species and raise error because the solvent is not listed as one of the initial species.

For liquid phase generation, you can provide a list of species for which one concentration is held constant over time (Use the keyword `constantSpecies=[]` with species labels separated by “,”). To generate meaningful liquid phase oxidation mechanism, it is highly recommended to consider O<sub>2</sub> as a constant species. To consider pyrolysis cases, it is still possible to obtain a mechanism without this option. Expected results with Constant concentration option can be summarized with those 3 cases respectively presenting a generation with 0, 1 (oxygen only) and 2 constant species (oxygen and decane):



As it creates a mass lost, it is recommended to avoid to put any products as a constant species.

For sensitivity analysis, RMG-Py must be compiled with the DASPK solver, which is done by default but has some dependency restrictions. (See [License Restrictions on Dependencies](#) for more details.) Like for the simpleReactor, the `sensitivity` and `sensitivityThreshold` are optional arguments for when the user would like to conduct sensitivity analysis with respect to the reaction rate coefficients for the list of species given for `sensitivity`.

Sensitivity analysis is conducted for the list of species given for `sensitivity` argument in the input file. The normalized concentration sensitivities with respect to the reaction rate coefficients  $\text{dln}(C_i)/\text{dln}(k_j)$  are saved to a csv file with the file name `sensitivity_1_SPC_1.csv` with the first index value indicating the reactor system and the second naming the index of the species the sensitivity analysis is conducted for. Sensitivities to thermo of individual species is also saved as semi normalized sensitivities  $\text{dln}(C_i)/\text{d}(G_j)$  where the units are given in  $1/(\text{kcal mol}^{-1})$ . The `sensitivityThreshold` is set to some value so that only sensitivities for  $\text{dln}(C_i)/\text{dln}(k_j) > \text{sensitivityThreshold}$  or  $\text{dln}C_i/\text{d}(G_j) > \text{sensitivityThreshold}$  are saved to this file.

Note that in the RMG job, after the model has been generated to completion, sensitivity analysis will be conducted in one final simulation (sensitivity is not performed in intermediate iterations of the job).

Notes: `sensitivity`, `sensitivityThreshold` and `constantSpecies` are optionnal keywords.

### 1.15.1 Equation of state

Specifying a `liquidReactor` will have two effects:

1. disable the ideal gas law renormalization and instead rely on the concentrations you specified in the input file to initialize the system.
2. prevent the volume from changing when there is a net stoichiometry change due to a chemical reaction ( $A = B + C$ ).

### 1.15.2 Solvation thermochemistry

The next correction for liquids is solvation effects on the thermochemistry. By specifying a solvent in the input file, we load the solvent parameters to use.

The free energy change associated with the process of transferring a molecule from the gas phase to the solvent phase at constant  $T$  and  $P$  is defined as the free energy of solvation. Commonly, the standard state of the ideal gas and ideal solution at equal and dilute solute concentrations, also known as the Ben-Naim standard state, is used for solvation free energy ( $\Delta G_{\text{solv}}^*$ ) [BenNaim1987]. Solvation energy is added to the gas phase Gibbs free energy as a correction to estimate the free energy of the compound in a liquid phase:

$$\Delta G_{\text{liquid}}^* \approx \Delta G_{\text{f,gas}}^o + \Delta G_{\text{solv}}^* \quad (1.1)$$



Many different methods have been developed for computing solvation energies among which continuum dielectric and force field based methods are popular. Not all of these methods are easy to automate, and many are not robust i.e. they either fail or give unreasonable results for certain solute-solvent pairs. CPU time and memory (RAM) requirements are also important considerations. A fairly accurate and fast method for computing  $\Delta G_{\text{solv}}^*$ , which is used in RMG, is the LSER approach described below.

### Use of thermo libraries in liquid phase system

As it is for gas phase simulation, thermo libraries listed in the input files are checked first to find thermo for a given species and return the first match. As it exists two types of thermo libraries, (more details on [thermo libraries](#)), thermo of species matching a library in a liquid phase simulation is obtained following those two cases:

If library is a “liquid thermo library”, thermo data are directly used without applying solvation on it.

If library is a “gas thermo library”, thermo data are extracted and then corrections are applied on it using the [LSER method](#) for this specific species-solvent system.

---

**Note:** Gas phase libraries can be declared first, liquid thermo libraries will still be tested first but the order will be respected if several liquid libraries are provided.

---

### Use of Abraham LSER to estimate thermochemistry at 298 K

The Abraham LSER provides an estimate of the the partition coefficient ( $K$ ) of a solute (component 2) between the vapor phase and a particular solvent (component 1) at 298 K:

$$\log_{10} K = c + eE + sS + aA + bB + lL \quad (1.2)$$

where the partition coefficient is the ratio of the equilibrium concentrations of the solute in liquid and vapor phases

$$K = \frac{c_{2,\text{liquid}}}{c_{2,\text{gas}}} \quad (1.3)$$

The Abraham model is used in RMG to estimate  $\Delta G_{\text{solv}}^*$  which is related to the  $K$  of a solute according to the following expression:

$$\begin{aligned} \Delta G_{\text{solv}}^*(298\text{K}) &= -RT \ln K \\ &= -2.303RT \log_{10} K \end{aligned} \quad (1.4)$$

The variables in the Abraham model represent solute ( $E, S, A, B, V, L$ ) and solvent descriptors ( $c, e, s, a, b, v, l$ ) for different interactions. The  $sS$  term is attributed to electrostatic interactions between the solute and the solvent (dipole-dipole interactions related to solvent dipolarity and the dipole-induced dipole interactions related to the polarizability of the solvent) [Vitha2006], [Abraham1999], [Jalan2010]. The  $lL$  term accounts for the contribution from cavity formation and dispersion (dispersion interactions are known to scale with solute volume [Vitha2006], [Abraham1999]. The  $eE$  term, like the  $sS$  term, accounts for residual contributions from dipolarity/polarizability related interactions for solutes whose blend of dipolarity/polarizability differs from that implicitly built into the  $S$  parameter [Vitha2006], [Abraham1999], [Jalan2010]. The  $aA$  and  $bB$  terms account for the contribution of hydrogen bonding between the solute and the surrounding solvent molecules. H-bonding interactions require two terms as the solute (or solvent) can act as acceptor (donor) and vice versa. The descriptor  $A$  is a measure of the solute’s ability to donate a hydrogen bond (acidity) and the solvent descriptor  $a$  is a measure of the solvent’s ability to accept a hydrogen bond. A similar explanation applies to the  $bB$  term [Vitha2006], [Abraham1999], [Poole2009].

The enthalpy change associated with solvation at 298 K can be calculated from the Mintz LSER. Mintz et al. ([Mintz2007], [Mintz2007a], [Mintz2007b], [Mintz2007c], [Mintz2007d], [Mintz2008], [Mintz2008a], [Mintz2009]) have developed a linear correlation similar to the Abraham model for estimating  $\Delta H_{\text{solv}}^*$ :

$$\Delta H_{\text{solv}}^*(298\text{K}) = c' + a'A + b'B + e'E + s'S + l'L \quad (1.5)$$

where  $A$ ,  $B$ ,  $E$ ,  $S$  and  $L$  are the same solute descriptors used in the Abraham model for the estimation of  $\Delta G_{\text{solv}}^*$ . The lowercase coefficients  $c'$ ,  $a'$ ,  $b'$ ,  $e'$ ,  $s'$  and  $l'$  depend only on the solvent and were obtained by fitting to experimental data.

RMG's database has a solute library that contains the solute descriptors of around 300 compounds and it is located at `RMG-database/input/solvation/libraries/solute.py` in RMG-database. For the compounds that are not found in the solute library, the group additivity method is used to estimate the solute descriptors as described below under *Group additivity method for solute descriptor estimation*.

The solvent descriptors ( $c$ ,  $e$ ,  $s$ ,  $a$ ,  $b$ ,  $l$ ,  $c'$ ,  $a'$ ,  $b'$ ,  $e'$ ,  $s'$ ,  $l'$ ) are largely treated as regressed empirical coefficients. The solvent descriptors are fitted by Chung et al. ([Chung2021]) using experimental solute parameter, solvation free energy, and solvation enthalpy data collected from various sources. The Abraham solvent parameters ( $c$ ,  $e$ ,  $s$ ,  $a$ ,  $b$ ,  $v$ ,  $l$ ) are provided in RMG's database for 196 pure solvents and 3 binary mixture solvents for solvation free energy calculations. The Mintz solvent parameters ( $c'$ ,  $a'$ ,  $b'$ ,  $e'$ ,  $s'$ ) are provided for 69 pure solvents in RMG's database for solvation enthalpy calculations. A full list of solvents and their solvent parameters can be found on (1) [the RMG-database git repository](#) or (2) [the RMG website](#). If RMG-database is installed, these solvent information can be found in `RMG-database/input/solvation/libraries/solvent.py`.

You can also search for a solvent by SMILES string using a sample ipython notebook located at `RMG-Py/ipython/estimate_solvation_thermo_and_search_available_solvents.ipynb`. This ipython notebook takes a SMILES string as an input and checks whether the given compound is found in RMG's database. It also returns the Abraham and Mintz solvent parameters for the matched solvent. In addition, the ipython notebook shows sample solvation free energy and enthalpy calculations for solute-solvent pairs.

### Estimation of $\Delta G_{\text{solv}}^*$ at other temperatures: linear extrapolation

To estimate  $\Delta G_{\text{solv}}^*$  at temperatures other than 298 K, a simple linear extrapolation can be employed. For this approach, the enthalpy and entropy of solvation are assumed to be independent of temperature. The entropy of solvation,  $\Delta S_{\text{solv}}^*$  (298K), is calculated from  $\Delta G_{\text{solv}}^*$  (298K) and  $\Delta H_{\text{solv}}^*$  (298K) estimated from the Abraham and Mintz LSERs.

$$\Delta S_{\text{solv}}^*(298\text{K}) = \frac{\Delta H_{\text{solv}}^*(298\text{K}) - \Delta G_{\text{solv}}^*(298\text{K})}{298\text{K}} \quad (1.6)$$

Then  $\Delta G_{\text{solv}}^*$  at other temperatures is approximated by simple extrapolation assuming linear temperature dependence.

$$\Delta G_{\text{solv}}^*(T) = \Delta H_{\text{solv}}^*(298\text{K}) - T \Delta S_{\text{solv}}^*(298\text{K}) \quad (1.7)$$

This method provides a rapid, first-order approximation of the temperature dependence of solvation free energy. However, since the actual solvation enthalpy and entropy vary with temperature, this approximation will deviate at temperatures far away from 298 K. Looking at several experimental data, this approximation seems reasonable up to ~ 400 K.

### Estimation of $\Delta G_{\text{solv}}^*$ at other temperatures: temperature-dependent model

This method uses a piecewise function of K-factor to estimate more accurate temperature dependent solvation free energy. The K-factor at infinite dilution ( $K_{2,1}^\infty$ ), also known as the vapor-liquid equilibrium ratio, is defined as the ratio of the equilibrium mole fractions of the solute (component 2) in the gas and the liquid phases of the solvent (component 1):

$$K_{2,1}^\infty = \frac{y_2}{x_2} \quad (1.8)$$

Recently, Chung et al. ([Chung2020]) has shown that the following piecewise function combining two separate correlations ([Japas1989], [Harvey1996]) can accurately predict the K-factor from room temperature up to the critical temperature of the solvent

$$\text{For } T \leq 0.75T_c : \quad T_r \ln K_{2,1}^\infty = A + B(1 - T_r)^{0.355} + C(T_r)^{0.59} \exp(1 - T_r) \quad (1.9)$$

$$\text{For } 0.75T_c \leq T < T_c : \quad T_r \ln K_{2,1}^\infty = D \left( \frac{\rho_1^l}{\rho_{c,1}} - 1 \right) \quad (1.10)$$

where  $A, B, C, D$  are empirical parameters unique for each solvent-solute pair,  $T_c$  is the critical temperature of the solvent,  $T_r$  is the reduced temperature ( $T_r = \frac{T}{T_c}$ ),  $\rho_1^l$  is the saturated liquid phase density of the solvent, and  $\rho_{c,1}$  is the critical density of the solvent. The transition temperature,  $0.75T_c$ , has been empirically chosen. All calculations are performed at the solvent's saturation pressures such that K-factor is only a function of temperature.

Solvation free energy can be calculated from K-factor from the following relation

$$\Delta G_{\text{solv}}^* = RT \ln \left( \frac{K_{2,1}^\infty \rho_1^g}{\rho_1^l} \right) \quad (1.11)$$

where  $\rho_1^g$  is the saturated gas phase density of the solvent.

To solve for the four empirical parameters ( $A, B, C, D$ ), we need four equations. The first two can be obtained by enforcing the continuity in values and temperature gradient of the piecewise function at the transition temperature. The last two can be obtained by making the K-factor value and its temperature gradient at 298 K match with those estimated from the solvation free energy and enthalpy at 298 K. These lead to the following four linearly independent equations to solve:

$$\text{At } T = 298\text{K} : \quad A + B(1 - T_r)^{0.355} + C(T_r)^{0.59} \exp(1 - T_r) = T_r \ln K_{2,1}^\infty(298\text{ K}) \quad (1.12)$$

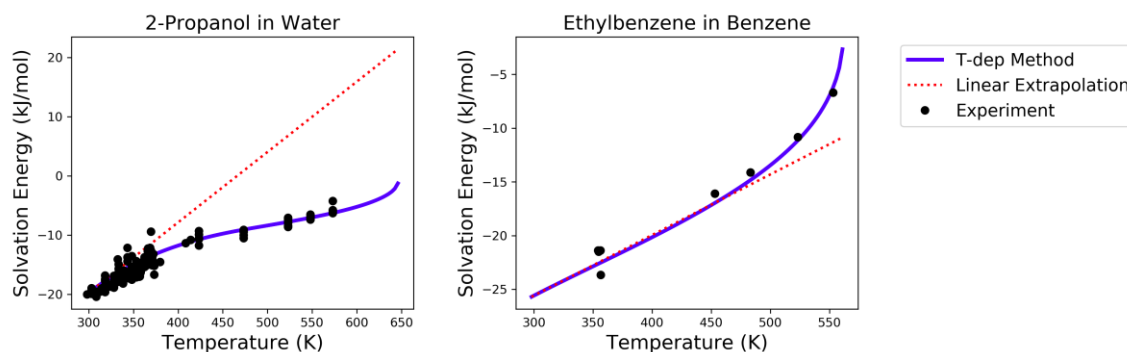
$$\text{At } T = 298\text{K} : \quad -\frac{0.355B}{T_c}(1 - T_r)^{-0.645} + \frac{C \exp(1 - T_r)}{T_c} (0.59(T_r)^{-0.41} - (T_r^*)^{0.59}) = \left. \frac{d(T_r \ln K_{2,1}^\infty)}{dT} \right|_{T=298\text{ K}} \quad (1.13)$$

$$\text{At } T = 0.75T_c : \quad A + B(1 - T_r)^{0.355} + C(T_r)^{0.59} \exp(1 - T_r) = D \left( \frac{\rho_1^l}{\rho_{c,1}} - 1 \right) \quad (1.14)$$

$$\text{At } T = 0.75T_c : \quad -\frac{0.355B}{T_c}(1 - T_r)^{-0.645} + \frac{C \exp(1 - T_r)}{T_c} (0.59(T_r)^{-0.41} - (T_r)^{0.59}) = \left. \frac{D}{\rho_{c,1}} \frac{d\rho_1^l}{dT} \right|_{T=0.75T_c} \quad (1.15)$$

The temperature dependent liquid phase and gas phase densities of solvents can be evaluated at the solvent's saturation pressure using CoolProp [Bell2014]. CoolProp is an open source fluid modeling software based on Helmholtz energy equations of state. It provides accurate estimations of fluid properties over the wide ranges of temperature and pressure for a variety of fluids. With known solvents' densities, one can easily find the empirical parameters of the piecewise functions by solving the linear equations above without using any experimental data.

This method has been tested for 47 solvent-solute pairs over a wide range of temperature, and the mean absolute error of solvation free energies has been found to be 1.6 kJ/mol [Chung2020]. Sample plots comparing the predictions made by this temperature dependent method and the linear extrapolation method are shown below. The experimental data are obtained from the Dortmund Databank integrated in SpringerMaterials [DDBST2014].



A sample ipython notebook script for temperature dependent K-factor and solvation free energy calculations can be found under `$RMG-Py/ipython/temperature_dependent_solvation_free_energy.ipynb`. These calculations are also available on a web browser from the RMG website: [Solvation Search](#).

However not every solvent listed in the RMG solvent database is available in CoolProp. Here is a list of solvents that are available in CoolProp and therefore are available for temperature dependent solvation calculations:

1. benzene
2. cyclohexane
3. decane
4. dichloroethane
5. dodecane
6. ethanol
7. heptane
8. hexane
9. nonane
10. octane
11. pentane
12. toluene
13. undecane
14. water

### Current status of temperature dependent $\Delta G_{\text{solv}}^*$ in RMG liquid reactor

Currently, RMG uses the linear extrapolation method to estimate solvation free energy at temperatures other than 298 K. The work is in progress to implement the temperature dependent solvation free energy estimation for available solvents.

### Group additivity method for solute descriptor estimation

Group additivity or group contribution is a convenient way of estimating the thermochemistry for thousands of species sampled in a typical mechanism generation job. Use of the Abraham Model in RMG requires a similar approach to estimate the solute descriptors ( $A$ ,  $B$ ,  $E$ ,  $L$ , and  $S$ ). RMG uses the group additivity method devised by Chung et al. [Chung2021] for solute descriptor estimation. The solute descriptor group additivity follows the same scheme as the RMG's group additivity method for gas phase thermochemistry estimation, which is explained in [Thermochemistry Estimation](#) and [Thermo Database](#). It estimates the solute descriptors by dividing a molecule into atom-centered (AC) functional groups and summing the contribution from all groups. Additionally, RMG implements ring strain correction (RSC) and long distance interaction (LDI) groups to account for more advanced structural effects that cannot be captured by the atom-based approach. E.g.:

$$E, S, A, B, \text{ or } L = \sum_{i=1}^{N_{\text{atom}}} \text{AC}_i + \sum_{j=1} \text{RSC}_j + \sum_{k=1} \text{LDI}_k$$

where  $N_{\text{atom}}$  is the number of heavy atoms in a molecule and RSC and LDI corrections are applied for each ring cluster and long distance interaction group found in a molecule, respectively.

While most molecules follow the equation above, halogenated molecules are treated differently in RMG for solute descriptor estimation: all halogen atoms are first replaced by hydrogen atoms, then the group additivity estimate is made

on the replaced structure, and halogen corrections are lastly added for each halogen atom to get the final prediction as shown below:

$$E, S, A, B, \text{ or } L = \sum_{i=1}^{N_{\text{atom}*}} AC_i + \sum_{j=1} RSC_j + \sum_{k=1} LDI_k + \sum_{l=1}^{N_{\text{halogen}}} \text{Halogen}_l$$

$$= (E, S, A, B, \text{ or } L)_{\text{replaced compound}} + \sum_{l=1}^{N_{\text{halogen}}} \text{Halogen}_l$$

where the subscript ‘replaced compound’ denotes the compound whose halogen atoms are replaced by hydrogen atoms, and  $N_{\text{atom}*}$  and  $N_{\text{halogen}}$  represent the number of non-halogen heavy atoms and the number of halogen atoms in a molecule, respectively. We take this unique approach because it allows one to use the experimental solute parameter data of a replaced compound and simply apply halogen corrections to get more accurate estimates for a halogenated compound.

For radical species, RMG uses the hydrogen bond increment (HBI) method developed by Lay et al. [Lay] to estimate the solute descriptors. The HBI method first saturates the compound, gets the estimate using the saturated structure, and applies the radical corrections for each radical site using the original structure as shown below:

$$E, S, A, B, \text{ or } L = (E, S, A, B, \text{ or } L)_{\text{saturated}} + \sum_{m=1}^{N_{\text{radical}}} \text{radical}_m$$

where the subscript ‘saturated’ denotes the compound whose radical sites are saturated and  $N_{\text{radical}}$  is the number of radical sites in a molecule. If the solute descriptors for the saturated structure are available in the RMG-database solute library, the group additivity approach will use the library data and apply the HBI corrections to get the estimates for the radical. If the solute descriptors for the saturated structure are not available in the solute library, RMG will use the group additivity approach to estimate the solute descriptors for the saturated structure and apply the HBI corrections.

If a species is a radical and contains any halogen atoms, RMG’s solute descriptor group additivity method will first saturate the compound and check whether the saturated form can be found in the solute libraries. If yes, it uses the solute data of the saturated form and applies the HBI corrections on the original molecule. If the saturated form cannot be found in the solute libraries, it then replaces the halogen atoms with hydrogen atoms and checks whether the saturated, replaced form can be found in the solute libraries. If yes, it uses the solute data of the saturated, replaced form, applies a halogen correction for each halogenated site on the saturated form, and finally performs the HBI corrections on the original molecule. If the saturated, replaced form cannot be found in the solute libraries, it computes the solute data for the saturated, replaced form using group additivity, applies a halogen correction for each halogenated site on the saturated form, and finally performs the HBI corrections on the original molecule.

A sample ipython script that shows the solute parameter group additivity calculations, solvation free energy and enthalpy calculations can be found at `RMG-Py/ipython/estimate_solvation_thermo_and_search_available_solvents.ipynb`.

The group contribution databases for the solute descriptors can be found under `RMG-database/input/solvation/groups/` in RMG-database. Each particular type of group contribution is stored in a file with the extension `.py`, e.g. ‘groups.py’:

file	Type of group contribution
group.py	group additive values (ACs)
ring.py	monocyclic ring corrections (RSCs)
polycyclic.py	polycyclic ring corrections (RSCs)
longDistanceInteraction_cyclic.py	aromatic ortho, meta, para correction (LDIs)
longDistanceInteraction_noncyclic.py	gauche interaction correction (LDIs)
halogen.py	halogen corrections (halogens)
radical.py	hydrogen bond increments (HBIs)

Like many other entities in RMG, the database of each type of group contribution is organized in a hierarchical tree, and is defined at the bottom of the database file.

More information on hierarchical tree structures in RMG can be found here: [Introduction](#).

For information on the estimated prediction errors of the group additivity method, please refer to the work by Chung et al. [[Chung2021](#)]

### 1.15.3 Diffusion-limited kinetics

The next correction for liquid-phase reactions is to ensure that bimolecular reactions do not exceed their diffusion limits. The theory behind diffusive limits in the solution phase for bimolecular reactions is well established ([[Rice1985](#)]) and has been extended to reactions of any order ([[Flegg2016](#)]). The effective rate constant of a diffusion-limited reaction is given by:

$$k_{\text{eff}} = \frac{k_{\text{diff}} k_{\text{int}}}{k_{\text{diff}} + k_{\text{int}}} \quad (1.16)$$

where  $k_{\text{int}}$  is the intrinsic reaction rate, and  $k_{\text{diff}}$  is the diffusion-limited rate, which is given by:

$$k_{\text{diff}} = \left[ \prod_{i=2}^N \hat{D}_i^{3/2} \right] \frac{4\pi^{\alpha+1}}{\Gamma(\alpha)} \left( \frac{\sigma}{\sqrt{\Delta_N}} \right)^{2\alpha} \quad (1.17)$$

where  $\alpha = (3N - 5)/2$  and

$$\hat{D}_i = D_i + \frac{1}{\sum_{m=1}^{i-1} D_m^{-1}} \quad (1.18)$$

$$\Delta_N = \frac{\sum_{i=1}^N D_i^{-1}}{\sum_{i>m} (D_i D_m)^{-1}} \quad (1.19)$$

$D_i$  are the individual diffusivities and  $\sigma$  is the Smoluchowski radius, which would usually be fitted to experiment, but RMG approximates it as the sum of molecular radii. RMG uses the McGowan method for estimating radii, and diffusivities are estimated with the Stokes-Einstein equation using experimental solvent viscosities ( $\eta(T)$ ):

$$D_i = \frac{k_B T}{6\pi \eta r_i} \quad (1.20)$$

$$\sigma = \sum_{i=1}^N r_i \quad (1.21)$$

$$r_i = \frac{\left( 100 \frac{3}{4} \frac{V_i}{\pi N_A} \right)^{1/3}}{100} \quad (1.22)$$

where  $k_B$  is the Boltzmann constant,  $N_A$  is the Avogadro number,  $r_i$  is the individual molecular radius in meters, and  $V_i$  is the individual McGowan volume in cm<sup>3</sup>/mol divided by 100, which is equivalent to the Abraham solute parameter,  $V$ .

In a unimolecular to bimolecular reaction, for example, the forward rate constant ( $k_f$ ) can be slowed down if the reverse rate ( $k_{r,\text{eff}}$ ) is diffusion-limited since the equilibrium constant ( $K_{eq}$ ) is not affected by diffusion limitations. In cases where both the forward and the reverse reaction rates are multimolecular, the forward rate coefficients limited in the forward and reverse directions are calculated and the limit with the smaller forward rate coefficient is used.

The viscosity of the solvent is calculated Pa.s using the solvent specified in the command line and a correlation for the viscosity using parameters  $A, B, C, D, E$ :

$$\ln \eta = A + \frac{B}{T} + C \log T + DT^E \quad (1.23)$$

The viscosity parameters ( $A$ ,  $B$ ,  $C$ ,  $D$ ,  $E$ ) are provided for 150 pure solvents in RMG's database, which can be found under (1) [the RMG-database git repository](#) or (2) [the RMG website](#). If RMG-database is installed, these viscosity parameters can be found in `RMG-database/input/solvation/libraries/solvent.py`.

You can also check whether a compound of interest has viscosity parameters in RMG-database by using a SMILES string and a sample ipython notebook located at `RMG-Py/ipython/estimate_solvation_thermo_and_search_available_solvents.ipynb`.

To build accurate models of liquid phase chemical reactions you will also want to modify your kinetics libraries or correct gas-phase rates for intrinsic barrier solvation corrections (coming soon).

### 1.15.4 Example liquid-phase input file, no constant species

This is an example of an input file for a liquid-phase system:

```
# Data sources
database(
    thermoLibraries = ['primaryThermoLibrary'],
    reactionLibraries = [],
    seedMechanisms = [],
    kineticsDepositories = ['training'],
    kineticsFamilies = 'default',
    kineticsEstimator = 'rate rules',
)

# List of species
species(
    label='octane',
    reactive=True,
    structure=SMILES("C(CCCCC)CC"),
)

species(
    label='oxygen',
    reactive=True,
    structure=SMILES("[O][O]"),
)

# Reaction systems
liquidReactor(
    temperature=(500,'K'),
    initialConcentrations={
        "octane": (6.154e-3,'mol/cm^3'),
        "oxygen": (4.953e-6,'mol/cm^3')
    },
    terminationTime=(5,'s'),
)

solvation(
    solvent='octane'
)

simulator(
```

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```
    atol=1e-16,
    rtol=1e-8,
)

model(
    toleranceKeepInEdge=1E-9,
    toleranceMoveToCore=0.01,
    toleranceInterruptSimulation=0.1,
    maximumEdgeSpecies=100000
)

options(
    units='si',
    generateOutputHTML=False,
    generatePlots=False,
    saveSimulationProfiles=True,
)
```

### 1.15.5 Example liquid-phase input file, with constant species

This is an example of an input file for a liquid-phase system with constant species:

```
# Data sources
database(
    thermoLibraries = ['primaryThermoLibrary'],
    reactionLibraries = [],
    seedMechanisms = [],
    kineticsDepositories = ['training'],
    kineticsFamilies = 'default',
    kineticsEstimator = 'rate rules',
)

# List of species
species(
    label='octane',
    reactive=True,
    structure=SMILES("C(CCCCC)CC"),
)

species(
    label='oxygen',
    reactive=True,
    structure=SMILES("[O][O]"),
)

# Reaction systems
liquidReactor(
    temperature=(500, 'K'),
    initialConcentrations={
        "octane": (6.154e-3, 'mol/cm^3'),
        "oxygen": (4.953e-6, 'mol/cm^3')
    }
)
```

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```

    },
    terminationTime=(5, 's'),
    constantSpecies=['oxygen'],
)

solvation(
    solvent='octane'
)

simulator(
    atol=1e-16,
    rtol=1e-8,
)

model(
    toleranceKeepInEdge=1E-9,
    toleranceMoveToCore=0.01,
    toleranceInterruptSimulation=0.1,
    maximumEdgeSpecies=100000
)

options(
    units='si',
    generateOutputHTML=False,
    generatePlots=False,
    saveSimulationProfiles=True,
)

```

## 1.16 Heterogeneous Catalysis Systems and Surface Reactions

RMG can now be used to study heterogenous catalysis and surface reactions. Initially developed in a fork of RMG called RMG-Cat ([Goldsmith2017]), this is now a part of the main RMG software. Several surface specific features need to be considered when setting up an input file for surface reaction mechanism generation, as they cause certain aspects of it to deviate from the standard gas-phase RMG input file.

### 1.16.1 Catalyst properties

A new block `catalystProperties()` should be added for specifying the catalyst surface to be used in the mechanism generation. It includes the surface site density of the metal surface (`surfaceSiteDensity`), which is the amount of active catalytic sites per unit surface area. It varies depending on the catalyst in question, but is held constant across simulations. This block should also contain the reference adatom binding energies (see linear scaling section below).

One can also specify a specific metal of interest, and RMG will load corresponding binding energies from the metal database by using `metal`. The full database of available metals can be found in `input/surface/libraries/metal.py`.

Here is an example catalyst properties block for Pt(111):

```
catalystProperties(  
    metal = Pt111  
)
```

Here is an example custom catalyst properties block for Pt(111):

```
catalystProperties(  
    bindingEnergies = {  
        'H': (-2.754, 'eV/molecule'),  
        'O': (-3.811, 'eV/molecule'),  
        'C': (-7.025, 'eV/molecule'),  
        'N': (-4.632, 'eV/molecule'),  
    },  
    surfaceSiteDensity=(2.483e-9, 'mol/cm^2'),  
)
```

### 1.16.2 Reactor specifications

For surface chemistry, RMG can model constant temperature and volume systems. The temperature, initial pressure, initial mole fractions of the reactant species, initial surface coverages, catalytic surface area to volume ratio in the reactor, and surface site density are defined for each individual reaction system in the input file. As for the simple reactor model in RMG, the initial mole fractions are defined in a dictionary with the keys being names of species corresponding to molecules given in the species block. The `initialGasMoleFractions` dictionary should contain gas-phase species, the `initialSurfaceCoverages` dictionary should contain adsorbates and vacant sites. Both will be normalized if the values given do not sum to 1.00. The ratio of catalyst surface area to gas phase volume (*surfaceVolumeRatio*) is determined by reactor geometry, and so may be different in each `surfaceReactor` simulation.

The following is an example of a surface reactor system for catalytic combustion of methane over a Pt catalyst:

```
surfaceReactor(  
    temperature=(800, 'K'),  
    initialPressure=(1.0, 'bar'),  
    initialGasMoleFractions={  
        "CH4": 0.0500,  
        "O2": 0.1995,  
        "N2": 0.7505,  
    },  
    initialSurfaceCoverages={  
        "X": 1.0,  
    },  
    surfaceVolumeRatio=(1.0e4, 'm^-1'),  
    terminationConversion = { "CH4":0.9 },  
    terminationRateRatio=0.01  
)
```

## Adsorbate representation

Adsorbates are represented using chemical graph theory (ChemGraph), such that atoms are represented by nodes and bonds between them by edges. This way each adsorbate is represented by an adjacency list. Specific to heterogeneous chemistry and surface reactions is the metal-adsorbate bond for adsorbates. Firstly, there needs to be a species representation for the binding site in the RMG-Cat input file. This can be added as follows:

```
species(
    label='X',
    reactive=True,
    structure=adjacencyList("1 X u0"),
)
```

The surface binding sites have an element X which has two atom-types: either vacant, Xv, or occupied, Xo in which case it has a molecule adsorbed on it.

Adsorbates in RMG-Cat can currently have one or two surface binding sites, and can be bound to the sites with single, double, triple, or quadruple bonds. The following is an example for the adjacency list of adsorbed methoxy with one binding site:

```
1 X u0 p0 c0 {3,S}
2 C u0 p0 c0 {3,S} {4,S} {5,S} {6,S}
3 O u0 p2 c0 {1,S} {2,S}
4 H u0 p0 c0 {2,S}
5 H u0 p0 c0 {2,S}
6 H u0 p0 c0 {2,S}
```

Additionally, the adsorbates in RMG-Cat can be physisorbed (have a van der Waals bond to the surface). The adjacency lists for physisorbed species are structured the same way as for other adsorbates, except that there is no bond edge for the binding. The atom representing the surface site (X) must still be included. Following is an adjacency list for physisorbed methane:

```
1 X u0 p0 c0
2 C u0 p0 c0 {3,S} {4,S} {5,S} {6,S}
3 H u0 p0 c0 {2,S}
4 H u0 p0 c0 {2,S}
5 H u0 p0 c0 {2,S}
6 H u0 p0 c0 {2,S}
```

This implementation currently does not distinguish between different binding sites on a given facet. Instead, the lowest energy binding site for a given adsorbate is assumed, consistent with the mean-field approach of the kinetics ([Goldsmith2017]).

### 1.16.3 Thermochemistry

RMG will first check thermochemistry libraries for adsorbates. Failing that, the gas phase thermochemistry will be used and an adsorption correction added. The gas phase thermochemistry will be estimated using the methods specified for regular gas phase species (libraries, automated quantum mechanics, machine learning, group additivity, etc.) and the adsorption correction estimated as described below. Finally, the adsorbed species will have its energy changed using linear scaling relationships, to allow for metals other than Platinum(111) to be simulated. These methods are all described below.

## Use of thermo libraries for surface systems

For surface species, thermo libraries provided in the input files are checked first for an exact match of a given adsorbate, and those thermodynamic properties are used.

In order to predict the thermodynamic properties for species that are not in the database, RMG-Cat uses a precompiled adsorption correction with the thermodynamic properties of the gas-phase precursor ([Goldsmith2017]).

Following is an example for how a thermo library for species adsorbed on platinum is provided in the input file database module:

```
thermoLibraries=['surfaceThermoPt111']
```

This can be added along with other gas-phase reaction libraries for coupling of gas-phase and surface reactions. For a full list of libraries check <https://rmg.mit.edu/database/thermo/libraries/> or the folder RMG-database/input/thermo/libraries/ in your RMG database.

## Adsorption correction estimation

The folder RMG-database/input/thermo/groups/ contains the adsorption corrections for the change in thermodynamic properties of a species upon adsorption from the gas-phase. Currently the database has adsorption corrections for nickel (adsorptionNi.py) and platinum (adsorptionPt.py).

An example of an adsorption correction entry is shown below:

```
entry(
    index = 40,
    label = "C-*R3",
    group =
    """
1 X  u0 p0 c0 {2,S}
2 C  u0 p0 c0 {1,S} {3,[S,D]} {4,[S,D]}
3 R  u0 px c0 {2,[S,D]}
4 R  u0 px c0 {2,[S,D]}
    """,
    thermo=ThermoData(
        Tdata=[300, 400, 500, 600, 800, 1000, 1500], 'K'),
        Cpdata=[-0.45, 0.61, 1.42, 2.02, 2.81, 3.26, 3.73], 'cal/(mol*K)'),
        H298=(-41.64, 'kcal/mol'),
        S298=(-32.73, 'cal/(mol*K)'),
    ),
    shortDesc="""Came from CH3 single-bonded on Pt(111)""",
    longDesc="""Calculated by Katrin Blondal at Brown University using statistical_
↳mechanics
        (files: compute_NASA_for_Pt-adsorbates.ipynb and compute_NASA_for_Pt-gas_
↳phase.ipynb).
        Based on DFT calculations by Jelena Jelic at KIT.
        DFT binding energy: -1.770 eV.
        Linear scaling parameters: ref_adatom_C = -6.750 eV, psi = -0.08242 eV,
↳gamma_C(X) = 0.250.

    CR3
    |
    *****
```

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```
"""
)
```

Here, R in the label C-\*R3 represents any atom, where the H atoms in methyl have been replaced by wild cards. This enables RMG-Cat to determine which species in the thermo database is the closest match for the adsorbate in question, using a hierarchical tree for functional groups. This is defined at the bottom of the adsorption corrections files, e.g.:

```
tree(
"""
L1: R*
  L2: R*single_chemisorbed
    L3: C*
      L4: Cq*
      L4: C#*R
        L5: C#*CR3
        L5: C#*NR2
        L5: C#*OR
      L4: C=*R2
        L5: C=*RCR3
        L5: C=*RNR2
        L5: C=*ROR
      L4: C=* (=R)
        L5: C=* (=C)
        L5: C=* (=NR)
      L4: C-*R3
        L5: C-*R2CR3
        ...
```

When RMG-Cat has found the closest match, it reads the corresponding adsorption correction from the database and uses it with the thermo of the original adsorbate's gas-phase precursor to estimate its enthalpy, entropy and heat capacity.

## Linear scaling relations

In surface reaction mechanism generation with RMG-Cat, linear scaling relations are used to investigate surface reaction systems occurring on surfaces that do not have DFT-based values in the database ([Mazeau2019]). This is especially useful for alloy catalysts as conducting DFT calculations for such systems is impractical. Linear scaling relations for heterogeneous catalysis are based on the finding of Abild-Pedersen et al. ([Abild2007]) that the adsorption energies of hydrogen-containing molecules of carbon, oxygen, sulfur, and nitrogen on transition metal surfaces scale linearly with the adsorption energy of the surface-bonded atom. Using this linear relationship, the energy of a species ( $AH_x$ ) on any metal M2 can be estimated from the known energy on metal M1,  $\Delta E_{M1}^{AH_x}$ , and the adsorption energies of atom A on the two metals M1 and M2 as follows:

$$\Delta E_{M2}^{AH_x} = \Delta E_{M1}^{AH_x} + \gamma(x)(\Delta E_{M2}^A - \Delta E_{M1}^A), \quad (1.24)$$

where

$$\gamma(x) = (x_{max} - x)/x_{max}, \quad (1.25)$$

is the slope of the linear relationship between ( $AH_x$ ) and A, and ( $x_{max}$ ) is the maximum number of hydrogen atoms that can bond to the central atom A. Since the adsorption energy of ( $AH_x$ ) is proportional to adsorption energies on different metals, full calculations for every reaction intermediate on every metal are not necessary. Therefore, having this implemented in RMG-Cat allows for independent model generation for any metal surface. By effect it enables the expedient, high-throughput screening of catalysts for any surface catalyzed reaction of interest ([Mazeau2019]).

Because of this feature, it is required to provide the adsorption energies of C, N, O and H on the surface being investigated in the input file for RMG-Cat to generate a mechanism. The following is an example using the default binding energies of the four atoms on Pt(111). Deviating from these values will result in adsorption energies being modified, even for species taken from the thermochemistry libraries:

```
bindingEnergies = { # default values for Pt(111)
    'H': (-2.754, 'eV/molecule'),
    'O': (-3.811, 'eV/molecule'),
    'C': (-7.025, 'eV/molecule'),
    'N': (-4.632, 'eV/molecule'),
}
```

## 1.16.4 Reactions and kinetics

### Reaction families and libraries for surface reaction systems

In the latest version of the RMG database, surface reaction families have been added. These include adsorption/desorption, bond fission and H abstraction ([Goldsmith2017]). For surface reaction families to be considered in the mechanism generation, the ‘surface’ kinetics family keyword needs to be included in the database section of the input file as follows:

```
kineticsFamilies=['surface', 'default']
```

This allows for RMG-Cat to consider both surface and gas reaction families. If including only surface reactions is desired, that can be attained by removing the ‘default’ keyword.

For surface reactions proposed by reaction families that do not have an exact match in the internal database of reactions, Arrhenius parameters are estimated according to a set of rules specific to that reaction family. The estimation rules are derived automatically from the database of known rate coefficients and formulated as Brønsted-Evans-Polanyi relationships ([Goldsmith2017]).

The user can provide a surface reaction library containing a set of preferred rate coefficients for the mechanism. Just like for gas-phase reaction libraries, values in the provided reaction library are automatically used for the respective proposed reactions. The reactions in the reaction library are not required to be a part of the predefined reaction families ([Goldsmith2017]).

Following is an example where a mechanism for catalytic partial oxidation of methane on platinum by Quiceno et al. ([Deutschmann2006]) is provided as a reaction library in the database section of the input file:

```
reactionLibraries = [('Surface/CPOX_Pt/Deutschmann2006', False)]
```

Gas-phase reaction libraries should be included there as well for accurate coupled gas-phase/surface mechanism generation.

The following is a list of the current pre-packaged surface reaction libraries in RMG-Cat:

Library	Description
Surface/Deutschmann_Ni	Steam- and CO <sub>2</sub> -Reforming as well as Oxidation of Methane over Nickel-Based Catalysts
Surface/CPOX_Pt/Deutschmann2006	High-temperature catalytic partial oxidation of methane over platinum

### 1.16.5 Coverage Dependence

An Arrhenius-like expression can be used to describe the effect of the coverage ( $\theta_k$ ) of species  $k$  on the forward rate constant for a given surface reaction. RMG has the capability to account for such coverage dependent kinetics, as specified in the following equation:

$$k_f = AT^b \exp\left(-\frac{E_a}{RT}\right) \prod_k 10^{a_k \theta_k} \theta_k^{m_k} \exp\left(\frac{-E_k \theta_k}{RT}\right) \quad (1.26)$$

where the parameters  $a_k$ ,  $m_k$ , and  $E_k$  are the modifiers for the pre-exponential, temperature exponent, and activation energy from species  $k$ .

#### input file specifications

Coverage dependent parameters are applied if the “coverage\_dependence” attribute is set to “True” in the catalyst properties block:

```
catalystProperties(
    metal = Pt111
    coverageDependence=True,
)
```

By default, this field is false.

#### Coverage block in families and libraries

Coverage dependent parameters can be added to a family or library reaction by specifying a dictionary in the “coverage\_dependence” field, with the names of the species serving as the keys. Nested within that dictionary is a dictionary of the coverage dependent parameters for each species. For example:

```
entry(
    index = 5,
    label = "NH_X + X <=> N_X + H_X",
    kinetics = SurfaceArrhenius(
        A = (7.22E20, 'cm^2/(mol*s)'),
        n = 0.0,
        Ea = (5.3, 'kcal/mol'),
        Tmin = (200, 'K'),
        Tmax = (3000, 'K'),
        coverage_dependence = {'N_X': {'a':0.0, 'm':0.0, 'E':(15.5, 'kcal/mol')},
                               'H_X': {'a':0.0, 'm':0.0, 'E':(1.0, 'kcal/mol')}}},
    ),
    shortDesc = u""Surface_Dissociation"",
    longDesc = u""
"The role of adsorbate-adsorbate interactions in the rate controlling step
and the most abundant reaction intermediate of NH3 decomposition on Ru"
D.G. Vlachos et al. (2004). Catalysis Letters 96, 13-22.
https://doi.org/10.1023/B:CATL.0000029523.22277.e1
This reaction used RMG's surface site density of Ru0001 = 2.630E-9(mol/cm^2) to
calculate the A factor.
A = 1.9E12(1/s)/2.630E-9(mol/cm^2) = 7.22E20 cm^2/(mol*s)
This is R5 in Table 2 (set A)
"
```

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```
"""  
    metal = "Ru",  
    facet = "0001",  
)
```

The species “N\_X” and “H\_X” are the coverage dependent species in this example, and they also happen to be species partaking in this reaction. However, any species that are listed in the species dictionary can also be used.

### 1.16.6 Examples

### Example input file: methane steam reforming

This is a simple input file steam reforming of methane

```
# Data sources
database(
  thermoLibraries=['surfaceThermoNi111', 'surfaceThermoPt111', 'primaryThermoLibrary', 'thermo_DFT_CCSDTF12_BAC'],
  reactionLibraries = [('Surface/Deutschmann_Ni', True)], # when Pt is used change the library to Surface/CP0X_Pt/Deutschmann2006
  seedMechanisms = [],
  kineticsDepositories = ['training'],
  kineticsFamilies = ['surface','default'],
  kineticsEstimator = 'rate rules',
)

catalystProperties(
  bindingEnergies = { # values for Ni(111)
    'H': (-2.892, 'eV/molecule'),
    'O': (-4.989, 'eV/molecule'),
    'C': (-6.798, 'eV/molecule'),
    'N': (-5.164, 'eV/molecule'),
  },
  surfaceSiteDensity=(3.148e-9, 'mol/cm^2'), # values for Ni(111)
)

# List of species

species(
  label='CH4',
  reactive=True,
  structure=SMILES("[CH4]"),
)

#species(
#  label='water',
#  reactive=True,
#  structure=adjacencyList(
#    """
#1  O  u0  p2  {2,S}  {3,S}  {4,vdW}
#2  H  u0  p0  {1,S}
#"""
#  )
#)
```

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```
#3 H u0 p0 {1,S}
#4 X u0 p0 {1,vdW}
#"""),
#)

#species(
#    label='c2h4',
#    reactive=True,
#    structure=adjacencyList(
#        """
#1 C u0 p0 c0 {2,D} {3,S} {4,S}
#2 C u0 p0 c0 {1,D} {5,S} {6,S}
#3 H u0 p0 c0 {1,S}
#4 H u0 p0 c0 {1,S}
#5 H u0 p0 c0 {2,S}
#6 H u0 p0 c0 {2,S}
#"""),
#)

species(
    label='O2',
    reactive=True,
    structure=adjacencyList(
        """
1 O u1 p2 c0 {2,S}
2 O u1 p2 c0 {1,S}
"""),
)

species(
    label='CO2',
    reactive=True,
    structure=SMILES("O=C=O"),
)

species(
    label='H2O',
    reactive=True,
    structure=SMILES("O"),
)

species(
    label='H2',
    reactive=True,
    structure=SMILES("[H][H]"),
)

species(
    label='CO',
    reactive=True,
    structure=SMILES("[C-]#[O+]"),
)

```

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```
species(  
    label='C2H6',  
    reactive=True,  
    structure=SMILES("CC"),  
)  
  
species(  
    label='CH2O',  
    reactive=True,  
    structure=SMILES("C=O"),  
)  
  
species(  
    label='CH3',  
    reactive=True,  
    structure=SMILES("[CH3]"),  
)  
  
species(  
    label='C3H8',  
    reactive=True,  
    structure=SMILES("CCC"),  
)  
  
species(  
    label='H',  
    reactive=True,  
    structure=SMILES("[H]"),  
)  
  
species(  
    label='C2H5',  
    reactive=True,  
    structure=SMILES("C[CH2]"),  
)  
  
species(  
    label='CH3OH',  
    reactive=True,  
    structure=SMILES("CO"),  
)  
  
species(  
    label='HCO',  
    reactive=True,  
    structure=SMILES("[CH]=O"),  
)  
  
species(  
    label='CH3CHO',  
    reactive=True,
```

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```

    structure=SMILES("CC=O"),
)

species(
    label='OH',
    reactive=True,
    structure=SMILES("[OH]"),
)

species(
    label='C2H4',
    reactive=True,
    structure=SMILES("C=C"),
)

#-----
species(
    label='site',
    reactive=True,
    structure=adjacencyList("1 X u0"),
)

#-----
# Reaction systems
surfaceReactor(
    temperature=(1000, 'K'),
    initialPressure=(1.0, 'bar'),
    initialGasMoleFractions={
        "CH4": 1.0,
        "O2": 0.0,
        "CO2": 1.2,
        "H2O": 1.2,
        "H2": 0.0,
        "CH3OH": 0.0,
        "C2H4": 0.0,
    },
    initialSurfaceCoverages={
        "site": 1.0,
    },
    surfaceVolumeRatio=(1.e5, 'm^-1'),
    terminationConversion = { "CH4":0.9,},
    terminationTime=(0.01, 's'),
)

simulator(
    atol=1e-18,
    rtol=1e-12,
)

model(
    toleranceKeepInEdge=0.0,
    toleranceMoveToCore=1e-6,
    toleranceInterruptSimulation=0.1,

```

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```

    maximumEdgeSpecies=100000
)

options(
    units='si',
    generateOutputHTML=True,
    generatePlots=False, # Enable to make plots of core and edge size etc.. But takes
    ↪ a lot of the total runtime!
    saveEdgeSpecies=True,
    saveSimulationProfiles=True,
    verboseComments=True,
)

```

### Example input file: methane oxidation

This is an input file for catalytic partial oxidation (CPOX) of methane

```

# Data sources
database(
    thermoLibraries=['surfaceThermoPt111', 'primaryThermoLibrary', 'thermo_DFT_
    ↪ CCSDTF12_BAC', 'DFT_QCI_thermo'], # 'surfaceThermoPt' is the default. Thermo data is
    ↪ derived using bindingEnergies for other metals
    reactionLibraries = [('Surface/CPOX_Pt/Deutschmann2006_adjusted', False)], # when
    ↪ Ni is used change the library to Surface/Deutschmann_Ni
    seedMechanisms = [],
    kineticsDepositories = ['training'],
    kineticsFamilies = ['surface', 'default'],
    kineticsEstimator = 'rate rules',
)

catalystProperties(
    metal = 'Pt111'
)

species(
    label='CH4',
    reactive=True,
    structure=SMILES("[CH4]"),
)

species(
    label='O2',
    reactive=True,
    structure=adjacencyList(
        """
1 0 u1 p2 c0 {2,S}
2 0 u1 p2 c0 {1,S}
"""),
)

```

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```

species(
    label='N2',
    reactive=False,
    structure=SMILES("N#N"),
)

species(
    label='vacantX',
    reactive=True,
    structure=adjacencyList("1 X u0"),
)

# If you would like to forbid the bidentate form of absorbed CO2 from your model,
# use the following `CO2_bidentate` forbidden structure
# forbidden(
#     label='CO2_bidentate',
#     structure=SMILES("O=C(*)O*"),
# )

#-----
# Reaction systems
surfaceReactor(
    temperature=(800, 'K'),
    initialPressure=(1.0, 'bar'),
    initialGasMoleFractions={
        "CH4": 0.1,
        "O2": 0.2,
        "N2": 0.7,
    },
    initialSurfaceCoverages={
        "vacantX": 1.0,
    },
    surfaceVolumeRatio=(1.e5, 'm^-1'),
    terminationConversion = { "CH4":0.99,},
    terminationTime=(0.1, 's'),
)

simulator(
    atol=1e-18,
    rtol=1e-12,
)

model(
    toleranceKeepInEdge=0.0,
    toleranceMoveToCore=1e-5,
    toleranceInterruptSimulation=0.1,
    maximumEdgeSpecies=100000,
)

options(
    units='si',
    generateOutputHTML=True,

```

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```
generatePlots=False, # Enable to make plots of core and edge size etc. But takes_
↪ a lot of the total runtime!
saveEdgeSpecies=True,
saveSimulationProfiles=True,
)
```

## Additional Notes

Other things to update: \* table of atom types in users/rmg/database/introduction.rst \* table of atom types in reference/molecule/atomtype.rst

## 1.17 Frequently Asked Questions

### 1.17.1 Introduction

We have compiled some common questions about installing and using RMG below. For any other questions related to RMG and its usage and installation, please post an issue on our [GitHub issues page](#), where you can also search for any previous reports of your issue. Alternatively, you can also ask questions via the [RMG-Py chat room](#) or by contacting us directly at [rmg\\_dev@mit.edu](mailto:rmg_dev@mit.edu).

### 1.17.2 Installing RMG

#### 1. How can I install RMG-Py without Anaconda?

Usually we don't recommend installing RMG-Py without Anaconda because it takes longer and is easier to get trouble with package management. But one still can try direct installation on Linux or MacOS by following [Linux instruction](#) or [MacOS instruction](#). The RMG team does not use this install approach internally any more, so these instructions are not actively maintained.

#### 2. Why does RMG-Py not work natively on Windows?

One major challenge with supporting Windows is ensuring that all of our dependencies support Windows. This becomes non-trivial as we add more dependencies to support increasing RMG functionality. Ensuring that code within RMG is platform-agnostic is also challenging, since it is rarely the first priority for new development because our main focus is on research.

#### 3. What is the recommended way to run RMG-Py on Windows?

The currently recommended way to run RMG on Windows is to set up a Linux environment. There are multiple ways you can approach this. Windows 10 supports a Linux subsystem which allows one to set up a Linux environment within Windows without using virtualization. You can find instructions on setting up RMG within the Linux subsystem [here](#).

Another option would be to set up a full Linux virtual machine using something like VirtualBox or VMWare Workstation. The benefit of this option is being able to run in a full Linux environment. However, running two operating systems simultaneously does result in excess resource overhead, so it may not be suitable for running extended RMG jobs. Instructions for setting up a virtual machine can be found [here](#).

A third option that we are currently beginning to explore using [Docker](#), which is a container-based infrastructure which shares the same benefits as a virtual machine but with less overhead. There are some test images of RMG-Py which can be found on [Docker Hub](#) if you would like to give this a try. More detailed instructions will be made available once we officially support this approach.

#### 4. Windows binary installation gives ``WindowsError: [Error 5]``?

Error 5 is access is denied, so this is either a permissions error, or an issue with the Windows file lock. [These posts](#) suggest rebooting the computer (in case it's a file lock), and running the anaconda prompt, from which you run `conda create -c rmg --name rmg_env rmg rmgdatabase`, as an administrator (in case it's a permissions error). Please checkout one example from a user having [Windows binary installation issue](#).

### 1.17.3 Running RMG

#### 1. How do I run a basic RMG job?

Please see step-by-step instructions in the either the [binary](#) or [source](#) installation instructions. In general, the syntax is

```
rmg.py input.py
```

if the RMG-Py directory has been properly added to PATH. For the binary installation, this is done automatically, but you will need to do this yourself if installing from source.

For information on writing an RMG input file, please see the [documentation](#).

#### 2. Why did I get ImportError: No module named graph when trying to run RMG?

This error is commonly seen when RMG is run before compiling. The graph module just happens to be one of the first Cython modules to be imported. To resolve this, compile RMG using the make command while in the main RMG-Py directory.

#### 3. Why did I get ImportError: No module named cantera when trying to run RMG?

This error is commonly seen when RMG is run without properly setting up the Anaconda environment. The cantera module happens to be one of the first dependencies to be imported. To resolve this, activate the RMG environment using `conda activate rmg_env`. If the environment has not already been created, create the environment according to the [Linux installation instructions](#).

#### 4. What is an UndeterminableKineticsError?

This is a common cause of crashed RMG jobs. It is often due to inconsistencies in how reaction templates are defined in RMG-database, and occasionally due to inconsistencies in resonance structure generation. Unfortunately, this type of error can be very difficult to debug. You can post such issues to our [GitHub issues page](#).

#### 5. What is an InvalidMicrocanonicalRateError?

This is another common cause of crashed RMG jobs when using the pressure dependence module. It is due to a failure to converge the microcanonical rate calculation for a pressure dependent network. It can be due to a variety of factors, such as poor thermochemistry or rate constants. Unfortunately, there is currently no good way to debug and fix these types of errors.

#### 6. Why did I get Segmentation fault:11 after installing RMG on my machine?

**Segmentation fault** is a typical error in C code, caused by a program trying to read or write an illegal memory location, i.e. one it is not allowed to access. The most common cause in RMG is a conflict between two different versions of a shared library. RMG has some dependencies which are written in C++, e.g. rdkit, openbabel. If you compile one of these with a different version of some compiler library, or you compile RMG using one version and run it with another, you will often get a Segmentation fault. Chances are those packages are not up to date, or maybe your environmental variable PATH is messed up so that the wrong version of something is being found. Please see one example from a user having same [Segmentation fault issue](#).

#### 7. Why did I get IOError: [Errno 13] Permission denied: 'C:\\\\RMG.log'

You do not have permission to write to the log file. Try running the RMG from a different folder that you do have write permission to, such as within your user's documents directory, or else try running the command prompt as an Administrator (so that you have write permission everywhere). See for example [issue #817](#).

## 1.17.4 Miscellaneous

### 1. Why can't my adjacency lists be read any more?

The adjacency list syntax changed in July 2014. The minimal requirement for most translations is to prefix the number of unpaired electrons with the letter *u*.

Example old syntax:

```
HXD13
1    C 0      {2,D}
2    C 0 {1,D} {3,S}
3    C 0 {2,S} {4,D}
4    C 0 {3,D} {5,S}
5 *1 C 0 {4,S} {6,S}
6 *2 C 0 {5,S}
```

Example new syntax:

```
HXD13
1    C u0      {2,D}
2    C u0 {1,D} {3,S}
3    C u0 {2,S} {4,D}
4    C u0 {3,D} {5,S}
5 *1 C u0 {4,S} {6,S}
6 *2 C u0 {5,S}
```

The new syntax, however, allows much greater flexibility, including definition of lone pairs, partial charges, wildcards, and molecule multiplicities, and was necessary to allow us to add Nitrogen chemistry. See `rmgpy.molecule.adjlist` for details of the new syntax.

## 1.18 Release Notes

### 1.18.1 RMG-Py Version 3.2.0

Date: July 13, 2022

- **RMG-Py**

- Transport: Added halogens transport corrections to boiling point when estimating critical properties using group additivity
- Updated solvation thermo GAV method to use more groups
- Made it optional to generate\_resonance\_structures when loading species dicts
- Added filter so radical/lone pair/formal charge is not added to surface site when generating resonance structures
- Forbid surface bidentate vdW species
- Added get\_react\_thermo function to avoid deepcopy



- Added decay framework for handling species RMG templates think exist, but really aren't wells
  - Added check to prevent multiple surface bonds from forming through a single adatom
  - Added multidentate adsorption correction for thermo estimation
  - Added error checks to make MOPAC calculations more robust
  - Added features to preserve atom order and template labels when generating reactions
  - Added coverage dependent effects to surface kinetics
  - Added support for halogen families in autogen tree script
  - Enabled pyrims for RMG Simulations and Edge Analysis
  - Added Liquid-Surface Reactor for RMG Electrocat
  - Added support for forbidden structures, more general than forbidden molecules
  - Removed hard-coded template matching code for Bimolec hydroperoxide decomposition
  - Added support for 2-parameter Troe reactions, only had 3-parameter Troe before
  - Included noncyclic long distance GAV correction for halogen regardless of its existence in the cycle
  - Added support for pdep networks with halogens
  - Added atom labels to molecule to\_group method in order to keep the atom labels during conversion
  - Moved rmgrc to template file so user's settings won't be overwritten every pull from RMG-Py
  - Implemented two backup conformer embedding algorithms for robustness
  - Added Nitrogen groups to transport
  - Removed check for adsorbate getting adsorbed again which prevents Surface\_Dissociation\_to\_Bidentate family
  - Modified the liquid reactor to be able to simulate as CSTR, semi-batch, and/or vapor liquid mass transfer interface
  - Added fragment code to rmgpy/molecule
- **Auto Generated Trees**
    - Enabled estimator to ascend autogenerated rate tree if uncertainty is too high in a lower node
    - Made some major improvements to automated tree extension generation and the cascade algorithm
    - Added support for quadruple bonds in auto tree generation
    - Added binding energies for N-S and C#S
    - Removed hard-coded special treatment for Peroxyl Disproportionation family during template matching
    - Increased ArrheniusBM fitting temperature upper limit to 2000K for RMG-database rate trees
    - Skipped number of products check for ATG tree generation of Intra\_R\_Add\_Endocyclic and Intra\_R\_Add\_Exocyclic
- **RMS**
    - Added surface reactions to RMS yaml format
- **Arkane**
    - Added check for convergence and other common errors in QM parsers

- Updated the documentation that tabulates which levels of theory are supported by Arkane
- Read actual scan angles for rotor calculations
- Corrected Fourier fitting in torsion.pyx
- Added Psi4 ESS adapter to Arkane
- Added commit strings for RMG-Py and RMG-database to Arkane logs
- Added BAC confidence interval estimates to Arkane logs
- Added leave-one-out cross-validation for evaluating BAC fits
- Enabled parsing of scan log files with linear bend (something like L 1 2 3 B)
- Enabled assignment of PES (angles vs energies) directly in the Arkane input file
- Added a readme file for Arkane
- Updated QChem parser to only return the negative frequency from the last frequency block instead of the first

- **Bugfixes**

- Added check for multiplicity of reverse products if the family template reactants have multiplicity constraints
- Added check for vdW multiplicity constraints in forward direction
- Added check to see that empty surface site template group only matches empty surface site structure (and not vdW species with empty site)
- Fixed regex bug in checking multiplicity of adjacency list
- Fixed bug where RMG can output mechanisms in which two species have the same name
- Added QM fallback to ML or GAV in case of bad conformer ID error from rdkit
- Fixed many broken links in documentation
- Fixed species missing metal attribute error
- Fixed some automated tree generation parallelization bugs
- Changed tree generation get\_training\_set method to use deepcopy to clear atom labels and to parse out the metal from the entry
- Added a save\_order attribute to some methods to preserve atom order in cases that need it
- Fixed load chemkin function to allow extended elements and species that start with digits
- Handle string data properly when averaging children solute
- Fixed bug in get\_w0 where a\_dict didn't match the molecule because it was made before the molecule was deepcopied
- Added check for pdep net reactions when removing species to prevent forbidden species from ending up in net reactions
- Fixed bug where add\_atom\_labels\_for\_reaction mislabels reactants if family is its own reverse
- Fixed bug where save\_training\_reactions occasionally mixes up atom labels
- Added Ctc atom type to prevent RMG from crashing when trying to make [C+]#[C-] molecule, which was then added to the forbidden structures
- Fixed bug where generate\_resonance\_structure does not preserve atom when keep\_isomorphic=False and save\_order=True

- Fixed bugs related to RMS object construction, particularly Multi/Pdep/Arrhenius and falloff
- Added check to always draw CO as ‘CO’ instead of ‘OC’
- Converted ThermoData object to a NASA object for compatibility with RMS
- Corrected pyrms core/edge species/reaction handling for phase systems
- Fixed incorrect reading in load\_chemkin\_file for surface species with site density specified
- Added properties so group can be pickled without losing important information like ring membership
- **Testing**
  - Updated reference number of reactions for Arkane test\_reactions unit test
  - Changed molecule for rmgpy/data/thermoTest.py test\_identifying\_missing\_group test because group is no longer missing
  - Added continuous integration test for links in documentation
  - Changed kinetics database tests to look for auto\_generated tag instead of the hardcoded family list
  - Updated rmg test data with new 2+2 cycloaddition species and reactions
  - Remove cti file generation from regression tests to avoid Cantera IO error
  - Added tests to check number of reactants and products defined in ATG rate rules
- **Miscellaneous**
  - Added check to only publish documentation documentation from RMG official fork
  - Fixed RMG-Py 3.1.0 release note bullet formatting
  - Changed installation instructions for WSL users to install graphviz system wide to include all dependencies
  - Changed get\_all\_solute\_data function for RMG-website use in order to apply halogen or radical correction on top of library or GAV
  - Added openSUSE installation instructions
  - Changed default branch to main
  - Changed rmg.py shebang to use python-jl instead of python3 for compatibility with RMS/pyrms
  - Updated ketoenol template image to 1,3 sigmatropic rearrangement
  - Updated 2+2\_cycloaddition images in documentation
  - Added licensing information to the README file
  - Updated installation instructions with main instead of master branch, latest Anaconda link, and ssh instead of https clone from github
  - Added support for Sticking Reactions in HTML reports
  - Added reminder in documentation to activate rmg\_env before making tests
  - Check that family tree is not autogenerated before calling add\_rules\_from\_training and fill\_rules\_by\_averaging\_up
  - Added warning to not to call add\_rules\_from\_training and fill\_rules\_by\_averaging\_up on ATG trees, and return statement before error
  - Replaced BurkeH2O2 library with PrimaryH2O2 in relevant RMG examples

### 1.18.2 RMG-Database Version 3.2.0

Date: July 13, 2022

- **Thermochemistry**

- **Identified and fitted thermo for missing groups using the following libraries:**

- ‘Klippenstein\_Glarborg2016’, ‘BurkeH2O2’, ‘thermo\_DFT\_CCSDTF12\_BAC’, ‘DFT\_QCI\_thermo’, ‘primaryThermoLibrary’, ‘primaryNS’, ‘NitrogenCurran’, ‘NOx2018’, ‘FFCM1(-)’, ‘SulfurLibrary’, ‘SulfurGlarborgH2S’, ‘SABIC\_aromatics’

- Added more solutes and solvents to the solvent library

- Updated GAV method for solvation thermo to use more groups

- **Added the following new halogen thermo libraries:**

- \* CHOF\_G4

- \* CHOCI\_G4

- \* CHOBr\_G4

- \* CHOFCI\_G4

- \* CHOCIBr\_G4

- \* CHOFCBr\_G4

- \* CHOFCIBr\_G4

- \* Chlorination

- \* halogens

- \* 2-BTP

- \* 2-BTP\_G4

- Added new halogens group entries for group.py, radical.py nonring.py, and longDistanceInteraction\_noncyclic.py

- Added the following species to the primaryThermoLibrary: F, HF, F2, Br, HBr, Br2, NO, NO2, CO, OCCCCO

- Updated halogen group entries with molecule symmetry number correction

- Added corrections for overestimation of triplet and multidentate adsorbates

- Added CO2, COOH, and HCOO to the Pt(111) thermo database

- Added halogens statmech library

- Added F/Cl/Br-benzene group additivity values

- Added “heavy halogen interaction” long distance thermo group

- Added thermo library with 1D rotor scans for species in ketoenol, retroene, and 1,3 sigmatropic rearrangement training reactions

- **Kinetics**

- Added coverage-dependent kinetics for surface reactions

- **Added the following new families:**

- \* Surface\_Adsorption\_Dissociative\_Double

- \* Surface\_Abstraction\_Beta\_double\_vdW

- \* Surface\_Abstraction\_Beta
- \* XY\_elimination\_hydroxy
- \* Intra halogen migration family
- \* 1,3 sigmatropic rearrangement
- **Autogenerated the following family trees:**
  - \* Birad\_recombination
  - \* Diels alder addition
  - \* Substitution\_O
  - \* Ketoenol
  - \* Retroene
  - \* Disproportionation
  - \* Cyclopentadiene\_scission
  - \* 1,3\_NH3\_elimination
  - \* CO Disproportionation
  - \* Peroxyl Disproportionation
  - \* Bimolec\_Hydroperoxide\_Decomposition
  - \* 1,3\_sigmatropic\_rearrangement
  - \* 2+2\_cycloaddition
- Merged all 2+2\_cycloaddition families in to one 2+2\_cycloaddition family
- Added aromatic H abstraction rates by Hou et al.
- Added PrimaryH2O2 library with rates by Konnov
- Added surface library reactions for ammonia
- Added more nodes to Surface\_Adsorption\_Double, Surface\_Adsorption\_Single, Surface\_Adsorption\_vdW, Surface\_Dissociation, and Surface\_Dissociation\_Beta families
- Added new halogens kinetics families and libraries
- Added new rates and refit retroene rate tree
- Added new rates and refit ketoenol rate tree
- Added new rates and refit Intra R Add Endo/Exocyclic rate trees
- Added training reactions for Diels Alder Addition family
- Added training reactions and groups related to PAH formation
- **Transport**
  - Added NIST transport library for fluorines
  - Added new halogen transport groups
  - Added Nitrogen groups to transport
- **QM Corrections**
  - Added frequency scaling factors AEC and BAC for  $\omega$ B97X-D3/def2-TZVP and B97-D3/def2-mSVP

- Added notebooks demonstrating how to update AEC and BAC
- Updated AECs for CCSD(T)-F12/cc-pVXZ-F12 st X = D, T
- Added frequency factor for b2plypd3/def2tzvp
- **Updated BAC using correct frequency scaling factor for:**
  - \* wB97X-D3/def2-TZVP
  - \* B97-D3/def2-mSVP
  - \* CCSD(T)-F12/cc-pVTZ-F12// $\omega$ B97X-D3/def2-TZVP
  - \* CCSD(T)-F12/cc-pVDZ-F12// $\omega$ B97X-D3/def2-TZVP

- **Bugfixes**

- Fixed the number of unpaired radicals in surface vdW families
- Fixed typos in training reactions field names
- Fixed enthalpy errors in adsorption corrections for O-containing species on Pt(111)
- Fixed some errors in surface training reaction rates
- Fixed some minor errors in the solvent library
- Fixed typos in coverage dependent kinetics parameters
- Used forbidden group to fix error where unsymmetric head node leads to Undeterminable Kinetics Error
- Removed duplicates in XY\_addition\_multiplebond
- Fixed typo in R\_Recombination training reaction units
- Fixed incorrectly imported species H2CCC and C3H2 in the CurranPentane library
- Fixed master to main in trigger script
- Added the missing reactant and product number in the intra\_R\_Add families
- Fixed Intra\_R\_Add\_Endocyclic/Exocyclic families by generating from the ring opening direction and enumerating backbones

- **Miscellaneous**

- Updated Github Actions workflow for better handling of dual RMG-Py and RMG-database pull requests
- Added the Blowers-Masel tree generation notebook
- Added [C-]#[C+] to forbidden structures
- Added thermally forbidden 2pi + 2pi cycloaddition to forbidden structures
- Changed Github Actions to run on main branch instead of master
- Updated 2+2\_cycloaddition reaction family images

### 1.18.3 RMG-Py Version 3.1.0

Date: April 23, 2021

We recommend creating a new conda environment using the latest environment.yml as many dependencies have changed, and upgrading an existing environment is always troublesome.

- **RMG-Py**

- Added support for Bromine
- Added improved method to calculate temperature dependent solvation free energy
- Made Rank 1 accuracy correspond to 0.2 kcal/mol instead of 0 kcal/mol
- Improvements to Group Additivity comments, in particular adding missing group comments
- Added support for trimolecular units in ArrheniusBM fits
- Improvements to profiling
- Use kekulized structures for transport estimation
- Automatic tree generation script improvements
- Properly short circuit is\_isomorphic when strict=False
- Added block for specifying species tuples to react when starting an RMG run
- Improve ArrheniusBM fitting to a single reaction
- Improvements in bidentate thermochemistry estimation
- Added new surface attributes for metals and facets
- Added support for Phosphorus
- Enable use LSRs to scale thermo from different metals and enable proper use of training reactions from different metals
- Added maximumSurfaceSites constraint

- **Arkane**

- Added frequency scaling factors for apfd/deef2tzvp and wb97xd/def2svp
- Kinetics and pdep sensitivities additionally saved in YAML format
- Enable automatic isodesmic reaction generation
- AECs, BACs and frequency scaling factors moved from Arkane to RMG-database
- Added functionality for Petersson and Melius BAC fitting using Arkane and the reference database
- Enabled two parameter Arrhenius fit option
- Added functionality for fitting AECs
- Added classes to standardize model chemistry definitions
- Use adjlists instead of smiles when saving

- **Bugfixes**

- QMTP updated to work with g16 executable
- Fixed various Sticking Coefficient bugs
- Fixed issues with Surface Arrhenius reactions written in the reverse being converted to ArrheniusEP instead of SurfaceArrheniusBEP

- Fixed NaN handling in the explorer tool's steady state solve
- Fixed `determine_qm_software` for Orca
- Fixed bug where `elementary_high_p` library reactions with more than the maximum number of atoms for pdep never entered the edge
- Fixed bug related to pdep networks having sources not contained in the core
- Fixed various profiling bugs
- Fixed issue with indexing when merging models
- Fixed bug with ranged liquid reactors
- Fixed bug with loading of autogenerated trees in Arkane
- Fixed bug related to collision limit violation checks in `LiquidReactor`
- Fixed bug related to `Pmin` and `Pmax` definition in `SurfaceReactor`
- Fixed bugs in global uncertainty analysis for `LiquidReactor`
- Fixed bug related to the units of reverse rate constants for reactions involving surface species
- Fixed bug in Molecule isomorphism where it would simply assume the given initial map was correct
- Remove deprecated `matplotlib warn` keyword
- Fixed bug related to reading Chebyshev forms in Chemkin files
- Fixed reference concentration for surface species when calculating `Kc`
- Fixed issue with the reaction generation using the reverse of `Surface_ElleyRideal_Addition_MultipleBond`
- Fixed bug with `adlist` multiplicity line being mistaken as the species name
- Fixed bug with the library to training notebook
- Remove temporary seed mechanisms if they exist from a previous run

- **Miscellaneous**

- Modified `find_parameter_sources_and_assign_uncertainties` to regenerate `chem.inp` as needed
- Added option to save atom order when labeling template reactions
- Added option to ignore atom type errors when creating molecule objects
- Enable use of `critical_distance_factor` in `from_xyz`
- Improved SIGINT handling when calling `lpsolve`
- Enable H-bond drawing
- Improvements to debug messages
- Updated dependencies `cclib` and `OpenBabel`

Note that the upgrade to `OpenBabel v3+` will change the interpretation of some ambiguous SMILES strings that use the lower-case aromatics notation. Although we think the new interpretation is not wrong, it might be different from previous versions, so take care.



### 1.18.4 RMG-Database Version 3.1.0

Date: April 23, 2021

- **Thermochemistry**
  - Added groups and library for Iodine
  - Added additional solvent parameters
  - Updated SABIC\_aromatics thermo library added s3\_5\_7\_ane thermo library and updated polycyclic groups
  - Renaming of adsorption libraries
- **Kinetics**
  - Added kinetic library and training reactions for Iodine
  - Added training reactions for peroxy families
  - Prevent forbidden [2pi+2pi] thermal cycloaddition for  $C=C + C=C$
  - Removed incorrectly transcribed training reaction for  $CH_3OH + O_2 \Rightarrow CH_3O + HO_2$
  - Added H\_Abstraction training reactions
  - Creation of the retroene family uses automatic tree generation
  - Added Surface Dissociation Double vdW, Surface Dissociation vdW, Surface Migration and Eley-Rideal, Surface Addition Single vdW, Surface Abstraction vdW, Surface Dual adsorption vdW, Surface Dissociation Beta, Surface Adsorption Abstraction vdW and Surface\_DoubleBond\_to\_Bidentate families
  - Updated Surface Dissociation, Surface Abstraction, Surface Adsorption Dissociative, Surface Adsorption Single and Surface Bidentate Dissociation families
  - Added assorted Nitrogen catalysis training reactions
  - Allow CO insertion to  $H-C(R)=O$
- **QM Corrections**
  - Updated AECs and added frequency scaling factor for wB97M-V/def2-TZVPD
  - Standardized level of theory specifications
- **Bug fixes**
  - Fixed Cds-CdSH node reference
  - Fixed typos causing thermo discontinuities for H2\_ads and O-NH2-ads
  - Fixed enthalpy error for O-NH2\_ads
  - Corrected structure of H2CC in JetSurF2.0, Klippenstein\_Glarborg2016, and Narayanaswamy
  - Fixed Ni211 binding energies
- **Miscellaneous**
  - Fix indexing of importChemkinLibrary.py script
  - Moved AEC, BAC and frequency scale factor data from RMG-Py into RMG-database
  - Added notebook for fitting polycyclic thermo groups
  - New surface attributes

### 1.18.5 RMG-Py Version 3.0.0

Date: December 16, 2019

This release represents a major milestone in RMG development and includes many backwards-incompatible changes, most notably Python 3 compatibility and major API changes. Users switching to RMG 3 will need to create new conda environments and update any scripts which access the API. We recommend using the *futurize* script from python-future for updating scripts for Python 3 and the provided *rmg2to3.py* script for updating scripts for RMG 3.

- **Python 3 #1724**

- RMG is now compatible with Python 3.7 and newer
- RMG v2.x versions will no longer be supported
- **API changes**
  - \* Method, function, and argument names have been standardized to use snake\_case across RMG and Arkane
  - \* Input file related code was not changed, in order to continue support for existing syntax
  - \* Conversion script has been provided to aid transition (scripts/rmg2to3.py)
  - \* Standardized submodule names in the rmgpy.tools module #1794
- **Accompanying changes**
  - \* Reduction and scoop\_framework modules have been removed
  - \* New/updated hash and comparison methods for Species/Molecule/Atom/Bond classes
  - \* DDE thermochemistry estimator has been replaced by chemprop
  - \* Update example IPython notebooks #1735
  - \* Update global uncertainty module to work with MUQ 2 and Python 3 #1738
- Miscellaneous clean up and bug fixes following transition #1741, #1744, #1752, #1759, #1785, #1802, #1798, #1799, #1808

- **Arkane**

- Improvements and refactoring of job output file creation and content #1607
- Fix kinetics fitting bug #1672
- Improvements to automatic network exploration tool #1647
- Support for ND classical and semi-classical rotor calculations #1640, #1849
- Support for 2D quantum mechanical rotor calculations using Q2DTor #1640
- Support for providing absolute file paths #1685
- Output RMG-style libraries #1769
- Check for error termination in Gaussian log files #1766
- Support for parsing Orca log files #1749
- Support for parsing MP2, double hybrid DFT, CCSD, and CCSD(T) energies from Gaussian log files #1815
- Support for TeraChem log files #1788
- Miscellaneous bug fixes #1810

- **New features and other additions**

- Additional options for heterocycles in MLEstimator #1621
- Automatic tree generation algorithm implementation completed #1486, #1675, #1848
- New simulation restart approach using seed mechanisms (old pickle-based method removed) #1641
- Added new MBSampledReactor type for simulating molecular beam experiments (does not support model generation) #1669
- Improvements to group additivity thermo estimates for aromatics and sulfur species #1731, #1751
- Improvements to solvation correction determination with multiple resonance structures #1832
- Add support for reading and writing extended element syntax in Chemkin NASA polynomials #1636
- Add support for fitting negative Arrhenius rates (found in MultiArrhenius data) #1834
- **Bug fixes**
  - Fix numpy rcond usage to restore support for older numpy versions #1670
  - Fix bug with duplicate library reactions when using RMG generated seed mechanisms #1676
  - Move parse\_command\_line\_arguments to facilitate importing in binary package #1717
  - Fix issues with is\_identical\_to methods of kinetics models #1705
  - Fix cython issue with make\_object definitions #1817
  - Fix issue with estimating solvation corrections for radicals #1773
  - Fix parsing of certain types of RMG generated reaction comments #1842
  - Fix identifier generation for surface species using OpenBabel #1842
  - Fix mole fraction normalization for SimpleReactor #1809
  - Fix permissions error when writing seed mechanisms in WSL #1796
  - Fix issue with restarting from job without reaction filters #1847
- **Other**
  - Improvements to mergeModels.py script #1649
  - Miscellaneous performance improvements #1677, #1765,
  - Raise errors when NaN is encountered in solver #1679
  - Allow sulfur species to have valence 12 in resonance algorithm #1751
  - Add support for maxproc argument to generate\_reactions module #1780
  - Display atom index when drawing groups #1758
  - Update sensitivity example #1805
  - Update commented input file #1806
  - Generate reverse reaction recipes in reverse order of the forward recipe #1829
  - Add iodine to Chemkin elements list #1825
  - Remove unnecessary duplicate checking for seed mechanisms #1824
  - Organize examples for running RMG scripts #1840
  - Increase RDKit version requirement to avoid memory leak #1851
  - Logging changes #1721, #1755

- Documentation updates #1680, #1709, #1767, #1781, #1784, #1807, #1845

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### 1.18.6 RMG-database Version 3.0.0

Date: December 16, 2019

- **Thermochemistry**
  - Add new models for chemprop estimator to replace dde models #351
  - Revamp GAVs for oxygenated sulfur species #360
  - Add polycyclic GAVs for various strained molecules #333
- **Kinetics**
  - New automatically generated tree for R\_Recombination #334, #369
  - Refine root template for 1,2\_NH3\_elimination #350
  - New DMSOxy kinetics family #360
  - Add DMS related training reactions to H\_abstraction #360
- **Bug fixes**
  - Fix drawing for 2+2\_cycloaddition\_Cd #345
  - Fix incorrect SMILES in solute database #348
  - Fix incorrect adjacency list for HON in kinetics libraries #350
  - Fix typo in solvent parameters #357
- **Miscellaneous**
  - Update scripts and IPython notebooks for Python 3 #364

### 1.18.7 RMG-Py Version 2.4.1

Date: July 23, 2019

- **Bugfixes**
  - Improve error handling in NASA as\_dict method #1630
  - Fixes to Fluorine atomtypes #1656
  - Fix pressure dependent network generation #1658
  - Add support for reversing PDepArrhenius with MultiArrhenius rates #1659
- **Arkane**
  - Implement ZPE scaling factor #1619
  - Refactor infrastructure for bond additivity corrections #1605
  - Add frequency scale factors for wb97xd/def2tzvp and apfd/def2tzvpp #1653
  - Fix frequency scale factors in example files #1657
  - Get element counts from conformers #1651

- **Miscellaneous**

- Update conda environment files #1623, #1644
- Output RMS (Reaction Mechanism Simulator) format mechanism files #1629
- Properly clean up files after running tests #1645
- Documentation fixes #1650
- Improve `as_dict` and `make_object` by making them recursive #1643

### 1.18.8 RMG-Py Version 2.4.0

Date: June 14, 2019

- **Heterogeneous catalysis!**

- **RMG-cat fork has been merged #1573**
  - \* Introduce `SurfaceReactor`
  - \* Thermo estimation for adsorbed species
  - \* Surface reaction generation and kinetics estimation
- Introduce Van der Waals bonds (order 0) and quadruple bonds (order 4) #1542

- **Arkane**

- Automatically detect rotor symmetry #1526
- Introduce new YAML files for storing and loading species `statmech` data #1402, #1551
- Don't create species dictionary file if there are no structures #1528
- Improvements to network explorer tool #1545
- Improved class inheritance for quantum log file classes #1571
- Automatic determination of optical isomers and symmetry using `symmetry` package #1571
- Parse CCSD(T) energies from Molpro output #1592
- Automatically determine molecule linearity #1601
- Determine frequency scaling factor based on `geom/freq` method rather than `sp` method #1612
- Improve logging related to energy barriers #1575
- Ensure that translational mode is calculated for atoms #1620

- **Miscellaneous features**

- New `enumerate_bonds` method of `Molecule` to generate dictionary of bond types #1525
- Introduce `RMGObject` parent class to support YAML dumping and loading #1402, #1540
- Add support for fluorine atomtypes #1543
- Introduce `ArrheniusBM` class for Blower-Masel kinetics #1461
- Allow defining and using co-solvents for solvent libraries #1558
- Introduce `strict` option to perform isomorphism between species/molecules while ignoring electrons and bond orders #1329
- `Molecule` and `Species` objects can be instantiated by providing `SMILES` or `InChI` argument directly, and the identifiers can be accessed via the `SMILES` and `InChI` attributes #1329

- Parallelization has been completely refactored using Python multiprocessing module in replacement of scoop, currently supports parallel reaction generation and QMTP #1459
- Improvements to usability of uncertainty analysis functionality #1593
- **Bug fixes**
  - Various fixes for supporting mono-atomic molecules in Arkane #1513, #1521
  - Ensure keras\_backend is set consistently #1535
  - Fix handling of disconnected graphs in VF2 isomorphism algorithm #1538
  - Ignore hydrogen bonds when converting to RDKit molecule #1552
  - Other miscellaneous bugs #1546, #1556, #1593, #1600, #1622
- **Backward incompatible changes**
  - Hydrogen bonds are now order 0.1 (instead of 0) #1542
- **New dependencies**
  - pyyaml (required) #1402
  - scikit-learn (required) #1461
  - textgenrnn (optional) #1573
- **Other**
  - Windows binaries are no longer officially supported. The new recommended way to use RMG on Windows computers is via a virtual machine or through the Linux subsystem. See documentation for updated installation instructions. #1531, #1534
  - Documentation updates #1544, #1567
  - Logging/exception improvements #1538, #1562
  - PEP-8 improvements #1566, #1592, #1596
  - Solver output files (png/csv) now report moles instead of mole fractions #1542
  - Replace global RMGDatabase object if the database is reloaded #1565
  - Print ML generated quote upon completion of RMG jobs #1573
  - Infrastructure for automatically generated reaction rate trees #1461
  - Testing related changes #1597, #1599
  - Updates to example Jupyter notebooks #1541, #1593

### 1.18.9 RMG-database Version 2.4.0

Date: June 14, 2019

- **Heterogeneous catalysis!**
  - RMG-cat fork has been merged #309
  - **New kinetics families**
    - \* Surface\_Adsorption\_Single
    - \* Surface\_Adsorption\_vdW
    - \* Surface\_Adsorption\_Dissociative

- \* Surface\_Dissociation
- \* Surface\_Abstraction
- \* Surface\_Adsorption\_Double
- \* Surface\_Dissociation\_vdW
- \* Surface\_Adsorption\_Bidentate
- \* Surface\_Bidentate\_Dissociation
- \* Surface\_Recombination (deprecated, use Surface\_Dissociation instead)
- **New thermo group types**
  - \* adsorptionNi
  - \* adsorptionPt
- **New thermo libraries**
  - \* surfaceThermoNi
  - \* surfaceThermoPt
- **New kinetics families**
  - 1,2\_NH3\_elimination #326
  - 1,3\_NH3\_elimination #326
- **New kinetics libraries**
  - HydrazinePDep #326
- **New transport libraries**
  - OneDMinN2 #326
- **Kinetics training reaction additions**
  - 1,2\_shiftC #306
  - Intra\_R\_Add\_Endocyclic #306, #258
  - Intra\_R\_Add\_Exocyclic #306, #258, #331
  - Intra\_ene\_reaction #306
  - R\_Addition\_COm #306
  - R\_Addition\_MultipleBond #306, #258
  - R\_Recombination #306, #326
  - Intra\_H\_migration #306
  - H\_Abstraction #326
- **Kinetics library additions**
  - primaryNitrogenLibrary #326
  - Lai\_Hexylbenzene #258
- **Thermo library additions**
  - CBS\_QB3\_1dHR, thermo\_DFT\_CCSDTF12\_BAC #319
  - primaryNS #326

- Lai\_Hexylbenzene #258
- **Thermo group additions**
  - ring, polycyclic, radical #258
- **Changes**
  - [adjlist] kinetics/libraries/Klippenstein\_Glarborg2016 #308
  - [labels] thermo/libraries/CBS\_QB3\_1dHR, Narayanaswamy #306
  - [units] kinetics/libraries/Sulfur/GlarborgMarhsall, Nitrogen\_Dean\_and\_Bozzelli, primaryNitrogenLibrary, primarySulfurLibrary #311
  - [units] R\_Addition\_MultipleBond/training, R\_Recombination/training #312
  - [adjlist] kinetics/libraries/GRI-Mech3.0-N #313
  - [adjlist] thermo/libraries/GRI-Mech3.0-N, GRI-Mech3.0 #313
  - [rates] Disproportionation/training, R\_Addition\_MultipleBond/training #326
  - [labels] kinetics/libraries/NOx2018 #326
  - [labels, attributes] kinetics/libraries/Nitrogen\_Dean\_and\_Bozelli #326
  - [labels] kinetics/librariesNitrogen\_Glarbog\_Gimenez\_et\_al, Nitrogen\_Glarborg\_Zhang\_et\_al #326
  - [labels, adjlist] thermo/libraries/BurcatNS #326
  - [labels] thermo/libraries/NOx2018, NitrogenCurran #326
  - [labels] transport/libraries/NOx2018 #326
  - [adjlist] Intra\_R\_Add\_Endocyclic/training #332
  - [value] thermo/groups/ring/12dioxetane #327
  - [adjlist] thermo/libraries/GRI-Mech3.0 #336
  - [value] thermo/libraries/primaryThermoLibrary #338

### 1.18.10 RMG-Py Version 2.3.0

Date: Dec 20, 2018

- **Arkane (formerly CanTherm):**
  - CanTherm had been renamed to Arkane (Automated Reaction Kinetics And Network Exploration)
  - New network exploration functionality using RMG-database
  - Support for all elements has been added for reading quantum output files
  - New supporting information output file with rotational constants and frequencies
  - Known thermo and kinetics can be provided in addition to quantum information
  - Improve general user experience and error handling
- **New machine learning thermo estimator**
  - Estimate species thermochemistry using a graph convolutional neural network
  - Estimator trained on quantum calculations at B3LYP and CCSD(T)-F12 levels
  - Currently supports C/H/O/N, with an emphasis on cyclic molecules



- **Resonance:**
  - New pathways added for lone-pair multiple-bond resonance, replacing two pathways which were more specific
  - New pathways added for aryne resonance
  - Aromatic resonance pathways simplified and refactored to use filtration
  - Kekule structures are now considered unreactive structures
- **Miscellaneous changes:**
  - Isotope support added for reading and writing InChI strings
  - New branching algorithm for picking up feedback loops implemented (beta)
  - Global forbidden structure checking is now only done for core species for efficiency, which may lead to forbidden species existing in the edge
  - Minor improvements to symmetry algorithm to fix a few incorrect cases
- **Bug fixes:**
  - Fixed issue where react flags were being reset when filterReactions was used with multiple reactors, resulting in no reactions generated
  - File paths for collision violators log changed to output directory
  - Fixed bug in local uncertainty introduced by ranged reactor changes
  - Fixed bug with diffusion limitation calculations for multi-molecular reactions
  - Various other minor fixes

### 1.18.11 RMG-database Version 2.3.0

Date: Dec 20, 2018

- **Kinetics rules to training reactions**
  - All kinetics rules have been converted into training reactions by converting each group to the smallest molecule that matches it
  - Training reactions are preferred over rules because they correspond to a specific reaction and are therefore easier to update
  - This conversion is in anticipation of upcoming changes to trees in kinetics families
- **Additions:**
  - R\_Addition\_MultipleBond training reactions
  - intra\_NO2\_ONO\_conversion training reactions
  - SABIC\_aromatics thermo library (CBS-QB3, RRHO)
  - McGowan volumes for noble gases
  - More entries added to Lai\_Hexylbenzene libraries
  - Architecture and weights for neural network thermo estimator

### 1.18.12 RMG-Py Version 2.2.1

Date July 23, 2018

This release is minor patch which fixes a number of issues discovered after 2.2.0.

- **Collision limit checking:**
  - RMG will now output a list of collision limit violations for the generated model
- **Fixes:**
  - Ambiguous chemical formulas in SMILES lookup leading to incorrect SMILES generation
  - Fixed issue with reading geometries from QChem output files
  - React flags for reaction filter were not properly updated on each iteration
  - Fixed issue with inconsistent symmetry number calculation

### 1.18.13 RMG-Py Version 2.2.0

Date: July 5, 2018

- **New features:**
  - New ring membership attribute added to atoms. Can be specified in group adjacency lists in order to enforce ring membership of atoms during subgraph matching.
  - Reactors now support specification of T, P, X ranges. Different conditions are sampled on each iteration to optimally capture the full parameter space.
  - New termination type! Termination rate ratio stops the simulation when the characteristic rate falls to the specified fraction of the maximum characteristic rate. Currently not recommended for systems with two-stage ignition.
  - New resonance transitions implemented for species with lone pairs (particularly N and S containing species). A filtration algorithm was also added to select only the most representative structures.
  - Formal support for trimolecular reaction families.
  - New isotopes module allows post-processing of RMG mechanisms to generate a mechanism with isotopic labeling.
- **Changes:**
  - Library reactions can now be integrated into RMG pdep networks if the new elementary\_high\_p attribute is True
  - Library reactions may be duplicated by pdep reactions if the new allow\_pdep\_route attribute is True
  - Jupyter notebook for adding new training reactions has been revamped and is now located at `ipython/kinetics_library_to_training.ipynb`
  - Syntax for recommended families has changed to set notation instead of dictionaries, old style still compatible
  - Ranking system for database entries expanded to new 0-11 system from the old 0-5 system
  - Collision limit checking has been added for database entries
- **Cantherm:**
  - Improved support for MolPro output files

- Added iodine support
- Automatically read spin multiplicity from quantum output
- Automatically assign frequency scale factor for supported model chemistries
- Plot calculated rates and thermo by default
- New sensitivity analysis feature analyzes sensitivity of reaction rates to isomer/TS energies in pdep networks
- **Fixes:**
  - Properly update charges when creating product templates in reaction families
  - Excessive duplicate reactions from different resonance structures has been fixed (bug introduced in 2.1.3)
  - Fixed rate calculation for MultiPdepArrhenius objects when member rates have different plists
- **A more formal deprecation process is now being trialed. Deprecation warnings have been added to functions to be removed in version 2.3.0:**
  - All methods related to saving or reading RMG-Java databases and old-style adjacency lists
  - The group additivity method for kinetics estimation (unrelated to thermo group additivity)
  - The saveRestartPeriod option and the old method of saving restart files

#### 1.18.14 RMG-database Version 2.2.0

Date: July 5, 2018

- **Additions:**
  - New Intra\_R\_Add\_Exo\_Scission reaction family
  - New 1,2\_ShiftC reaction family
  - **New reaction families for peroxide chemistry in liquid systems**
    - \* Korcek\_step1\_cat
    - \* Bimolec\_Hydroperoxide\_Decomposition
    - \* Peroxyl\_Termination
    - \* Peroxyl\_Disproportionation
    - \* Baeyer-Villiger\_step1\_cat
    - \* Baeyer-Villiger\_step2
    - \* Baeyer-Villiger\_step2\_cat
  - Numerous new training reactions added to many families
- **Changes:**
  - New tree structure for Intra\_R\_Add\_Endocyclic with consideration for cyclic species
  - Multiple bond on ring is no longer allowed in Intra\_R\_Add\_Exocyclic and should react in Intra\_R\_Add\_Endocyclic instead
  - Entry ranks rescaled to new 0-11 ranking system
  - Global forbidden structures has been cleaned up, leading to significant performance improvement

- **Fixes:**
  - Corrected shape indices in NOx2018 transport library
  - Removed or corrected some kinetics entries based on collision limit check

### 1.18.15 RMG-Py Version 2.1.9

Date: May 1, 2018

- **Cantherm:**
  - Atom counts are no longer necessary in input files and are automatically determined from geometries
  - Custom atom energies can now be specified in input files
  - Removed atom energies for a few ambiguous model chemistries
  - Add atom energies for B3LYP/6-311+g(3df,2p)
- **Changes:**
  - Refactored molecule.parser and molecule.generator modules into molecule.converter and molecule.translator to improve code organization
  - SMILES generation now outputs canonical SMILES
  - Molecule.sortAtoms method restored for deterministic atom order
  - PDep reactions which match an existing library reaction are no longer added to the model
- **Fixes:**
  - Fix issue with reaction filter initiation when using seed mechanisms

### 1.18.16 RMG-database Version 2.1.9

Date: May 1, 2018

- **Chlorine:**
  - New Chlorinated\_Hydrocarbons thermo library
  - Added group additivity values and long distance corrections for chlorinated species
  - Added chlorine groups and training reactions to H\_Abstraction
- **Additions:**
  - New NOx2018 kinetics, thermo, and transport libraries
  - New N-S\_interactions kinetics library
  - New SulfurHaynes thermo library
  - Added species to SOxNOx thermo library from quantum calculations
- **Other changes:**
  - Renamed NOx and SOx kinetics libraries to PrimaryNitrogenLibrary and PrimarySulfurLibrary
  - S2O2, SOO2, SO2O2, and N2SH were globally forbidden due to inability to optimize geometries
- **Fixes:**
  - Corrected some A-factor units in Nitrogen\_Dean\_and\_Bozzelli kinetics library

### 1.18.17 RMG-Py Version 2.1.8

Date: March 22, 2018

- **New features:**
  - Chlorine and iodine atom types have been added, bringing support for these elements to RMG-database
  - Forbidden structures now support Molecule and Species definitions in addition to Group definitions
- **Changes:**
  - Reaction pair generation will now fall back to generic method instead of raising an exception
  - Removed sensitivity.py script since it was effectively a duplicate of simulate.py
  - Thermo jobs in Cantherm now output a species dictionary
  - Fitted atom energy corrections added for B3LYP/6-31g\*\*
  - Initial framework added for hydrogen bonding
  - Renamed molepro module and associated classes to molpro (MolPro) to match actual spelling of the program
  - Chemkin module is now cythonized to improve performance
- **Fixes:**
  - Allow delocalization of triradicals to prevent hysteresis in resonance structure generation
  - Fix reaction comment parsing issue with uncertainty analysis
  - Fix numerical issue causing a number of pressure dependent RMG jobs to crash
  - Template reactions from seed mechanisms are now loaded as library reactions if the original family is not loaded
  - Fix issues with degeneracy calculation for identical reactants

### 1.18.18 RMG-database Version 2.1.8

Date: March 22, 2018

- **Changes:**
  - Corrected name of JetSurf2.0 kinetics and thermo libraries to JetSurf1.0
  - Added actual JetSurf2.0 kinetics and thermo libraries
  - Updated thermo groups for near-aromatic radicals, including radical and polycyclic corrections

### 1.18.19 RMG-Py Version 2.1.7

Date: February 12, 2018

- **Charged atom types:**
  - Atom types now have a charge attribute to cover a wider range of species
  - New atom types added for nitrogen and sulfur groups
  - Carbon and oxygen atom types renamed following new valence based naming scheme
- **Ring perception:**

- Ring perception methods in the Graph class now use RingDecomposerLib
- This includes the `getSmallestSetOfSmallestRings` methods and a newly added `getRelevantCycles` method
- The set of relevant cycles is unique and generally more useful for chemical graphs
- This also fixes inaccuracies with the original SSSR method
- **Other changes:**
  - Automatically load reaction libraries when using a seed mechanism
  - Default kinetics estimator has been changed to rate rules instead of group additivity
  - Kinetics families can now be set to be irreversible
  - Model enlargement now occurs after each reactor simulation rather than after all of them
  - Updated bond additivity corrections for CBS-QB3 in Cantherm
- **Fixes:**
  - Do not print SMILES when raising `AtomTypeError` to avoid further exceptions
  - Do not recalculate thermo if a species already has it
  - Fixes to parsing of family names in seed mechanisms

### 1.18.20 RMG-database Version 2.1.7

Date: February 12, 2018

- **Charged atom types:**
  - Update adjlists with new atom types across the entire database
  - Added sulfur groups to all relevant kinetics families
  - New thermo group additivity values for sulfur/oxygen species
- **Additions:**
  - Benzene bonds can now react in `R_Addition_MultipleBond`
  - Many new training reactions and groups added in `R_Addition_MultipleBond`
  - New `Singlet_Val6_to_triplet` kinetics family
  - New Sulfur GlarborgBozzelli kinetics and thermo libraries
  - New Sulfur GlarborgMarshall kinetics and thermo libraries
  - New Sulfur GlarborgH2S kinetics and thermo libraries
  - New Sulfur GlarborgNS kinetics and thermo libraries
  - New NO<sub>x</sub> and NO<sub>x</sub>/LowT kinetics libraries
  - New SO<sub>x</sub> kinetics library
  - New BurcatNS thermo library
  - New SO<sub>x</sub>NO<sub>x</sub> thermo library
  - New `2+2_cycloaddition_CS` kinetics family
  - New `Cyclic_Thioether_Formation` kinetics family

- New Lai\_Hexylbenzene kinetics and thermo libraries
- **Changes:**
  - 1,2-Birad\_to\_alkene family is now irreversible
  - OxygenSingTrip kinetics library removed (replaced by Singlet\_Val6\_to\_triplet family)
  - Ozone is no longer forbidden
- **Fixes:**
  - Corrected adjlist for phenyl radical in JetSurf2.0 and USC-Mech-ii
  - Some singlet thermo groups relocated from radical.py to group.py

### 1.18.21 RMG-Py Version 2.1.6

Date: December 21, 2017

- **Model resurrection:**
  - Automatically attempts to save simulation after encountering a DASPK error
  - Adds species and reactions in order to modify model dynamics and fix the error
- **New features:**
  - Add functionality to read RCCSD(T)-F12 energies from MolPro log files
  - Add liquidReactor support to flux diagram generation
- **Other changes:**
  - Removed `rmgpy.rmg.model.Species` class and merged functionality into main `rmgpy.species.Species` class
  - Refactored parsing of RMG-generated kinetics comments from Chemkin files and fixed related issues
  - Refactored framework for generating reactions to reduce code duplication
  - Resonance methods renamed from `generateResonanceIsomers` to `generate_resonance_structures` across all modules
  - Raise `CpInf` to `Cphigh` for entropy calculations to prevent invalid results
- **Fixes:**
  - Update sensitivity analysis to use `ModelSettings` and `SimulatorSettings` classes introduced in v2.1.5
  - Fixed `generate_reactions` methods in `KineticsDatabase` to be directly usable again
  - Fixed issues with aromaticity perception and generation of aromatic resonance structures

### 1.18.22 RMG-database Version 2.1.6

Date: December 21, 2017

- **Additions:**
  - New training reactions added for [NH2] related H\_Abstractions
  - 14 new kinetics libraries related to aromatics formation (see RMG-database #222 for details)
- **Other changes:**
  - Removed some global forbidden groups which are no longer needed
  - Forbid CO and CS biradicals
  - Updated lone\_electron\_pair\_bond family and removed from recommended list
- **Fixes:**
  - Fixed unit errors in some H\_Abstraction and R\_Addition\_MultipleBond depositories

### 1.18.23 RMG-Py Version 2.1.5

Date: October 18, 2017

- **New bicyclic formula:**
  - Estimates polycyclic corrections for unsaturated bicyclics by adjusting the correction for the saturated version
  - Can provide a decent estimate in many cases where there is not an exact match
- **Other changes:**
  - Refactored simulation algorithm to properly add multiple objects per iteration
  - Print equilibrium constant and reverse rate coefficient values when using Cantherm to calculate kinetics
  - Speed up degeneracy calculation by reducing unnecessary operations
- **Fixes:**
  - Loosen tolerance for bond order identification to account for floating point error
  - Fixed uncertainty analysis to allow floats as bond orders
  - Fixed some comment parsing issues in uncertainty analysis
  - Added product structure atom relabeling for families added in RMG-database v2.1.5
  - Fixed issue with automatic debugging of kinetics errors due to forbidden structures

### 1.18.24 RMG-database Version 2.1.5

Date: October 18, 2017

- **Additions:**
  - New thermo groups added for species relevant in cyclopentadiene and natural gas pyrolysis
  - Added C2H4+O\_Klipp2017 kinetics library
- **Fixes:**
  - Prevent charged carbenes from reacting in Singlet\_Carbene\_Intra\_Disproportionation



- Updated H\_Abstraction rates in ethylamine library and corresponding training reactions

### 1.18.25 RMG-Py Version 2.1.4

Date: September 08, 2017

- **Accelerator tools:**

- Dynamics criterion provides another method to expand the mechanism by adding reactions to the core
- Surface algorithm enables better control of species movement to the core when using the dynamics criterion
- Multiple sets of model parameters can now be specified in a input file to allow different stages of model generation
- A species number termination criterion can now be set to limit model size
- Multiple items can now be added per iteration to speed up model construction
- New ModelSettings and SimulatorSettings classes for storing input parameters

- **New features:**

- Kinetics libraries can now be automatically generated during RMG runs to be used as seeds for subsequent runs
- Loading automatically generated seed mechanisms recreates the original template reaction objects to allow restarting runs from the seed mechanism
- Carbene constraints can now be set in the species constraint block using maxSingletCarbenes and maxCarbeneRadicals
- Chirality is now considered for determining symmetry numbers
- Thermodynamic pruning has been added to allow removal of edge species with unfavorable free energy (beta)

- **Other changes:**

- RMG-Py exception classes have been consolidated in the rmgpy.exceptions module
- Species labels will now inherit the label from a matched thermo library entry
- Sensitivity analysis is now available for LiquidReactor

- **Fixes:**

- Fixed sensitivity analysis following changes to the simulate method
- Add memory handling when generating collision matrix for pressure dependence
- Improved error checking for MOPAC
- Prevent infinite loops when retrieving thermo groups

- **Known issues:**

- Seed mechanisms cannot be loaded if the database settings are different from the original ones used to generate the seed

### 1.18.26 RMG-database Version 2.1.4

Date: September 08, 2017

- **New kinetics families for propargyl recombination route to benzene:**
  - Singlet\_Carbene\_Intra\_Disproportionation
  - Intra\_5\_membered\_conjugated\_C=C\_C=C\_addition
  - Intra\_Diels\_alder\_monocyclic
  - Concerted\_Intra\_Diels\_alder\_monocyclic\_1,2\_shift
  - Intra\_2+2\_cycloaddition\_Cd
  - Cyclopentadiene\_scission
  - 6\_membered\_central\_C-C\_shift
- **Renamed kinetics families:**
  - Intra\_Diels\_Alder → Intra\_Retro\_Diels\_alder\_bicyclic
  - H\_shift\_cyclopentadiene → Intra\_ene\_reaction
- **Other additions:**
  - Klippenstein\_Glarborg2016 kinetics and thermo libraries
  - Group additivity values added for singlet carbenes, which are no longer forbidden

### 1.18.27 RMG-Py Version 2.1.3

Date: July 27, 2017

- **Thermo central database:**
  - Framework for tracking and submitting species to a central database have been added
  - Following species submission, the central database will queue and submit quantum chemistry jobs for thermochemistry calculation
  - This is an initial step towards self-improving thermochemistry prediction
- **Rotor handling in Cantherm:**
  - Free rotors can now be specified
  - Limit number of terms used when fitting hinder rotor scans
  - Fixed bug with ZPE calculation when using hindered rotors
- **New reaction degeneracy algorithm:**
  - Use atom ID's to distinguish degenerate reactions from duplicates due to other factors
  - Degeneracy calculation now operates across all families rather than within each separately
  - Multiple transition states are now identified based on template comparisons and kept as duplicate reactions
- **Nodal distances:**
  - Distances can now be assigned to trees in reaction families
  - This enables better rate averages with multiple trees

- Fixed bug with finding the closest rate rule in the tree
- **New features:**
  - Added methods for automatically writing RMG-database files
  - New symmetry algorithm improves symmetry number calculations for resonant and cyclic species
  - Group additivity algorithm updated to apply new long distance corrections
  - Specific colliders can now be specified for pressure-dependent rates
  - Very short superminimal example added (hydrogen oxidation) for checking basic RMG operation
  - Cantera now outputs a Chemkin file which can be directly imported into Chemkin
- **Fixes:**
  - Fixed bug with negative activation energies when using Evans-Polanyi rates
  - Fixed walltime specification from command line when running RMG
  - Fixes and unit tests added for diffusionLimited module
- **Known issues:**
  - The multiple transition state algorithm can result in undesired duplicate reactions for reactants with multiple resonance structures

### 1.18.28 RMG-database Version 2.1.3

Date: July 27, 2017

- **Long-distance interaction thermo corrections:**
  - The gauche and int15 group files have been replaced by longDistanceInteraction\_noncyclic
  - New corrections for cyclic ortho/meta/para interactions are now available in longDistanceInteraction\_cyclic
- **Changes:**
  - Oa\_R\_Recombination family renamed to Birad\_R\_Recombination
  - More training reactions added for sulfur species in H\_Abstraction
  - RMG-database tests have been moved to RMG-Py

### 1.18.29 RMG-Py Version 2.1.2

Date: May 18, 2017

- **Improvements:**
  - New nitrogen atom types
  - Kinetics libraries can now be specified as a list of strings in the input file
  - New script to generate output HTML locally: generateChemkinHTML.py
  - New kekulization module replaces RDKit for generating Kekule structures
  - Benzene bonds can now be reacted in reaction families
  - Removed cantherm.geometry module due to redundancy with statmech.conformer

- **Fixes:**
  - Reaction direction is now more deterministic after accounting for floating point error
  - Multiple bugs with resonance structure generation for aromatics have been addressed

### 1.18.30 RMG-database Version 2.1.2

Date: May 18, 2017

- **Nitrogen improvements:**
  - Added ethylamine kinetics library
  - Updated group additivity values for nitrogen species
  - Added rate rules and training reactions for nitrogen species
- **Additions:**
  - New CO\_Disproportionation family
  - Added CurranPentane kinetics and thermo libraries
- **Fixes:**
  - Corrected some rates in FFCM1(-) to use MultiArrhenius kinetics
  - Corrected a few adjlists in FFCM1(-)

### 1.18.31 RMG-Py Version 2.1.1

Date: April 07, 2017

- **Uncertainty analysis:**
  - Local and global uncertainty analysis now available for RMG-generated models
  - Global uncertainty analysis uses MIT Uncertainty Quantification library, currently only supported on Linux systems
  - Examples for each module are available in localUncertainty.ipynb and globalUncertainty.ipynb
- **Fixes:**
  - Clar structure generation no longer intercepts signals
  - Fixes to SMILES generation
  - Fix default spin state of [CH]

### 1.18.32 RMG-database Version 2.1.1

Date: April 07, 2017

- **Additions:**
  - More species added to FFCM1(-) thermo library
- **Changes:**
  - Improved handling of excited species in FFCM1(-) kinetics library

- Replaced Klippenstein H<sub>2</sub>O<sub>2</sub> kinetics and thermo libraries with BurkeH<sub>2</sub>O<sub>2</sub>inN<sub>2</sub> and BurkeH<sub>2</sub>O<sub>2</sub>inArHe
- **Fixes:**
  - Corrected adjlists for some species in JetSurf2.0 kinetics and thermo libraries (also renamed from JetSurf0.2)
  - Correct multiplicities for [C] and [CH] in multiple libraries ([C] from 5 to 3, [CH] from 4 to 2)

### 1.18.33 RMG-Py Version 2.1.0

Date: March 07, 2017

- **Clar structure generation**
  - optimizes the aromatic isomer representations in RMG
  - lays the foundations for future development of poly-aromatic kinetics reaction families
- **Flux pathway analysis**
  - introduces an ipython notebook for post-generation pathway analysis (`ipython.mechanism_analyzer.ipynb`)
  - visualizes reactions and provides flux statistics in a more transparent way
- **Cantera mechanism**
  - automatically writes cantera version of RMG-generated mechanism at the end of RMG jobs
- **Fixes bugs**
  - upgrades pruning to fix new memory leaks introduced by recent functionalities
  - fixes the bug of duplicated species creation caused by `getThermoData` removing isomers unexpectedly
  - fixes restart file generation and parsing problems and users can choose restart mode again
  - upgrades bicyclic decomposition method such that more deterministic behaviors are ensured
  - change bond order type to float from string to improve RMG's symmetry calculation for species with multiple resonance structures

### 1.18.34 RMG-database Version 2.1.0

Date: March 07, 2017

- **Several new kinetics libraries added**
  - FFCM-1
  - JetSurF 0.2
  - Chernov\_aromatic\_only
  - Narayanaswamy\_aromatic\_only
  - 1989\_Stewart\_2CH<sub>3</sub>\_to\_C<sub>2</sub>H<sub>5</sub>\_H
  - 2005\_Senosaiin\_OH\_C<sub>2</sub>H<sub>2</sub>
  - 2006\_Joshi\_OH\_CO

- C6H5\_C4H4\_Mebel
- c-C5H5\_CH3\_Sharma
- **Several new thermochemistry libraries added**
  - FFCM-1
  - JetSurF 0.2
  - Chernov\_aromatic\_only
  - Narayanaswamy\_aromatic\_only
- **Improved kinetics tree accessibility**
  - adds database tests ensuring groups in the tree to be accessible
  - improves definitions of group structures in the kinetics trees to ensure accessibility
- New oxygenates thermo groups are added based Paraskeva et al.
- **Improved database tools**
  - `convertKineticsLibraryToTrainingReactions.ipynb` now can visualize groups of matched rate rules that training reactions hit
  - `exportKineticsLibrarytoChemkin.py` and `importChemkinLibrary.py` add more logging information on reaction sources

### 1.18.35 RMG-Py Version 2.0.0

Date: September 16, 2016

This release includes several milestones of RMG project:

- **Parallelization finally introduced in RMG:**
  - Generates reactions during `enlarge` step in parallel fashion (`rmgpy.rmg.react`)
  - Enables concurrent computing for QMTP thermochemistry calculations (`rmgpy.thermo.thermoengine`)
  - Instructions of running RMG parallel mode can be found [here for SLURM scheduler](#) and [here for SGE scheduler](#).
- **Polycyclic thermochemistry estimation improved:**
  - Extends group additivity method for polycyclics and estimates polycyclics of any large sizes by a heuristic method (bicyclics decomposition)
- **New tree averaging for kinetics:**
  - Fixes previous issue of incomplete generation of cross-level rate rules
  - Implements Euclidean distance algorithm for the selection of the best rate rules to use in `estimateKinetics`
  - Streamlines storage of kinetics comments for averaged rules, which can be analyzed by `extractSourceFromComments`
- **Database entry accessibility tests:**
  - Adds entry accessibility tests for future entries (`testing.databaseTest`)
- **Fixes bugs**

- fluxdiagram generation is now fixed, one can use it to generate short video of fluxdigram evolution
- mac environment yml file is introduced to make sure smooth RMG-Py installation and jobs on mac
- fixes failure of `checkForExistingSpecies` for polyaromatics species
- fixes execution failure when both pruning and pDep are turned on
- fixes pDep irreversible reactions
- fixes issue of valency of Cbf atom by dynamic benzene bond order assignment

### 1.18.36 RMG-database Version 2.0.0

Date: September 16, 2016

In conjunction with the release of RMG-Py v2.0.0, an updated package for the RMG-database has also been released. This release brings some new additions and fixes:

- **Polycyclic thermochemistry estimation improved:**
  - polycyclic database reorganized and more entries added in systematic way (`input.thermo.groups.polycyclic`)
- **Database entry accessibility tests:**
  - Fixes existing inaccessible entries in solvation/statmech/thermo of RMG-database

### 1.18.37 RMG-Py Version 1.0.4

Date: March 28, 2016

- **Cantera support in RMG (`rmgpy.tools.canteraModel`):**
  - Provides functions to help simulate RMG models using Cantera.
  - Has capability to generate cantera conditions and convert CHEMKIN files to cantera models, or use RMG to directly convert species and reactions objects to Cantera objects.
  - Demonstrative example found in `ipython/canteraSimulation.ipynb`
- **Module for regression testing of models generated by RMG (`rmgpy.tools.observableRegression`):**
  - Helps identify differences between two versions of models generated by RMG, using the “observables” that the user cares about.
- **Automatic plotting of simulations and sensitivities when generating models (`rmgpy.tools.plot`):**
  - Contains plotting classes useful for plotting simulations, sensitivities, and other data
  - Automatic plotting of simulations in the job’s solver folder when `saveSimulationProfiles` is set to True in the input file.
  - Sensitivities for top 10 most sensitivie reactions and thermo now plotted automatically and stored in the solver folder.
- **Improved thermochemistry estimation (mostly for cyclics and polycyclics)**
  - Add rank as an additional attribute in thermo database entries to determine trustworthiness
- **Bug fixes:**
  - Training reactions now load successfully regardless of `generateSpeciesConstraints` parameters
  - Transport data is now saved correctly to CHEMKIN `tran.dat` file and also imports successfully

- Fixes appending of reactions to CHEMKIN file when reaction libraries are desired to be appended to output
- Fixes writing of csv files for simulation and sensitivity results in Windows
- Fixes `Reaction.draw()` function to draw the entire reaction rather than a single species

### 1.18.38 RMG-Py Version 1.0.3

Date: February 4, 2016

This mini release contains the following updates:

- Pdep convergence issues in RMG-Py v1.0.2 are now fixed.
- RMG-database version information and anaconda binary version information is now recorded in RMG log file.

### 1.18.39 RMG-Py Version 1.0.2

Date: January 29, 2016

This new release adds several new features and bug fixes.

- Windows users can rejoice: RMG is now available in binary format on the Anaconda platform. Building by source is also much easier now through the Anaconda managed python environment for dependencies. See the updated [Installation Page](#) for more details
- Reaction filtering for speeding up model generation has now been added. It has been shown to speed up model convergence by 7-10x. See more details about how to use it in your RMG job [here](#). Learn more about the theory and algorithm on the [Rate-based Model Enlarging Algorithm](#) page.
- The RMG *native scripts* are now organized under the `rmgpy.tools` submodule for developer ease and better extensibility in external scripts.
- InChI conversion is now more robust for singlets and triplets, and augmented InChIs and InChI keys are now possible with new radical electron, lone pair, and multiplicity flags.
- Output HTML for visualizing models are now cleaned up and also more functional, including features to display thermo comments, display enthalpy, entropy, and free energy of reaction, as well as filter reactions by species. You can use this new visualization format either by running a job in RMG v1.0.2 or revisualizing your CHEMKIN file and species dictionary using the [visualization web tool](#).

### 1.18.40 RMG-database Version 1.0.2

Date: January 29, 2016

In conjunction with the release of RMG-Py v1.0.2, an updated package for the RMG-database has also been released. This release brings some new additions and fixes:

- New group additivity values for oxitene, oxerene, oexpane, and furan ring groups
- **Improvements to sulfur chemistry:**
  - Restructuring of radical trees in the kinetics families `SubstitutionS` and `intra_substitutionCS_cyclization`
  - A reaction library for di-tert-butyl sulfide



- Improvements for the `R_Addition_Multiple_Bond` kinetics family through new rate rules for the addition of allyl radical to double bonds in ethene, propene, and butene-like compounds, based on CBS-QB3 estimates from K. Wang, S.M. Villano, A.M. Dean, “Reactions of allylic radicals that impact molecular weight growth kinetics”, *PCCP*, 6255-6273 (2015).
- Several new thermodynamic and kinetics libraries for molecules associated with the pyrolysis of cyclopentadiene in the presence of ethene, based off of calculations from the paper A.G. Vandeputte, S.S. Merchant, M.R. Djokic, K.M. Van Geem, G.B. Marin, W. H. Green, “Detailed study of cyclopentadiene pyrolysis in the presence of ethene: realistic pathways from C<sub>5</sub>H<sub>5</sub> to naphthalene” (2016)

## 1.19 Credits

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- genindex
- modindex
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## ARKANE USER'S GUIDE

### 2.1 Introduction

**Arkane** (Automated Reaction Kinetics and Network Exploration) is a tool for computing the thermodynamic properties of chemical species and high-pressure-limit rate coefficients for chemical reactions using the results of a quantum chemistry calculation. Thermodynamic properties are computed using the rigid rotor-harmonic oscillator approximation with optional corrections for hindered internal rotors. Kinetic parameters are computed using canonical transition state theory with optional tunneling correction.

Arkane can also estimate pressure-dependent phenomenological rate coefficients  $k(T, P)$  for unimolecular reaction networks of arbitrary complexity. The approach is to first generate a detailed model of the reaction network using the one-dimensional master equation, then apply one of several available model reduction methods of varying accuracy, speed, and robustness to simplify the detailed model into a set of phenomenological rate coefficients. The result is a set of  $k(T, P)$  functions suitable for use in chemical reaction mechanisms. More information is available at [Allen et al.](#).

Arkane is developed and distributed as part of [RMG-Py](#), but can be used as a stand-alone application for Thermochemistry, Transition State Theory, and Master Equation chemical kinetics calculations.

Arkane is written in the [Python](#) programming language to facilitate ease of development, installation, and use.

Additional theoretical background can be found at [RMG's Theory Guide](#).

#### 2.1.1 License

Arkane is provided as free, open source code under the terms of the [MIT/X11 License](#). The full, official license is reproduced below

```
Copyright (c) 2002-2022 Prof. William H. Green (whgreen@mit.edu),  
Prof. Richard H. West (r.west@neu.edu) and the RMG Team (rmg_dev@mit.edu)
```

```
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## 2.2 Installation

### 2.2.1 Installing Arkane

Arkane can be obtained by installing the [RMG-Py](#) software, which includes all necessary dependencies.

Instructions to install RMG-Py can be found at the [RMG-Py Installation page](#).

Note that you'll need to choose between the Basic User or Developer installation instructions that are specific to your operating system. Modifying Arkane source code will require Developer installation. If you are only looking to run the code, the Basic User installation will work.

### 2.2.2 Installing Q2DTor

Q2DTor is a software for calculating the partition functions and thermodynamic properties of molecular systems with two or more torsional modes developed by David Ferro Costas ([david.ferro@usc.es](mailto:david.ferro@usc.es)) and Antonio Fernandez Ramos ([qf.ramos@usc.es](mailto:qf.ramos@usc.es)) at the Universidade de Santiago de Compostela. Arkane can integrate Q2DTor to compute the quantum mechanical partition function of 2D rotors.

For use of Q2DTor and HinderedRotor2D within Arkane please cite: D. Ferro-Costas, M. N. D. S. Cordeiro, D. G. Truhlar, A. Fernández-Ramos, *Comput. Phys. Commun.* 232, 190-205, 2018.

To install a Q2DTor version compatible with RMG run in the RMG-Py directory:

```
make q2dtor
```

## 2.3 Creating Input Files

### 2.3.1 Syntax

The format of Arkane input files is based on Python syntax. In fact, Arkane input files are valid Python source code, and this is used to facilitate reading of the file.

Each section is made up of one or more function calls, where parameters are specified as text strings, numbers, or objects. Text strings must be wrapped in either single or double quotes.

The following is a list of all the components of a Arkane input file for thermodynamics and high-pressure limit kinetics computations:

Component	Description
modelChemistry	Level of theory from quantum chemical calculations, see Model Chemistry table below
author	Author's name. Used when saving statistical mechanics properties as a .yaml file.
atomEnergies	Dictionary of atomic energies at modelChemistry level
frequencyScaleFactor	Reference by which to scale all frequencies
useHinderedRotors	True (by default) if hindered rotors are used, False if not
useAtomCorrections	True (by default) if atom corrections are used, False if not
useBondCorrections	True if bond corrections are used, False (by default) if not
bondCorrectionType	Petersson-type (default) or 'm' for Melius-type bond additivity corrections
useIsodesmicReactions	Isodesmic reactions are used to apply corrections. Will automatically turn on atom corrections and disable bond corrections
referenceSets	A list of reference sets to use for isodesmic reactions. By default if left blank only the main reference set is used, which is the recommended. All reference sets are located at RMG-database/input/reference_sets/
species	Contains parameters for non-transition states
transitionStates	Contains parameters for transition state(s)
reaction	Required for performing kinetic computations
statmech	Loads statistical mechanics parameters
thermo	Performs a thermodynamics computation
kinetics	Performs a high-pressure limit kinetic computation

For pressure dependent kinetics output, the following components are necessary:

Component	Description
network	Divides species into reactants, isomers, products and bath gases
pressureDependence	Defines parameters necessary for solving master equation

## 2.3.2 Model Chemistry

The first item in the input file should be a modelChemistry assignment with a string describing the model chemistry. The modelChemistry could either be in a *single point // frequency* format, e.g., *CCSD(T)-F12a/aug-cc-pVTZ//B3LYP/6-311++G(3df,3pd)*, just the *single point*, e.g., *CCSD(T)-F12a/aug-cc-pVTZ*, or a composite method, e.g., *CBS-QB3*.

Alternatively, modelChemistry can be specified using a LevelOfTheory or CompositeLevelOfTheory object. The basic syntax for LevelOfTheory is:

```
LevelOfTheory(
    method='B3LYP',
    basis='6-311++G(3df,3pd)'
)
```

See arkane/modelchem.py for additional options (e.g., software, solvent). Note that the software generally does not have to be specified because it is inferred from the provided quantum chemistry logs. An example CompositeLevelOfTheory is given by:

```
CompositeLevelOfTheory(
    freq=LevelOfTheory(
        method='B3LYP',
        basis='6-311++G(3df,3pd)'
    )
)
```

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```

energy=LevelOfTheory(
    method='CCSD(T)-F12',
    basis='aug-cc-pVTZ'
)
)

```

There are some methods that require the software to be specified. Currently, it is not possible to infer the software for such methods directly from the log files because Arkane requires the software prior to reading the log files. The methods for which this is the case are listed in the RMG-database in `input/quantum_corrections/lot_constraints.yml`.

Arkane uses the single point level to adjust the computed energies to the usual gas-phase reference states by applying atom and spin-orbit coupling energy corrections. Additionally, bond additivity corrections OR isodesmic reactions corrections can be applied (but not both). This is particularly important for `thermo()` calculations (see below). Note that the user must specify under the `species()` function the type and number of bonds for Arkane to apply bond additivity corrections. The frequency level is used to determine the frequency scaling factor if not given in the input file, and if it exists in Arkane (see the below table for existing frequency scaling factors). The example below specifies CBS-QB3 as the model chemistry:

```
modelChemistry = "CBS-QB3"
```

Also, the atomic energies at the single point level of theory can be directly specified in the input file by providing a dictionary of these energies in the following format:

```

atomEnergies = {
    'H': -0.499818,
    'C': -37.78552,
    'N': -54.520543,
    'O': -74.987979,
    'S': -397.658253,
}

```

The table below shows which model chemistries have atomization energy corrections (AEC), bond corrections (BC), and spin orbit corrections (SOC). It also lists which elements are available for a given model chemistry.

Model Chemistry	AEC	BC	SOC	Freq Scale	Supported Elements
'CBS-QB3'	v	v	v	v (0.990)	H, C, N, O, P, S
'CBS-QB3-Paraskevas'	v	v	v	v (0.990)	H, C, N, O, P, S
'G3'	v		v		H, C, N, O, P, S
'M08S0/MG3S*'	v		v		H, C, N, O, P, S
'M06-2X/cc-pVTZ'	v		v	v (0.955)	H, C, N, O, P, S
'Klip_1'	v		v		H, C, N, O
'Klip_2' uses $QCI(tz,qz)$ values	v		v		H, C, N, O
'Klip_3' uses $QCI(dz,qz)$ values	v		v		H, C, N, O
'Klip_2_cc' uses $CCSD(T)(tz,qz)$ values	v		v		H, C, O
'CCSD-F12/cc-pVDZ-F12'	v		v	v (0.947)	H, C, N, O
'CCSD(T)-F12/cc-pVDZ-F12_H-TZ'	v		v		H, C, N, O
'CCSD(T)-F12/cc-pVDZ-F12_H-QZ'	v		v		H, C, N, O
'CCSD(T)-F12/cc-pVnZ-F12', $n = D, T$	v	v	v	v	H, C, N, O, F, S, Cl
'CCSD(T)-F12/cc-pVQZ-F12'	v	v	v	v	H, C, N, O, S
'CCSD(T)-F12/cc-pVDZ-F12_noscale'	v		v		H, C, N, O
'CCSD(T)-F12/cc-pCVnZ-F12', $n = D, T, Q$	v		v	v	H, C, N, O

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Table 1 – continued from previous page

Model Chemistry	AEC	BC	SOC	Freq Scale	Supported Elements
'CCSD(T) - F12/aug-cc-pVnZ', $n = D, T, Q$	v		v	v	H, C, N, O, S
'CCSD(T) - F12/cc-pVTZ-f12(-pp),	v		v		H, C, N, O, S, I
'CCSD(T)/aug-cc-pVTZ(-pp),	v		v		H, C, O, S, I
'B-CCSD(T) - F12/cc-pVnZ-F12', $n = D, T, Q$	v		v		H, C, N, O, S
'B-CCSD(T) - F12/cc-pCVnZ-F12', $n = D, T, Q$	v		v		H, C, N, O
'B-CCSD(T) - F12/aug-cc-pVnZ', $n = D, T, Q$	v		v		H, C, N, O
'G03_PBEPBE_6-311++g_d_p'	v		v		H, C, N, O
'MP2_rmp2_pVnZ', $n = D, T, Q$	v		v	v	H, C, N, O
'FCI/cc-pVnZ', $n = D, T, Q$	v		v		C
'BMK/cbsb7'	v	v	v		H, C, N, O, P, S
'BMK/6-311G(2d,d,p)'	v	v	v		H, C, N, O, P, S
'B3LYP/6-311+G(3df,2p)'	v	v	v	v (0.967)	H, C, N, O, P, S
'B3LYP/6-31G(d,p)'	v	v		v (0.961)	H, C, O, S
'MRCI+Davidson/aug-cc-pV(T+d)Z'	v		v		H, C, N, O, S
'wb97x-d/aug-cc-pvtz'	v		v		H, C, N, O
'wb97x-d3/def2-tzvp'	v	v	v	v (0.984)	H, C, N, O, F, S, Cl, Br
'wb97m-v/def2-tzvpd'	v		v	v (1.002)	H, C, N, O, F, S, Cl, Br
'b97d-3/def2-msvp'	v	v	v	v (1.014)	H, C, N, O, F, S, Cl, Br

Notes:

- The 'CBS-QB3-Paraskevas' model chemistry is identical to 'CBS-QB3' except for BCs for C/H/O bonds, which are from Paraskevas et al. (DOI: 10.1002/chem.201301381) instead of Petersson et al. (DOI: 10.1063/1.477794). Beware, combining BCs from different sources may lead to unforeseen results.
- In 'M08S0/MG3S\*' the grid size used in the [QChem] electronic structure calculation utilizes 75 radial points and 434 angular points.
- Refer to paper by Goldsmith et al. (Goldsmith, C. F.; Magoon, G. R.; Green, W. H., *Database of Small Molecule Thermochemistry for Combustion. J. Phys. Chem. A* 2012, 116, 9033-9057) for definition of 'Klip\_2' ( $QCI(tz,qz)$ ) and 'Klip\_3' ( $QCI(dz,qz)$ ).

If a model chemistry other than the ones in the above table is used, then the user should supply the corresponding atomic energies (using `atomEnergies`) to get meaningful results. Bond corrections would not be applied in this case.

If a model chemistry or atomic energies are not available, then a kinetics job can still be run by setting `useAtomCorrections` to `False`, in which case Arkane will not raise an error for unknown elements. The user should be aware that the resulting energies and thermodynamic quantities in the output file will not be meaningful, but kinetics and equilibrium constants will still be correct.

### 2.3.3 Frequency Scale Factor

Frequency scale factors are empirically fit to experiment for different `modelChemistry`. Refer to NIST website for values (<http://cccbdb.nist.gov/vibscalejust.asp>). For CBS-QB3, which is not included in the link above, `frequencyScaleFactor` = 0.99 according to Montgomery et al. (*J. Chem. Phys.* 1999, 110, 2822-2827). The frequency scale factor is automatically assigned according to the supplied `modelChemistry`, if available (see above table). If not available automatically and not specified by the user, it will be assumed a unity value.

## 2.3.4 Species

Each species of interest must be specified using a `species()` function, which can be input in three different ways, discussed in the separate subsections below:

1. By pointing to the output files of quantum chemistry calculations, which Arkane will parse for the necessary molecular properties.
2. By directly entering the molecular properties.
3. By pointing to an appropriate YAML file.

Within a single input file, any of the above options may be used for different species.

### Option #1: Automatically Parse Quantum Chemistry Calculation Output

For this option, the `species()` function only requires two parameters, as in the example below:

```
species('C2H6', 'C2H6.py',
       structure = SMILES('CC'))
```

The first required parameter ('C2H6' above) is the species label, which can be referenced later in the input file and is used when constructing output files. For chemkin output to run properly, limit names to alphanumeric characters with approximately 13 characters or less.

The second parameter ('C2H6.py' above) points to the location of another python file containing details of the species. This file will be referred to as the species input file. The third parameter ('structure = SMILES('CC')' above) gives the species structure (either SMILES, adjacencyList, or InChI could be used). The structure parameter isn't necessary for the calculation, however if it is not specified a .yaml file representing an ArkaneSpecies will not be generated.

The species input file accepts the following parameters:

Parameter	Re-quired?	Description
bonds	op-tional	Type and number of bonds in the species
linear	op-tional	True if the molecule is linear, False if not
externalSymmetry	op-tional	The external symmetry number for rotation
spinMultiplicity	yes	The ground-state spin multiplicity (degeneracy)
opticalIsomers	op-tional	The number of optical isomers of the species
energy	yes	The ground-state 0 K atomization energy in Hartree (without zero-point energy) <b>or</b> The path to the quantum chemistry output file containing the energy
geometry	op-tional	The path to the quantum chemistry output file containing the optimized geometry
frequencies	yes	The path to the quantum chemistry output file containing the computed frequencies
rotors	op-tional	A list of <code>HinderedRotor()</code> and/or <code>FreeRotor()</code> objects describing the hindered/free rotors

The types and number of atoms in the species are automatically inferred from the quantum chemistry output and are used to apply atomization energy corrections (AEC) and spin orbit corrections (SOC) for a given `modelChemistry` (see [Model Chemistry](#)). If not interested in accurate thermodynamics (e.g., if only using `kinetics()`), then atom corrections can be turned off by setting `useAtomCorrections` to `False`.

The `bonds` parameter is used to apply bond additivity corrections (BACs) for a given `modelChemistry` if using Petersson-type BACs (`bondCorrectionType` = 'p'). If the species' structure is specified in the Arkane input file,



then the *bonds* attribute can be automatically populated. Including this parameter in this case will overwrite the automatically generated bonds. When using Melius-type BACs (`bondCorrectionType = 'm'`), specifying bonds is not required because the molecular connectivity is automatically inferred from the output of the quantum chemistry calculation. For a description of Petersson-type BACs, see Petersson et al., J. Chem. Phys. 1998, 109, 10570-10579. For a description of Melius-type BACs, see Anantharaman and Melius, J. Phys. Chem. A 2005, 109, 1734-1747.

Allowed bond types for the *bonds* parameter are, e.g., 'C-H', 'C-C', 'C=C', 'N-O', 'C=S', 'O=O', 'C#N'...

'O=S=O' is also allowed.

The order of elements in the bond correction label is important. The first atom should follow this priority: 'C', 'N', 'O', 'S', 'P', and 'H'. For bonds, use -/=/# to denote a single/double/triple bond, respectively. For example, for formaldehyde we would write:

```
bonds = {'C=O': 1, 'C-H': 2}
```

The parameter *linear* only needs to be specified as either True or False. The parameters *externalSymmetry*, *spinMultiplicity* and *opticalIsomers* only accept integer values. Note that *externalSymmetry* corresponds to the number of unique ways in which the species may be rotated about an axis (or multiple axes) and still be indistinguishable from its starting orientation (reflection across a mirror plane does not count as rotation about an axis). For ethane, we would write:

```
linear = False
externalSymmetry = 6
spinMultiplicity = 1
opticalIsomers = 1
```

The energy parameter is a dictionary with entries for different *modelChemistry*. The entries can consist of either floating point numbers corresponding to the 0 K atomization energy in Hartree (without zero-point energy correction), or they can specify the path to a quantum chemistry calculation output file that contains the species's energy. For example:

```
energy = {
    'CBS-QB3': Log('ethane_cbsqb3.log'),
    'Klip_2': -79.64199436,
}
```

In this example, the CBS-QB3 energy is obtained from a Gaussian log file, while the Klip\_2 energy is specified directly. The energy used will depend on what *modelChemistry* was specified in the input file. Arkane can parse the energy from a Gaussian, Molpro, or QChem log file, all using the same *Log* class, as shown below. The first (and required) argument for the *Log* class is the path to the log file. Optionally, a second keyword argument *check\_for\_errors=False* can be provided that will prevent Arkane from raising an exception if it finds an error in the QM job based on common phrases from the log file.

The input to the remaining parameters, *geometry*, *frequencies* and *rotors*, will depend on if hindered/free rotors are included. If *geometry* is not set, then Arkane will read the geometry from the *frequencies* file. Both cases are described below.

### Without Hindered/Free Rotors

In this case, only geometry and frequencies need to be specified, and they can point to the same or different quantum chemistry calculation output files. The geometry file contains the optimized geometry, while the frequencies file contains the harmonic oscillator frequencies of the species in its optimized geometry. For example:

```
geometry = Log('ethane_cbsqb3.log')  
  
frequencies = Log('ethane_freq.log')
```

In summary, in order to specify the molecular properties of a species by parsing the output of quantum chemistry calculations, without any hindered/free rotors, the `species()` function in the input file should look like the following example:

```
species('C2H6', 'C2H6.py')
```

and the species input file (C2H6.py in the example above) should look like the following:

```
bonds = {  
    'C-C': 1,  
    'C-H': 6,  
}  
  
linear = False  
  
externalSymmetry = 6  
  
spinMultiplicity = 1  
  
opticalIsomers = 1  
  
energy = {  
    'CBS-QB3': Log('ethane_cbsqb3.log'),  
    'Klip_2': -79.64199436,  
}  
  
geometry = Log('ethane_cbsqb3.log')  
  
frequencies = Log('ethane_freq.log')
```

### With Hindered/Free Rotors

In this case, geometry, frequencies and rotors need to be specified. The geometry and frequencies parameters must point to the **same** quantum chemistry calculation output file in this case. For example:

```
geometry = Log('ethane_freq.log')  
  
frequencies = Log('ethane_freq.log')
```

The geometry/frequencies log file must contain both the optimized geometry and the Hessian (matrix of partial second derivatives of potential energy surface, also referred to as the force constant matrix), which is used to calculate the harmonic oscillator frequencies. If Gaussian is used to generate the geometry/frequencies log file, the Gaussian input file must contain the keyword `iop(7/33=1)`, which forces Gaussian to output the complete Hessian.

1. Perform a geometry optimization.
2. Take the optimized geometry from step 1, and use it as the input to a freq job with the following input keywords:  
`#method basis-set freq iop(7/33=1)`

rotors is a list of `HinderedRotor()` and/or `HinderedRotor1DArray()` and/or `FreeRotor()` objects. Each `HinderedRotor()` object requires the following parameters:

Parameter	Required?	Description
scanLog	yes	The path to the Gaussian/Qchem log file, or a text/csv/yaml file containing the scan energies
pivots	yes	The indices of the atoms in the hindered rotor torsional bond
top	yes	The indices of all atoms on one side of the torsional bond (including the pivot atom)
symmetry	optional	The symmetry number for the torsional rotation (number of indistinguishable energy minima)
fit	optional	Fit to the scan data. Can be either <code>fourier</code> , <code>cosine</code> or <code>best</code> (default).

```
angle_unit: radians
energy_unit: kJ/mol
angles:
- 0.00000000000
- 0.1745329252
- 0.3490658504
      .
      .
      .
- 6.2831853072
energies:
- 0.0147251160
- 0.7223109804
- 2.6856059517
      .
      .
      .
- 0.00000000000
```

Angle (radians),Energy (kJ/mol)
0.0000000000,0.0147251160
0.1745329252,0.7223109804
0.3490658504,2.6856059517
0.5235987756,5.6856059517
0.6981317008,9.1856059517
0.8726646260,13.1856059517
1.0471975512,17.6856059517
1.2217304764,22.6856059517
1.3962634016,28.1856059517
1.5707963268,34.1856059517
1.7453292520,40.6856059517
1.9198621772,47.6856059517
2.0943951024,55.1856059517
2.2689280276,63.1856059517
2.4434609528,71.6856059517
2.6179938780,80.6856059517
2.7925268032,90.1856059517
2.9670597284,100.1856059517
3.1415926536,110.6856059517
3.3161255788,121.6856059517
3.4906585040,133.1856059517
3.6651914292,145.1856059517
3.8397243544,157.6856059517
4.0142572796,170.6856059517
4.1887902048,184.1856059517
4.3633231300,198.1856059517
4.5378560552,212.6856059517
4.7123889804,227.6856059517
4.8869219056,243.1856059517
5.0614548308,259.1856059517
5.2359877560,275.6856059517
5.4105206812,292.6856059517
5.5850536064,310.1856059517
5.7595865316,328.1856059517
5.9341194568,346.6856059517
6.1086523820,365.6856059517
6.2831853072,385.1856059517
6.4577182324,405.1856059517
6.6322511576,425.6856059517
6.8067840828,446.6856059517
6.9813170080,468.1856059517
7.1558499332,490.1856059517
7.3303828584,512.6856059517
7.5049157836,535.6856059517
7.6794487088,559.1856059517
7.8539816340,583.1856059517
8.0285145592,607.6856059517
8.2030474844,632.6856059517
8.3775804096,658.1856059517
8.5521133348,684.1856059517
8.7266462600,710.6856059517
8.9011791852,737.6856059517
9.0757121104,765.1856059517
9.2502450356,793.1856059517
9.4247779608,821.6856059517
9.5993108860,850.6856059517
9.7738438112,880.1856059517
9.9483767364,910.1856059517
10.1229096616,940.6856059517
10.2974425868,971.6856059517
10.4719755120,1003.1856059517
10.6465084372,1035.6856059517
10.8210413624,1069.1856059517
10.9955742876,1103.6856059517
11.1701072128,1139.1856059517
11.3446401380,1175.6856059517
11.5191730632,1213.1856059517
11.6937059884,1251.6856059517
11.8682389136,1291.1856059517
12.0427718388,1331.6856059517
12.2173047640,1373.1856059517
12.3918376892,1415.6856059517
12.5663706144,1459.1856059517
12.7409035396,1503.6856059517
12.9154364648,1549.1856059517
13.0899693900,1595.6856059517
13.2645023152,1643.1856059517
13.4390352404,1691.6856059517
13.6135681656,1741.1856059517
13.7881010908,1791.6856059517
13.9626340160,1843.1856059517
14.1371669412,1895.6856059517
14.3116998664,1949.1856059517
14.4862327916,2003.6856059517
14.6607657168,2059.1856059517
14.8352986420,2115.6856059517
15.0098315672,2173.1856059517
15.1843644924,2231.6856059517
15.3588974176,2291.1856059517
15.5334303428,2351.6856059517
15.7079632680,2413.1856059517
15.8824961932,2475.6856059517
16.0570291184,2539.1856059517
16.2315620436,2603.6856059517
16.4060949688,2669.1856059517
16.5806278940,2735.6856059517
16.7551608192,2803.1856059517
16.9296937444,2871.6856059517
17.1042266696,2941.1856059517
17.2787595948,3011.6856059517
17.4532925200,3083.1856059517
17.6278254452,3155.6856059517
17.8023583704,3229.1856059517
17.9768912956,3303.6856059517
18.1514242208,3379.1856059517
18.3259571460,3455.6856059517
18.5004900712,3533.1856059517
18.6750229964,3611.6856059517
18.8495559216,3691.1856059517
19.0240888468,3771.6856059517
19.1986217720,3853.1856059

### 2.3. Creating Input Files

(continued from previous page)

```
6.2831853072,0.0000000000
```

If a text file is feeded, it should satisfy the the following format:

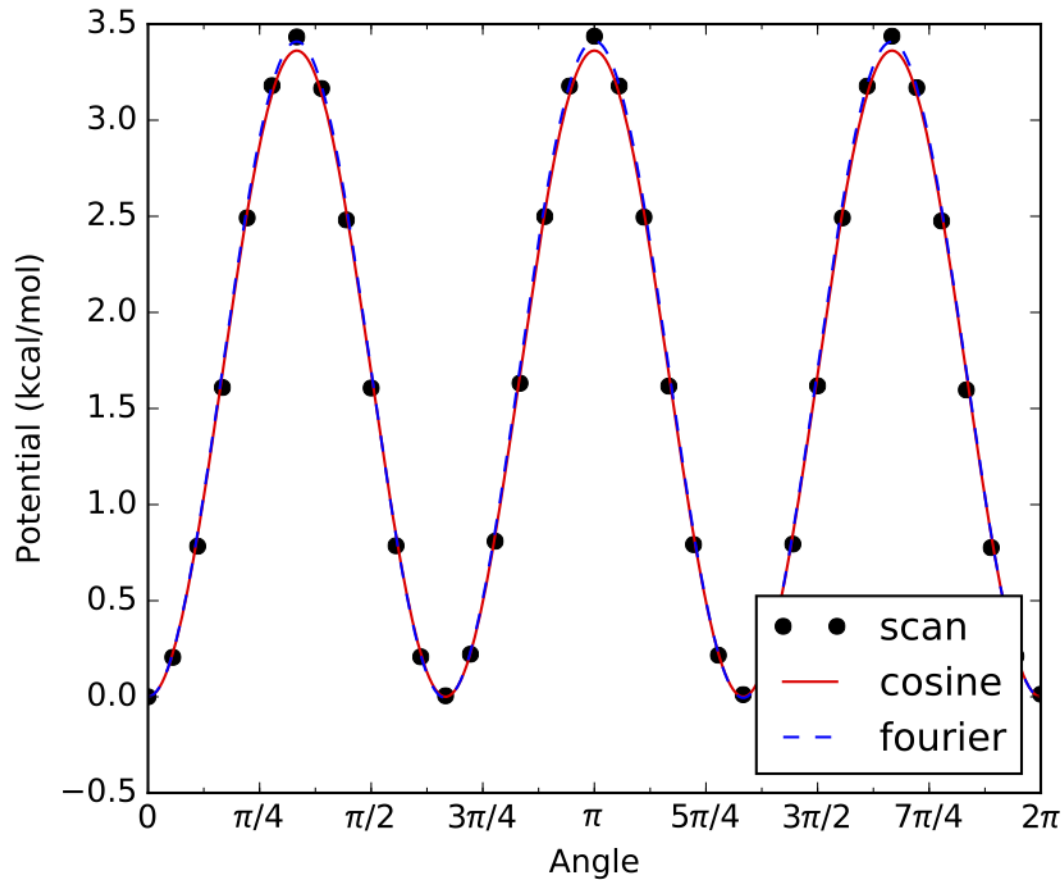
Angle (radians)	Energy (kJ/mol)
0.0000000000	0.0147251160
0.1745329252	0.7223109804
0.3490658504	2.6856059517
.	.
.	.
.	.
6.2831853072	0.0000000000

For all above options, the Energy can be in units of kJ/mol, J/mol (default), cal/mol, kcal/mol, cm<sup>-1</sup> or hartree, and the Angle can be either in radians (default) or in degrees. If `angle_unit` or `energy_unit` is not provided in the yaml file, the default unit will be used. If a header is included in either the csv file or the text file, units must be specified in parenthesis; otherwise, the column sequence will be assumed to be [angles, energies], and the default units will be used.

`HinderedRotor1DArray()` is an alternative way to define a hindered rotor without the need of a scan log file. The object requires the following parameters:

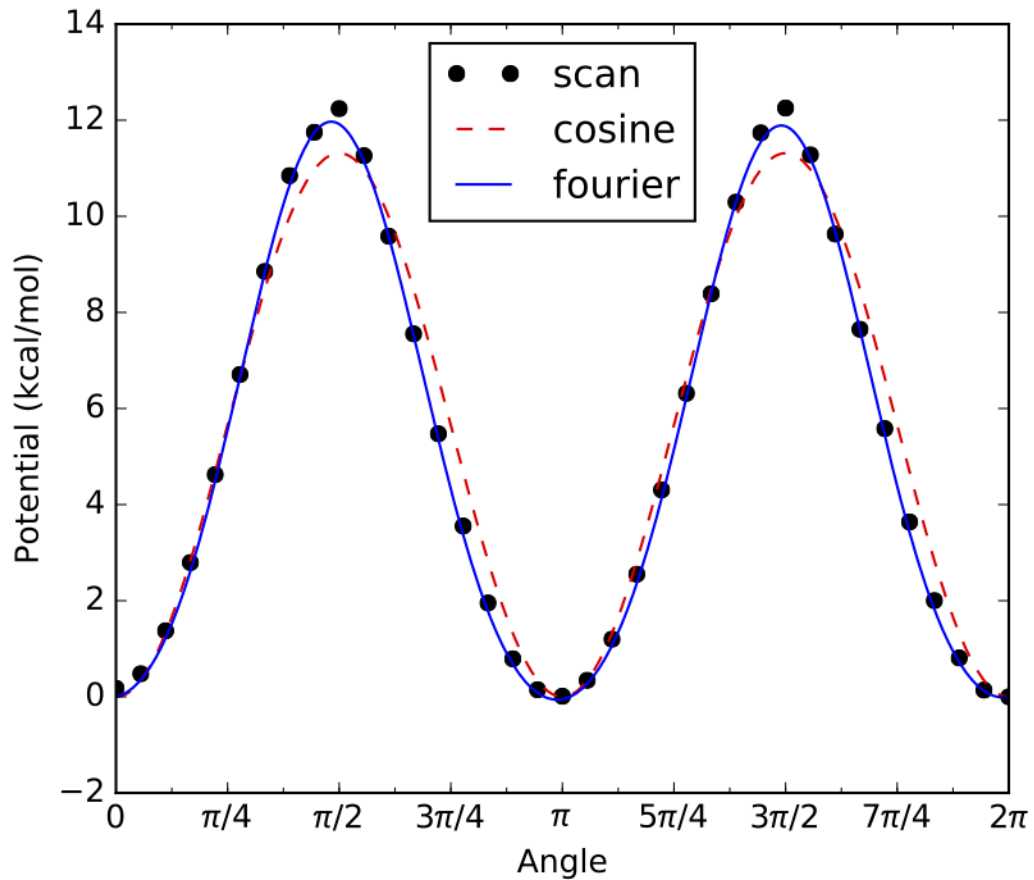
Parameter	Required?	Description
angles	yes	The angle values of the PES scan in unit of radians.
energies	yes	The energy values of the PES scan in unit of J/mol.
pivots	yes	The indices of the atoms in the hindered rotor torsional bond
top	yes	The indices of all atoms on one side of the torsional bond (including the pivot atom)
symmetry	optional	The symmetry number for the torsional rotation (number of indistinguishable energy minima)
fit	optional	Fit to the scan data. Can be either <code>fourier</code> , <code>cosine</code> or <code>best</code> (default).

For the above two objects, `symmetry` parameter will usually equal either 1, 2 or 3. It could be determined automatically by Arkane (by simply not specifying it altogether), however it is always better to explicitly specify it if it is known. If it is determined by Arkane, the log file will specify the determined value and what it was based on. Below are examples of internal rotor scans with these commonly encountered symmetry numbers. First, `symmetry = 3`:

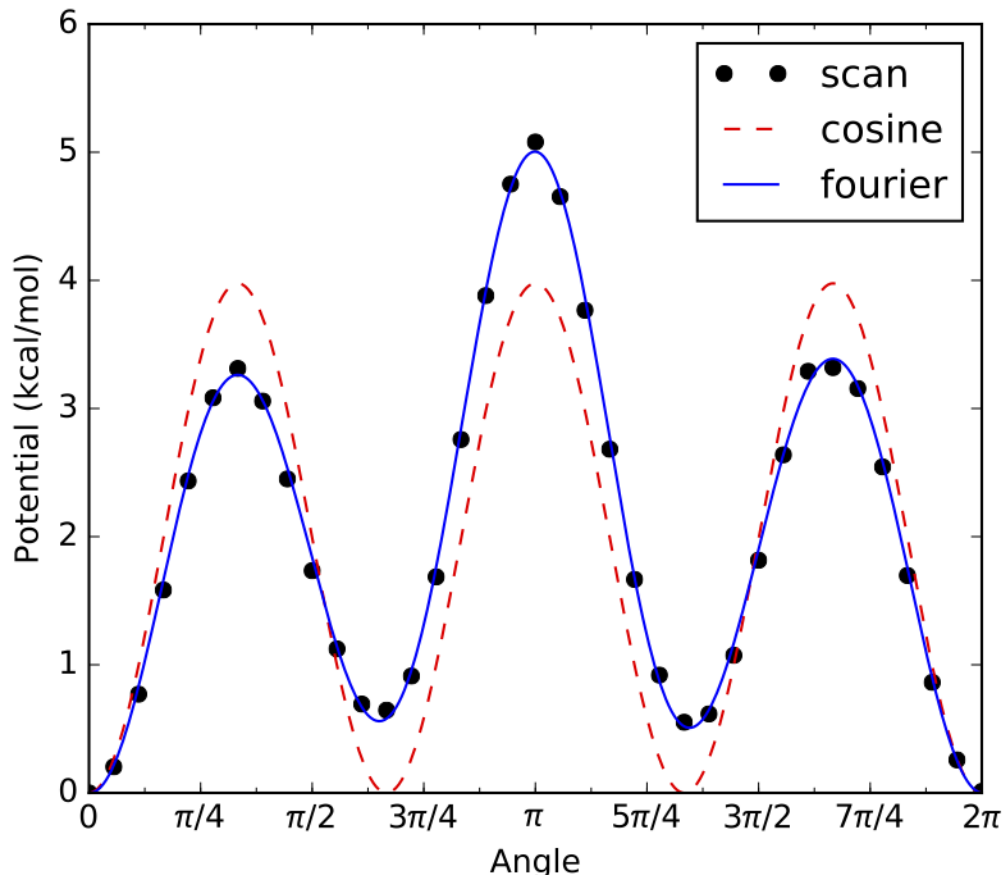


Internal rotation of a methyl group is a common example of a hindered rotor with  $\text{symmetry} = 3$ , such as the one above. As shown, all three minima (and maxima) have identical energies, hence  $\text{symmetry} = 3$ .

Similarly, if there are only two minima along the internal rotor scan, and both have identical energy, then  $\text{symmetry} = 2$ , as in the example below:



If any of the energy minima in an internal rotor scan are not identical, then the rotor has no symmetry (symmetry = 1), as in the example below:



For the example above there are 3 local energy minima, 2 of which are identical to each other. However, the 3rd minima is different from the other 2, therefore this internal rotor has no symmetry.

For practical purposes, when determining the symmetry number for a given hindered rotor simply check if the internal rotor scan looks like the `symmetry = 2` or `3` examples above. If it doesn't, then most likely `symmetry = 1`.

Each `FreeRotor()` object requires the following parameters:

Parameter	Description
<code>pivots</code>	The indices of the atoms in the free rotor torsional bond
<code>top</code>	The indices of all atoms on one side of the torsional bond (including the pivot atom)
<code>symmetry</code>	The symmetry number for the torsional rotation (number of indistinguishable energy minima)

Note that a `scanLog` is not needed for `FreeRotor()` because it is assumed that there is no barrier to internal rotation. Modeling an internal rotation as a `FreeRotor()` puts an upper bound on the impact of that rotor on the species's overall partition function. Modeling the same internal rotation as a `Harmonic Oscillator` (default if it is not specified as either a `FreeRotor()` or `HinderedRotor()`) puts a lower bound on the impact of that rotor on the species's overall partition function. Modeling the internal rotation as a `HinderedRotor()` should fall in between these two extremes.

To summarize, the species input file with hindered/free rotors should look like the following example (different options for specifying the same `rotors` entry are commented out):

```
bonds = {
    'C-C': 1,
```

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```

    'C-H': 6,
}

linear = False

externalSymmetry = 6

spinMultiplicity = 1

opticalIsomers = 1

energy = {
    'CBS-QB3': Log('ethane_cbsqb3.log'),
    'Klip_2': -79.64199436,
}

geometry = Log('ethane_freq.log')

frequencies = Log('ethane_freq.log')

rotors = [
    HinderedRotor(scanLog=Log('ethane_scan_1.log'), pivots=[1,5], top=[1,2,3,4],
↪symmetry=3, fit='best'),
    #HinderedRotor(scanLog=ScanLog('C2H6_rotor_1.txt'), pivots=[1,5], top=[1,2,3,4],
↪symmetry=3, fit='best'),
    #FreeRotor(pivots=[1,5], top=[1,2,3,4], symmetry=3),
]

```

Note that the atom labels identified within the rotor section should correspond to the indicated geometry.

## Multidimensional Hindered Rotors

For multidimensional hindered rotors, `geometry`, `frequencies` need to be specified in the same way described in detail in the last section. However, rotor files may be specified by either a 1D rotor scan file as in the last section (1D rotors only) or as a directory. The directory must contain a list of energy files in the format `something_name_rotorAngle1_rotorAngle2_rotorAngle3(...).log`.

For `HinderedRotor2D` (Quantum Mechanical 2D using Q2DTor):

Parameter	Description
<code>scandir</code>	file or directory containing scan energies
<code>pivots1</code>	The indices of the atoms in the first rotor torsional bond
<code>top1</code>	The indices of all atoms on one side of the first torsional bond (including the pivot atom)
<code>symmetry1</code>	The symmetry number of the first rotor
<code>pivots2</code>	The indices of the atoms in the second rotor torsional bond
<code>top2</code>	The indices of all atoms on one side of the second torsional bond (including the pivot atom)
<code>symmetry2</code>	The symmetry number of the second rotor
<code>symmetry</code>	Q2DTor simplifying symmetry code, default is none

For `HinderedRotorClassicalND` (Classical and Semiclassical ND rotors):



Parameter	Description
<code>scandir</code>	file or directory containing scan energies
<code>pivots</code>	The list of the indices of the atoms in each rotor torsional bond
<code>tops</code>	The list of the indices of all atoms on one side of each torsional bond (including the pivot atom)
<code>sigmas</code>	The list of symmetry numbers for each torsional bond
<code>semiclassical</code>	Indicates whether to use the semiclassical rotor correction (highly recommended)

The inputs are mostly the same as the last section except that `HinderedRotorClassicalND` takes lists of pivots, tops and sigmas instead of individual values. These rotor objects enable calculation of partition functions for multidimensional torsions that are particularly important for QOOH molecules and molecules involving intramolecular hydrogen bonding. It is worth noting that `HinderedRotor2D` can take on the order of hours to run. To mitigate this the `.evals` file in the directories `Q2DTor` directories are searched for automatically and used if present to reduce runtime to seconds. This means if you have run a system with `HinderedRotor2D` and wish to rerun the system and recalculate the `HinderedRotor2D` you should delete the `.evals` file. `HinderedRotorClassicalND` usually runs quickly for lower dimensional torsions.

### Additional parameters for pressure dependent networks

Additional parameters apply only to molecules in pressure dependent networks

Parameter	Required?	Description
<code>structure</code>	all species except bath gas	A chemical structure for the species defined using either SMILES, adjacencyList, or InChI
<code>molecularWeight</code>	optional for all species	The molecular weight, if not given it is calculated based on the structure
<code>reactive</code>	only bath gases	Boolean indicating whether the molecule reacts, set to <code>False</code> for bath gases. default is <code>True</code>
<code>collisionModel</code>	unimolecular isomers and bath gases	Transport data for the species
<code>energyTransferModel</code>	unimolecular isomers	Assigned with <code>SingleExponentialDown</code> model

The `structure` parameter is defined by SMILES, `adjList`, or InChI. For instance, either representation is acceptable for the acetone molecule:

```
structure = SMILES('CC(C)=O')

structure = adjacencyList("""1 C u0 p0 c0 {2,S} {5,S} {6,S} {7,S}
                             2 C u0 p0 c0 {1,S} {3,S} {4,D}
                             3 C u0 p0 c0 {2,S} {8,S} {9,S} {10,S}
                             4 O u0 p2 c0 {2,D}
                             5 H u0 p0 c0 {1,S}
                             6 H u0 p0 c0 {1,S}
                             7 H u0 p0 c0 {1,S}
                             8 H u0 p0 c0 {3,S}
                             9 H u0 p0 c0 {3,S}
                             10 H u0 p0 c0 {3,S}""")

structure = InChI('InChI=1S/C3H6O/c1-3(2)4/h1-2H3')
```

The `molecularWeight` parameter should be defined in the quantity format (`value`, `'units'`), for example:

```
molecularWeight = (44.04, 'g/mol')
```

If the `molecularWeight` parameter is not given, it is calculated by Arkane based on the chemical structure.

The `collisionModel` is defined for unimolecular isomers with the transport data using a `TransportData` object:

```
collisionModel = TransportData(sigma=(3.70,'angstrom'), epsilon=(94.9,'K'))
```

`sigma` and `epsilon` are Lennard-Jones parameters, which can be estimated using the Joback method on the [RMG website](#).

The `energyTransferModel` model available is a `SingleExponentialDown`.

- `SingleExponentialDown` - Specify `alpha0`, `T0` and `n` for the average energy transferred in a deactivating collision

$$\langle \Delta E_{\text{down}} \rangle = \alpha_0 \left( \frac{T}{T_0} \right)^n$$

An example of a typical `energyTransferModel` function is:

```
energyTransferModel = SingleExponentialDown(
    alpha0 = (0.5718,'kcal/mol'),
    T0 = (300,'K'),
    n = 0.85,
)
```

Parameters for the single exponential down model of collisional energy transfer are usually obtained from analogous systems in literature. For example, if the user is interested in a pressure-dependent network with overall molecular formula C7H8, the single exponential down parameters for toluene in helium available from literature could be used for all unimolecular isomers in the network (assuming helium is the bath gas). One helpful literature source for calculated exponential down parameters is the following paper: <http://www.sciencedirect.com/science/article/pii/S1540748914001084#s0060>

## Option #2: Directly Enter Molecular Properties

While it is usually more convenient to have Arkane parse molecular properties from the output of quantum chemistry calculations (see *Option #1: Automatically Parse Quantum Chemistry Calculation Output*) there are instances where an output file is not available and it is more convenient for the user to directly enter the molecular properties. This is the case, for example, if the user would like to use calculations from literature, where the final calculated molecular properties are often reported in a table (e.g., vibrational frequencies, rotational constants), but the actual output files of the underlying quantum chemistry calculations are rarely provided.

For this option, there are a number of required parameters associated with the `species()` function

Parameter	Required?	Description
<code>label</code>	yes	A unique string label used as an identifier
<code>E0</code>	yes	The ground-state 0 K enthalpy of formation (including zero-point energy)
<code>modes</code>	yes	The molecular degrees of freedom (see below)
<code>spinMultiplicity</code>	yes	The ground-state spin multiplicity (degeneracy), sets to 1 by default if not used
<code>opticalIsomers</code>	yes	The number of optical isomers of the species, sets to 1 by default if not used

The `label` parameter should be set to a string with the desired name for the species, which can be reference later in the input file.

```
label = 'C2H6'
```

The  $E_0$  ground state 0 K enthalpy of formation (including zero-point energy) should be given in the quantity format (value, 'units'), using units of either kJ/mol, kcal/mol, J/mol, or cal/mol:

```
E0 = (100.725, 'kJ/mol')
```

Note that if Arkane is being used to calculate the thermochemistry of the species, it is critical that the value of  $E_0$  is consistent with the definition above (0 K enthalpy of formation with zero-point energy). However, if the user is only interested in kinetics,  $E_0$  can be defined on any arbitrary absolute energy scale, as long as the correct relative energies between various `species()` and `transitionState()` are maintained. For example, it is common in literature for the energy of some reactant(s) to be arbitrarily defined as zero, and the energies of all transition states, intermediates and products are reported relative to that.

Also note that the value of  $E_0$  provided here will be used directly, i.e., no atom or bond corrections will be applied.

If you want Arkane to correct for zero point energy, you can either just place the raw units in Hartree (as if it were read directly from quantum):

```
E0 = 547.6789753223456
```

Or you can add a third argument to the Quantity specified whether zero-point energy is included or not:

```
E0 = (95.1, 'kJ/mol', 'e_electronic') # when zero point energy (ZPE) is not included,
↳- Arkane will add it
E0 = (95.1, 'kJ/mol', 'E0') # when ZPE is already included - Arkane will not add it
```

When specifying the `modes` parameter, define a list with the following types of degrees of freedom. To understand how to define these degrees of freedom, please click on the links below:

### Translational degrees of freedom

Class	Description
<code>IdealGasTranslation</code>	A model of three-dimensional translation of an ideal gas

### Rotational degrees of freedom

Class	Description
<code>LinearRotor</code>	A model of two-dimensional rigid rotation of a linear molecule
<code>NonlinearRotor</code>	A model of three-dimensional rigid rotation of a nonlinear molecule
<code>KRotor</code>	A model of one-dimensional rigid rotation of a K-rotor
<code>SphericalTopRotor</code>	A model of three-dimensional rigid rotation of a spherical top molecule

### Vibrational degrees of freedom

Class	Description
<code>HarmonicOscillator</code>	A model of a set of one-dimensional harmonic oscillators

Note that the `frequencies` provided here will be used directly, i.e., the `frequencyScaleFactor` will not be applied.

### Torsional degrees of freedom

Class	Description
<code>HinderedRotor</code>	A model of a one-dimensional hindered rotation
<code>FreeRotor</code>	A model of a one-dimensional free rotation

The `spinMultiplicity` is defined using an integer, and is set to 1 if not indicated in the `species()` function.

```
spinMultiplicity = 1
```

Similarly, the `opticalIsomers` is also defined using an integer, and is set to 1 if not used in the `species()` function.

```
opticalIsomers = 1
```

The following is an example of a typical `species()` function, based on ethane (different options for specifying the same internal rotation are commented out):

```
species(
    label = 'C2H6',
    E0 = (100.725, 'kJ/mol'),
    modes = [
        IdealGasTranslation(mass=(30.0469, 'amu')),
        NonlinearRotor(
            inertia = ([6.27071, 25.3832, 25.3833], 'amu*angstrom^2'),
            symmetry = 6,
        ),
        HarmonicOscillator(
            frequencies = ([818.917, 819.48, 987.099, 1206.81, 1207.06, 1396, 1411.35,
→ 1489.78, 1489.97, 1492.49, 1492.66, 2995.36, 2996.06, 3040.83, 3041, 3065.86, 3066.
→ 02], 'cm^-1'),
        ),
        HinderedRotor(
            inertia = (1.56768, 'amu*angstrom^2'),
            symmetry = 3,
            barrier = (11.2717, 'kJ/mol'),
        ),
        #HinderedRotor(
        #inertia = (1.56768, 'amu*angstrom^2'),
        #symmetry = 3,
        #fourier = (
        #    [
        #        [0.00458375, 0.000841648, -5.70271, 0.00602657, 0.0047446],
        #        [0.000726951, -0.000677255, 0.000207033, 0.000553307, -0.000503303],
        #    ],
        #    'kJ/mol',
        #),
        #),
        #FreeRotor(
        #    inertia = (1.56768, 'amu*angstrom^2'),
        #    symmetry = 3,
        #),
    ],
    spinMultiplicity = 1,
    opticalIsomers = 1,
)
```

Note that the format of the `species()` function above is identical to the `conformer()` function output by Arkane in `output.py`. Therefore, the user could directly copy the `conformer()` output of an Arkane job to another Arkane input file, change the name of the function to `species()` (or `transitionState()`, if appropriate, see next section) and run a new Arkane job in this manner. This can be useful if the user wants to easily switch a `species()` function from *Option #1: Automatically Parse Quantum Chemistry Calculation Output* to *Option #2: Directly Enter Molecular*

*Properties.*

### Additional parameters for pressure dependent networks

Additional parameters apply only to molecules in pressure dependent networks

Parameter	Required?	Description
structure	all species except bath gas	A chemical structure for the species defined using either SMILES, adjacencyList, or InChI
reactive	only bath gases	Boolean indicating whether the molecule reacts, set to <code>False</code> for bath gases. default is <code>True</code>
collisionModel	unimolecular isomers and bath gases	Transport data for the species
energyTransferModel	unimolecular isomers	Assigned with <code>SingleExponentialDown</code> model
thermo	optional	Thermo data for the species

The parameters `structure`, `molecularWeight`, `collisionModel` and `energyTransferModel` were already discussed above in [Option #1: Automatically Parse Quantum Chemistry Calculation Output](#).

When the `thermo` parameter is specified, Arkane will approximate the modes of vibration and energy from the thermodynamic parameters, and will utilize this in its solution of the pressure dependent network. This is analogous to how RMG calculates thermodynamic parameters for pressure dependent mechanisms.

The `thermo` parameter has the following syntax:

```
thermo = NASA(polynomials=[
    NASAPolynomial(coeffs=[3.81543,0.0114632,0.000281868,
                           -5.70609e-07,3.57113e-10,45814.7,14.9594],
                    Tmin=(10,'K'), Tmax=(510.16,'K')),
    NASAPolynomial(coeffs=[-1.32176,0.0893697,-5.78295e-05,
                           1.78722e-08,-2.11223e-12,45849.2,31.4869],
                    Tmin=(510.16,'K'), Tmax=(3000,'K'))
],
            Tmin=(10,'K'), Tmax=(3000,'K'))
```

### Option #3: Automatically Parse YAML files

Arkane automatically saves a `.yaml` file representing an `ArkaneSpecies` in an `ArkaneSpecies` folder under the run directory with the statistical mechanics properties of a species along with additional useful metadata. This process is triggered whenever a `thermo` calculation is ran for a species with a specified structure. To automatically generate such file in the first place, a species has to be defined using one of the other options above. The generated `.yaml` file could conveniently be used when referring to this species in subsequent Arkane jobs. We intend to create an online repository of Arkane `.yaml` files, from which users would be able to pick the desired species calculated at an appropriate level of theory (if available), and directly use them for kinetic or pressure-dependent calculations. Once such repository becomes available, a full description will be added to these pages.

### 2.3.5 Transition State

Transition state(s) are only required when performing kinetics computations. Each transition state of interest must be specified using a `transitionState()` function, which is analogous to the `species()` function described above. Therefore, the `transitionState()` function may also be specified in two ways: *Option #1: Automatically Parse Quantum Chemistry Calculation Output* and *Option #2: Directly Enter Molecular Properties*. Note that currently a transition state cannot be specified using a YAML file (Option #3).

The following is an example of a typical `transitionState()` function using Option #1:

```
transitionState('TS', 'TS.py')
```

Just as for a `species()` function, the first parameter is the label for that transition state, and the second parameter points to the location of another python file containing details of the transition state. This file will be referred to as the transition state input file, and it accepts the same parameters as the species input file described in *Option #1: Automatically Parse Quantum Chemistry Calculation Output*.

The following is an example of a typical `transitionState()` function using Option #2:

```
transitionState(
    label = 'TS',
    E0 = (267.403, 'kJ/mol'),
    modes = [
        IdealGasTranslation(mass=(29.0391, 'amu')),
        NonlinearRotor(
            inertia = ([6.78512, 22.1437, 22.2114], 'amu*angstrom^2'),
            symmetry = 1,
        ),
        HarmonicOscillator(
            frequencies = ([412.75, 415.206, 821.495, 924.44, 982.714, 1024.16, 1224.
→ 21, 1326.36, 1455.06, 1600.35, 3101.46, 3110.55, 3175.34, 3201.88], 'cm^-1'),
        ),
    ],
    spinMultiplicity = 2,
    opticalIsomers = 1,
    frequency = (-750.232, 'cm^-1'),
)
```

The only additional parameter required for a `transitionState()` function as compared to a `species()` function is frequency, which is the imaginary frequency of the transition state needed to account for tunneling. Refer to *Option #2: Directly Enter Molecular Properties* for a more detailed description of the other parameters.

### 2.3.6 Reaction

This is only required if you wish to perform a kinetics computation. Each reaction of interest must be specified using a `reaction()` function, which accepts the following parameters:

Parameter	Re-quired?	Description
<code>label</code>	All reactions	A name for the reaction
<code>reactants</code>	All reactions	A list of reactant species
<code>products</code>	All reactions	A list of product species
<code>transitionState</code>	All reactions	The transition state
<code>kinetics</code>	Optional	The high pressure-limit kinetics for the reaction, for pdep calculations
<code>tunneling</code>	Optional	The type of tunneling model (either 'Eckhart' or 'Wigner') to use for tunneling through the reaction barrier

The following is an example of a typical reaction function:

```
reaction(
    label = 'H + C2H4 <=> C2H5',
    reactants = ['H', 'C2H4'],
    products = ['C2H5'],
    transitionState = 'TS',
    tunneling='Eckart'
)
```

Note that the reactants and products must have been previously declared using a `species()` function, using the same name labels. Transition states must also be previously declared using a `transitionState()` function. The quantum tunneling factor method that may be assigned is either 'Eckart' or 'Wigner'.

The `kinetics` parameter is only useful in pressure dependent calculations. If the optional `kinetics` parameter is specified, Arkane will perform an inverse Laplace transform (ILT) on the high pressure-limit kinetics provided to estimate the microcanonical rate coefficients,  $k(E)$ , needed for the master equation (refer to Theory manual for more detail). This feature is useful for barrierless reactions, such as radical recombinations, which don't have an obvious transition state. If the ILT approach to calculating  $k(E)$  is taken, a placeholder `transitionState` must still be defined with an `E0` equal to the energy of the higher energy species it is connecting. If the optional `kinetics` entry is not specified, Arkane will calculate the required kinetic coefficients on its own. The `kinetics` entry is particularly useful to specify rates of barrierless reactions (for which Arkane cannot yet calculate high-pressure limit rates). The `kinetics` argument has the following syntax:

```
kinetics = Arrhenius(A=(2.65e6, 'm^3/(mol*s)'), n=0.0, Ea=(0.0, 'kcal/mol'), T0=(1, "K
↪")),
```

For high pressure limit kinetics calculations, specifying the `kinetics` parameter will just output the value specified by the `kinetics` parameter, without using transition state theory.

### 2.3.7 Thermodynamics

Use a `thermo()` function to make Arkane execute the thermodynamic parameters computation for a species. Pass the string label of the species you wish to compute the thermodynamic parameters for and the type of thermodynamics polynomial to generate (either 'Wilhoit' or 'NASA'). A table of relevant thermodynamic parameters will also be displayed in the output file.

Below is a typical `thermo()` execution function:

```
thermo('ethane', 'NASA')
```

### 2.3.8 High Pressure Limit Kinetics

Use a `kinetics()` function to make Arkane execute the high-pressure limit kinetic parameters computation for a reaction. The 'label' string must correspond to that of a defined `reaction()` function.

By default, Arkane outputs high pressure kinetic rate coefficients in the modified three-parameter Arrhenius equation format:

$$k(T) = A \left( \frac{T}{T_0} \right)^n \exp \left( -\frac{E_a}{RT} \right)$$

Alternatively, the user may request to output the rate in the classical two-parameter Arrhenius format:

$$k(T) = A \exp \left( -\frac{E_a}{RT} \right)$$

by passing `three_params = False` in the `kinetics()` function:

```
kinetics(  
label = 'H + C2H4 <=> C2H5',  
three_params = False,  
)
```

You have three options for specifying the temperature to which a modified/classical Arrhenius expression will be fit.

Give an explicit list of temperatures to fit:

```
kinetics(  
label = 'H + C2H4 <=> C2H5',  
Tlist = ([400,500,700,900,1100,1200], 'K'),  
)
```

Give minimum and maximum temperatures to fit:

```
kinetics(  
label = 'H + C2H4 <=> C2H5',  
Tmin = (400, 'K'), Tmax = (1200, 'K'), Tcount = 6,  
)
```

Use the default range to fit (298 K to 2500 K at 50 points spaced equally in 1/T space):



```
kinetics(label = 'H + C2H4 <=> C2H5')
```

If a sensitivity analysis is desired, simply add the conditions at which to calculate sensitivity coefficients in the following format, e.g.:

```
kinetics(
    label = 'HS00 <=> H00S',
    Tmin = (500, 'K'), Tmax = (3000, 'K'), Tcount = 15,
    sensitivity_conditions = [(1000, 'K'), (2000, 'K')]
)
```

The `output.py` file will show the rates at various temperatures including the quantum tunneling factor. Kinetic rates will also be added to the `chem.inp` file.

The output of a sensitivity analysis is saved into a `sensitivity` folder in the output directory. A text file, named with the reaction label, delineates the semi-normalized sensitivity coefficients  $d\ln(k)/dE_0$  in units of  $\text{mol/J}$  at all requested conditions. A horizontal bar figure is automatically generated per reaction with subplots for both the forward and reverse direction at all conditions.

## 2.3.9 Pressure Dependent Network Specification

To obtain pressure dependent rates, you need to add two different sections to the file. First, a declaration for the overall network must be given using the `network()` function, which specifies which species are contained in this reaction network. After that you will need to create a `pressureDependence()` block that indicates how the pressure dependence calculation should be conducted.

This section will go over the first of these sections, the `network()` function. This includes setting the following parameters:

Parameter	Description
<code>label</code>	A name for the network
<code>isomers</code>	A list of species participating in unimolecular reaction channels
<code>reactants</code>	A list of the species that participate in bimolecular reactant channels
<code>bathGas</code>	A dictionary of bath gases and their respective mole fractions, adding up to 1.0

Arkane is largely able to determine the molecular configurations that define the potential energy surface for your reaction network simply by inspecting the path reactions. However, you must indicate which unimolecular and bimolecular configurations you wish to include in the master equation formulation; all others will be treated as irreversible sinks.

Note that all species and bath gases used in the `network` function must have been previously declared with the same name labels in a previous `species` function in the input file.

You do not need to specify the product channels (infinite sinks) in this manner, as any configuration not marked as an isomer or reactant channel will be treated as a product channel.

An example of the `network` function is given below along with a scheme of the network:

```
network(
    label = 'acetyl + O2',
    isomers = [
        'acetylperoxy',
        'hydroperoxylvinoxy',
    ],
    reactants = [
```

(continues on next page)

(continued from previous page)

```

    ('acetyl', 'oxygen'),
],
bathGas = {
    'nitrogen': 0.4,
    'argon': 0.6,
}
)

```

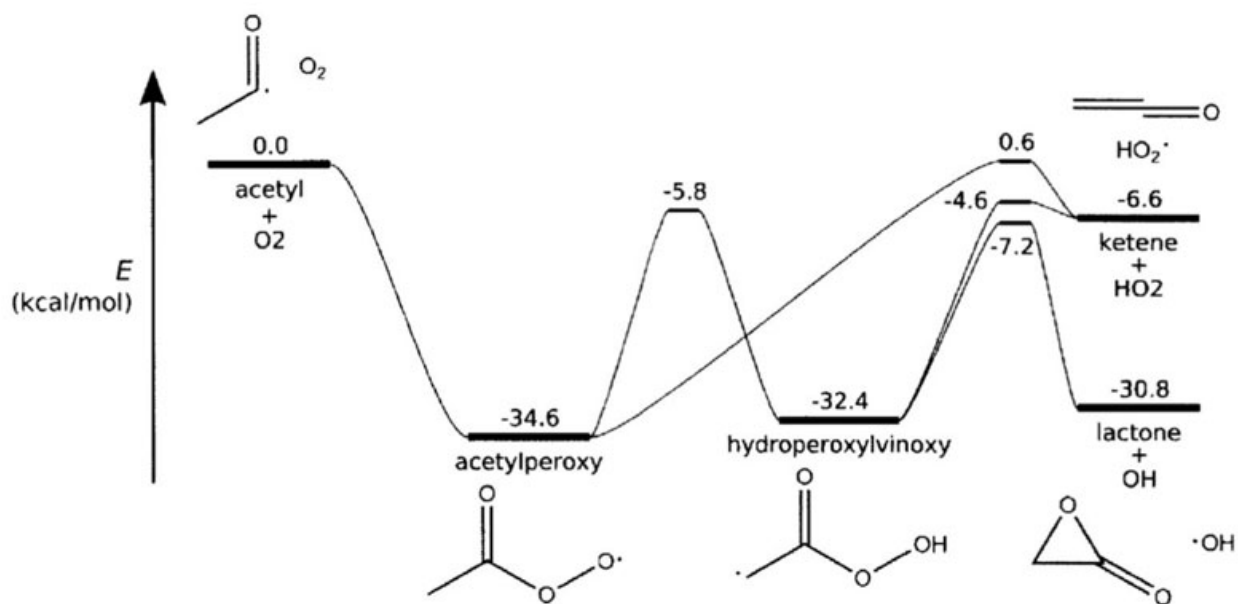


Image source: J.W. Allen, PhD dissertation, MIT 2013, calculated at the RQCISD(T)/CBS//B3LYP/6-311++G(d,p) level of theory

### 2.3.10 Pressure Dependent Rate Calculation

The overall parameters for the pressure-dependence calculation must be defined in a `pressureDependence()` function at the end of the input file. The parameters are:

Parameter	Re- quired?	Description
label	Yes	Use the name for the network declared previously
method	Yes	Method to use for calculating the pdep network. Use either 'modified strong collision', 'reservoir state', or 'chemically-significant eigenvalues'
interpolationModel	Yes	Select the output type for the pdep kinetics, either in 'chebyshev' or 'pdeparrhenius' (plog) format
activeKRotor	No	A flag indicating whether to treat the K-rotor as active or adiabatic (default True)
activeJRotor	No	A flag indicating whether to treat the J-rotor as active or adiabatic (default True)
Tmin/Tmax/Tcount or Tlist	Yes	Define temperatures at which to compute (and output) $k(T, P)$
Pmin/Pmax/Pcount or Plist	Yes	Define pressures at which to compute (and output) $k(T, P)$
maximumGrainSize	Yes	Defines the upper bound on grain spacing in master equation calculations.
minimumGrainCount	Yes	Defines the minimum number of grains in master equation calculation.
sensitivity_conditions	No	Specifies the conditions at which to run a network sensitivity analysis.

An example of the Pressure-dependent algorithm parameters function for the acetyl + O2 network is shown below:

```
pressureDependence(
    label='acetyl + O2',
    Tmin=(300.0, 'K'), Tmax=(2000.0, 'K'), Tcount=8,
    Pmin=(0.01, 'bar'), Pmax=(100.0, 'bar'), Pcount=5,
    #Tlist = ([300, 400, 600, 800, 1000, 1250, 1500, 1750, 2000], 'K')
    #Plist = ([0.01, 0.1, 1.0, 10.0, 100.0], 'bar')
    maximumGrainSize = (1.0, 'kcal/mol'),
    minimumGrainCount = 250,
    method = 'modified strong collision',
    #method = 'reservoir state',
    #method = 'chemically-significant eigenvalues',
    interpolationModel = ('chebyshev', 6, 4),
    #interpolationModel = ('pdeparrhenius'),
    #activeKRotor = True,
    activeJRotor = True,
    sensitivity_conditions = [[(1000, 'K'), (1, 'bar')], [(1500, 'K'), (10, 'bar')]]
)
```

## Temperature and Pressure Ranges

Arkane will compute the  $k(T, P)$  values on a grid of temperature and pressure points. Tmin, Tmax, and Tcount values, as well as Pmin, Pmax, and Pcount parameter values must be provided. Arkane will automatically choose the intermediate temperatures based on the interpolation model you wish to fit. This is the recommended approach.

Alternatively, the grid of temperature and pressure points can be specified explicitly using Tlist and/or Plist.

## Energy Grains

Determine the fineness of the energy grains to be used in the master equation calculations. Dictate the `maximumGrainSize`, and the `minimumGrainCount`.

## Sensitivity analysis

Arkane also has the ability to vary barrier heights and generate sensitivity coefficients as a function of changes in  $E_0$  with the `sensitivity_conditions` argument. For each desired condition, place its corresponding temperature and pressure within the list of `sensitivity_conditions`. See the example above for syntax.

The output of a sensitivity analysis is saved into a `sensitivity` folder in the output directory. A text file, named with the network label, delineates the semi-normalized sensitivity coefficients  $d\ln(k)/dE_0$  in units of  $\text{mol/J}$  for all network reactions (both directions if reversible) at all requested conditions. Horizontal bar figures are automatically generated per network reaction, showing the semi-normalized sensitivity coefficients at all conditions.

### 2.3.11 Atom Energy Fitting

Atom energies can be fitted using a small selection of species (see `SPECIES_LABELS` in `arkane/encorr/ae.py`). To do this, the single-point electronic energies calculated using the experimental geometries from the reference database of each of the species should be provided as a dictionary of the species labels and their energies in Hartree. Zero-point energies should not be included in the electronic energies. Each atom energy fitting calculation must be specified using a `ae()` function, which accepts the following parameters:

Parameter	Re- quired?	Description
<code>species_energies</code>	Yes	Dictionary of species labels and single-point energies
<code>level_of_theory</code>	No	Level of theory used as key if writing to the database dictionary
<code>write_to_database</code>	No	Write the atom energies to the database; requires <code>level_of_theory</code> (default: False)
<code>overwrite</code>	No	If atom energies already exist, overwrite them (default: False)

### 2.3.12 Bond Additivity Correction Fitting

If calculated data is available in the reference database, Arkane can fit and save bond additivity corrections (BACs). There are two different types available: Petersson-type (Petersson et al., J. Chem. Phys. 1998, 109, 10570-10579), which fits one parameter for each bond type, and Melius-type (Anantharaman and Melius, J. Phys. Chem. A 2005, 109, 1734-1747), which fits three parameters per atom type and an optional molecular parameter. Each BAC fitting calculation must be specified using a `bac()` function, which accepts the following parameters:

Parameter	Required?	Description
<code>level_of_theory</code>	Yes	Calculated data will be extracted from the reference database using this level of theory
<code>bac_type</code>	No	BAC type: 'p' for Petersson (default), 'm' for Melius
<code>train_names</code>	No	Names of training data folders in the RMG database (default: 'main')
<code>crossval_n_folds</code>	No	If 1, perform no cross-validation. If -1, perform leave-one-out cross-validation. If any other positive integer, perform k-fold cross-validation. (default: 1)
<code>idxs</code>	No	Only include reference species with these indices in the training data (default: None)
<code>exclude_idxs</code>	No	Exclude reference species with these indices from the training data (default: None)
<code>exclude_elements</code>	No	Exclude molecules with the elements in this list from the training data (default: None)
<code>charge</code>	No	Set the allowed charges ('neutral', 'positive', 'negative', or integers) for molecules in the training data (default: 'all')
<code>multiplicity</code>	No	Set the allowed multiplicities for molecules in the training data (default: 'all')
<code>weighted</code>	No	Weight the data to diversify substructures (default: False)
<code>write_to_database</code>	No	Write the BACs to the database; has no effect if doing cross-validation (default: False)
<code>overwrite</code>	No	If BACs already exist, overwrite them (default: False)
<code>fit_mol_corr</code>	No	Fit the optional molecular correction term (Melius only, default: True)
<code>global_opt</code>	No	Perform a global optimization (Melius only, default: True)
<code>global_opt_iter</code>	No	Number of global optimization iterations (Melius only, default: 10)

### 2.3.13 Examples

Perhaps the best way to learn the input file syntax is by example. To that end, a number of example input files and their corresponding output have been given in the `examples/arkane` directory.

### 2.3.14 Troubleshooting and FAQs

1) The network that Arkane generated and the resulting pdf file show abnormally large absolute values. What's going on?

This can happen if the number of atoms and atom types is not properly defined or consistent in your input file(s).

### 2.3.15 Arkane User Checklist

Using Arkane, or any rate theory package for that matter, requires careful consideration and management of a large amount of data, files, and input parameters. As a result, it is easy to make a mistake somewhere. This checklist was made to minimize such mistakes for users:

- Do correct paths exist for pointing to the files containing the electronic energies, molecular geometries and vibrational frequencies?

For calculations involving pressure dependence:

- Does the network pdf look reasonable? That is, are the relative energies what you expect based on the input?

For calculations using internal hindered rotors:

- Did you check to make sure the rotor has a reasonable potential (e.g., visually inspect the automatically generated rotor pdf files)?
- Within your input files, do all specified rotors point to the correct files?
- Do all of the atom label indices correspond to those in the file that is read by Log?
- Why do the fourier fits look so much different than the results of the ab initio potential energy scan calculations? This is likely because the initial scan energy is not at a minimum. One solution is to simply shift the potential with respect to angle so that it starts at zero and, instead of having Arkane read a Qchem or Gaussian output file, have Arkane point to a 'ScanLog' file. Another problem can arise when the potential at  $2\pi$  is also not [close] to zero.

## 2.4 Creating Input Files for Automated Pressure Dependent Network Exploration

### 2.4.1 Syntax

Network exploration starts from a pressure dependent calculation job so naturally it requires an input file containing everything required for a pressure-dependent calculation input file. In addition all species blocks must have a structure input and there must be a database block in the job. At the end of the pressure-dependent calculation input file you append an explorer block. For example

```
explorer(  
    source=['methoxy'],  
    explore_tol=0.01,  
    energy_tol=1e4,  
    flux_tol=1e-6,  
)
```

The source is a list containing either the label for a single isomer or the labels corresponding to a bimolecular source channel. The network is expanded starting from this starting isomer/channel.

### 2.4.2 Network Exploration

The `explore_tol` is a fraction of the flux from all net reactions from the source to the other channels in the network. Network expansion is done starting from just the network source using values from the rest of the Arkane job when available, otherwise from RMG. It cycles through all of the temperature and pressure points specified for fitting in the pressure dependence job and checks the total network leak rate at each one. Whenever this rate is greater than `explore_tol*kchar`, where `kchar` is the total flux from all net reactions away from the source, the outside isomer with the most leak is added to the network and reacted and the loop is flagged to cycle through all of the temperatures and pressures again. Once this loop is finished a `network_full.py` file is generated in the `pdep` directory that has the full explored network.

### 2.4.3 Network Reduction

`energy_tol` and `flux_tol` control reduction of the full network. This is highly recommended as the full model will often contain many unimportant reactions. How strict you decide to set these parameters should be related to how much you trust the thermo and rate information being used in the job.

`energy_tol` is related to the maximum difference in  $E_0$  allowed between a reaction TS and the source channel/isomer. A given reaction is deemed filterable at a given condition if  $\text{energy\_tol} * RT < E_{0\_TS} - E_{0\_source}$ . For example, if  $T = 1000 \text{ K}$  and `energy_tol` is set to 100 and the source energy is 100 ( $\text{kJ mol}^{-1}$ ), all reactions with a transition state energy more than  $100 * 8.314 \text{ (J K}^{-1} \text{ mol}^{-1}) * 1000 \text{ K} + 100 \text{ (kJ mol}^{-1}) = 931.4 \text{ (kJ mol}^{-1})$  will not be considered in the final network.

`flux_tol` is related to the solution of a steady state problem. In this problem a constant flux of 1.0 (choice of units irrelevant) is applied to the source channel/isomer while all  $A \Rightarrow B + C$  reactions are assumed to be irreversible. Under these conditions steady state concentrations of each isomer and the rates of every unimolecular reaction can be calculated. Since the input flux to the system is 1.0 to some degree these rates represent the fraction of the input flux passing through that reaction. When the flux through a reaction is less than `flux_tol` it is deemed filterable at that condition.

Overall a reaction is removed from the network if it is deemed filterable by both methods (if both specified) at every temperature and pressure combination. After reduction a `network_reduced.py` file is generated in the `pdep` directory containing the reduced network.

## 2.5 Running Arkane

To execute an Arkane job, invoke the command

```
$ python Arkane.py INPUTFILE
```

The absolute or relative paths to the `Arkane.py` file as well as to the input file must be given.

The job will run and the results will be saved in the same directory as the input file. If you wish to save the output elsewhere, use the `-o/-output` option, e.g.

```
$ python Arkane.py INPUTFILE -o OUTPUTFILE
```

### 2.5.1 Drawing Potential Energy Surface

Arkane contains functionality for automatically generating an image of the potential energy surface for a reaction network. This is done automatically and outputted in pdf format to a file called `network.pdf`.

### 2.5.2 Log Verbosity

You can manipulate the amount of information logged to the console window using the `-q/-quiet` flag (for quiet mode), the `-v/-verbose` flag (for verbose mode), or the `-d/-debug` flag (for debug mode). The former causes the amount of logging information shown to decrease; the latter two cause it to increase.

### 2.5.3 Suppressing plot creation

Arkane by default will generate many plot files. By adding the `-p/-no-plot` flag, Arkane will not generate any plots, reducing file size of output and increasing the calculation speed.

### 2.5.4 Help

To view help information and all available options, use the `-h/-help` flag, e.g.

```
$ python Arkane.py -h
```

## 2.6 Parsing Output Files

### 2.6.1 Thermodynamic and High-pressure Limit Kinetics Calculations

The syntax of Arkane output files closely mirrors that of the input files. For each `thermo()` function in the input file, there will be a corresponding `thermo()` function in the output file containing the computed thermodynamic model. Similarly, For each `kinetics()` function in the input file, there will be a corresponding `kinetics()` function in the output file containing the computed kinetics model.

### 2.6.2 Pressure-Dependent Calculations

The output file contains the entire contents of the input file. In addition, the output file contains a block of `pdepreaction()` calls. The parameters of each `pdepreaction()` block match those of the `reaction()` block from the input file, except that no transition state data is given and the `kinetics` are by definition pressure-dependent.

A `pdepreaction()` item is printed for each reaction pathway possible in the network. Each reaction is reversible. Reactions in the opposite direction are provided as commented out, so a user can choose to use them if she/he desires.

### 2.6.3 Chemkin Output File

In addition to the `output.py` which contains the thermodynamic, kinetic, and pressure dependent results from an Arkane run, a Chemkin input file, `chem.inp` is also returned. This file contains species and their thermodynamic parameters for each species that has the `thermo()` in the input file. The file also contains kinetics, both pressure dependent and high pressure limit, which have the `kinetics()` or `pressureDependence()` module called.

For the output file to function, all the names of species should be in valid chemkin format. The butanol and ethyl examples both show how to obtain a valid chemkin file.

The `chem.inp` file can be used in Chemkin software package or converted to a Cantera input file for use in Cantera software.



## 2.6.4 Log File

A log file containing similar information to that displayed on the console during Arkane execution is also automatically saved. This file has the name `Arkane.log` and is found in the same directory as the output file. The log file accepts logging messages at an equal or greater level of detail than the console; thus, it is often useful (and recommended) to examine both if something unexpected has occurred.

The `examples/arkane` directory contains both Arkane input files and the resulting output files.

## 2.6.5 Species Dictionary

Any species that had the `thermo()` method called and had the structure defined in the Arkane input file will also have an RMG style adjacency list representation in `species_dictionary.txt`. This allows the user to input the corresponding thermo and kinetics into RMG in various ways described in the RMG user guide.

## 2.7 Frequently Asked Questions

**Are there other software packages for investigating pressure-dependent reaction networks?**

Yes. The following is an (out of date, written in 2010) illustrative list of such packages:

Name	Method(s)	Language	Author(s)
MultiWell	stochastic	Fortran	J. R. Barker <i>et al</i>
UNIMOL	CSE	Fortran	R. G. Gilbert, S. C. Smith
ChemRate	CSE	C++ <sup>1</sup>	V. Mokrushin, W. Tsang
Variflex	CSE	Fortran	S. J. Klippenstein <i>et al</i>
MESMER	CSE (+ RS)	C++	S. H. Robertson <i>et al</i>
CHEMDIS <sup>2</sup>	MSC	Fortran	A. Y. Chang, J. W. Bozzelli, A. M. Dean

(MSC = modified strong collision, RS = reservoir state, CSE = chemically-significant eigenvalues)

Many of the above packages also provide additional functionality beyond the approximate solving of the master equation. For example, Variflex can be used for variational transition state theory calculations, while ChemRate provides a (Windows) graphical user interface for exploring a database of experimental data and physical quantities.

## 2.8 Credits

**Author:** Joshua W. Allen ([joshua.w.allen@gmail.com](mailto:joshua.w.allen@gmail.com))

**P.I.:** Prof. William H. Green ([whgreen@mit.edu](mailto:whgreen@mit.edu))

The author acknowledges the Green group for helping put the software through its paces and providing suggestions for its improvement.

Arkane is based upon work supported by the [King Abdullah University of Science and Technology](#).

- [genindex](#)
- [modindex](#)
- [search](#)

<sup>1</sup> Uses MFC for Windows graphical user interface

<sup>2</sup> No longer distributed

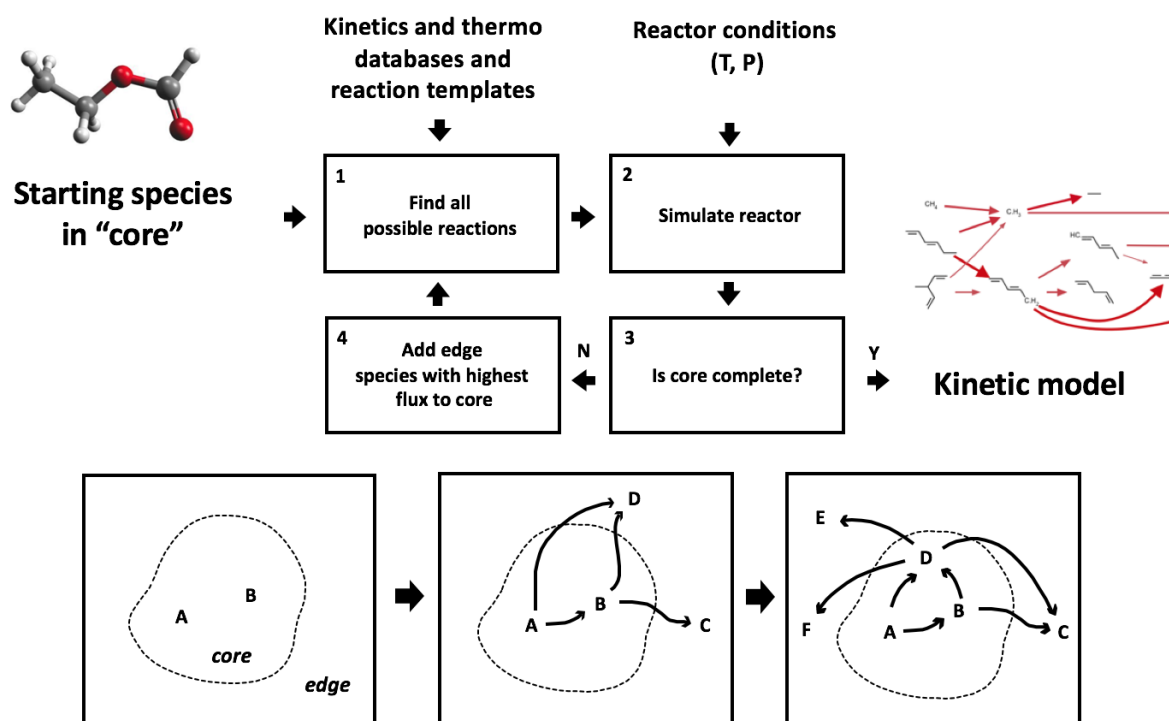


## THEORY GUIDE

The theoretical foundations to some of the parts of RMG and Arkane are described in greater detail in these sections.

### 3.1 RMG Theory Guide

#### 3.1.1 Rate-based Model Enlarging Algorithm



To construct a mechanism, the user must specify an initial set of species and the initial conditions (temperature, pressure, species concentrations, etc.). RMG reacts the initial species in all possible ways according to its known reaction families, and it integrates the model in time. RMG tracks the rate (flux) at which each new “edge” species is produced, and species (and the reactions producing them) that are produced with significant fluxes are incorporated into the model (the “core”). These new core species are reacted with all other core species in the model to generate a new set of edge species and reactions. The time-integration restarts, and the expanded list of edge species is monitored for significant species to be included in the core. The process continues until all significant species and reactions have been included.

in the model. The definition of a “significant” rate can be specified by the user by taking the following definition for a single species rate:

$$R_i = \frac{dC_i}{dt}$$

and the following definition for the reaction system’s characteristic rate, which is the sum of all **core** species rates:

$$R_{char} = \sqrt{\sum_j R_j^2} \quad \text{species } j \in \text{core}$$

When a species  $i \in \text{edge}$  exceeds a “significant” rate equal to  $\epsilon R_{char}$ , it is added to the core. The parameter  $\epsilon$  is the user-specified `toleranceMoveToCore` that can be adjusted under the *model tolerances* in the *RMG Input File*.

For more information on rate-based model enlargement, please refer to the papers [Gao2016] or [Susnow1997].

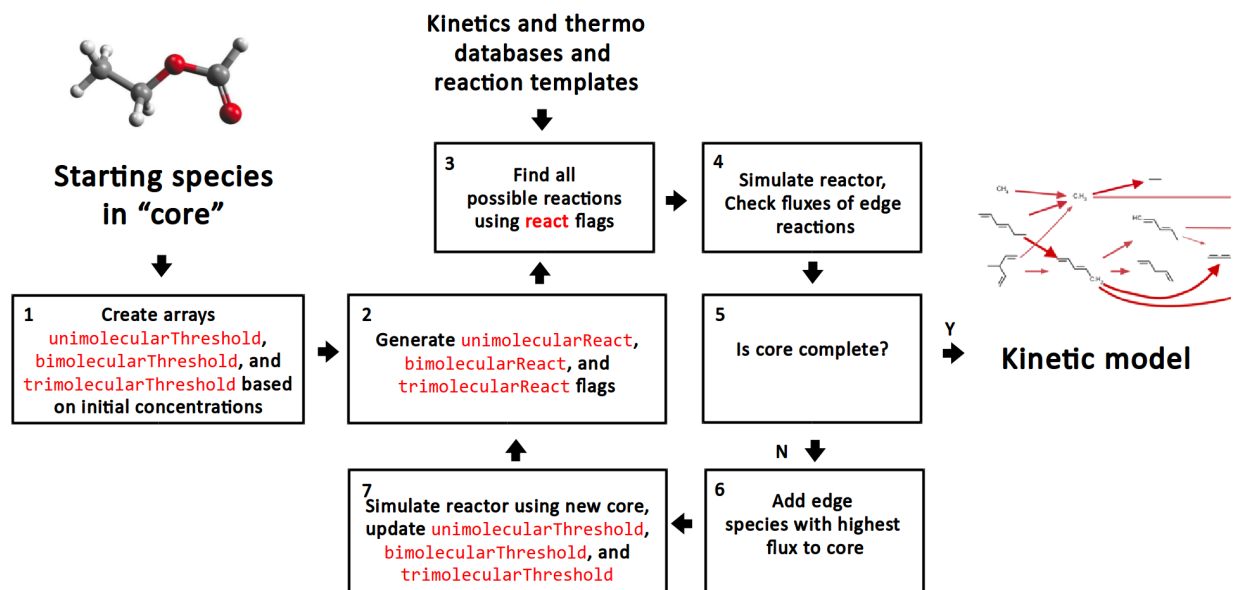
## Filtering Reactions within the Rate-based Algorithm

Filtering reactions in the react step in the flux-based algorithm attempts to speed up model generation by attacking the pain point. RMG has trouble converging when generating models for large molecules because it searches for reactions on the order of  $(n_{\text{reaction sites}})^{n_{\text{species}}}$ .

The original algorithm performs in the following manner:

1. Reacts species together (slow)
2. Determines which reactions are negligible (fast)

By filtering reactions we add a pre-filtering step before step 1 which prevents species from reacting together when the reactions are expected to be negligible throughout the simulation.



Here, `unimolecularThreshold`, `bimolecularThreshold`, and `trimolecularThreshold` are binary arrays storing flags for whether a species or a pair of species are above a reaction threshold. For a unimolecular rate, this threshold is set to True if the unimolecular rate of reaction  $k$  for a species  $A$

$$R_{unimolecular} = k_{threshold} C_A > \epsilon R_{char}$$

at any given time  $t$  in the reaction system, where  $k_{threshold} = \frac{k_B T}{h}$

For a bimolecular reaction occurring between species A and B, this threshold is set to True if the bimolecular rate

$$R_{\text{bimolecular}} = k_{\text{threshold}} C_A C_B > \epsilon R_{\text{char}}$$

where  $k_{\text{threshold}} = \text{filterThreshold}$ . `filterThreshold` is set by the user in the input file and its default value is  $10^8 \frac{\text{m}^3}{\text{mol}\cdot\text{s}}$ . This is on the same order of magnitude as the collision limit for two hydrogen atoms at 1000 K. In general, it is recommended to set `filterThreshold` such that  $k_{\text{threshold}}$  is slightly greater than the maximum rate constants one expects to be present in the system of interest. This will ensure that very fast reactions are not accidentally filtered out.

Similarly, for a trimolecular reaction, the following expression is used:

$$R_{\text{trimolecular}} = k_{\text{threshold}} C_A C_B C_C > \epsilon R_{\text{char}}$$

where  $k_{\text{threshold}} = 10^{-3} \cdot \text{filterThreshold} \frac{\text{m}^6}{\text{mol}^2\cdot\text{s}}$ . Based on extending Smoluchowski theory to multiple molecules, the diffusion limit rate constant for trimolecular reactions (in  $\frac{\text{m}^6}{\text{mol}^2\cdot\text{s}}$ ) is approximately three orders of magnitude smaller than the rate constant for bimolecular reactions (in  $\frac{\text{m}^3}{\text{mol}\cdot\text{s}}$ ). It is assumed here that Smoluchowski theory gives a sufficient approximation to collision theory in the gas phase.

When the liquid-phase reactor is used, the diffusion limits are calculated using the Stokes-Einstein equation instead. For bimolecular reactions, this results in

$$k_{\text{threshold}}[\text{m}^3/\text{mol}/\text{s}] = 22.2 \frac{T[\text{K}]}{\mu[\text{Pa}\cdot\text{s}]}$$

and for trimolecular

$$k_{\text{threshold}}[\text{m}^6/\text{mol}^2/\text{s}] = 0.11 \frac{T[\text{K}]}{\mu[\text{Pa}\cdot\text{s}]}$$

where  $\mu$  is the solvent viscosity. The coefficients in the above equations were obtained by using a representative value of the molecular radius of 2 Angstrom. More details on the calculation of diffusion limits in the liquid phase can be found in [the description of liquid-phase systems](#) under *diffusion-limited kinetics*.

Three additional binary arrays `unimolecularReact`, `bimolecularReact`, and `trimolecularReact` store flags for when the `unimolecularThreshold`, `bimolecularThreshold`, or `trimolecularThreshold` flag shifts from False to True. RMG reacts species when the flag is set to True.

### 3.1.2 Prune Edge Species

When dealing with complicated reaction systems, RMG calculation would easily hit the computer memory limitation. Memory profiling shows most memory especially during memory limitation stage is occupied by edge species. However, most edge species in fact wouldn't be included in the core (or final model). Thus, it's natural to get rid of some not "so useful" edge species during calculation in order to achieve both low memory consumption and mechanism accuracy. Pruning is such a way.

#### Key Parameters in Pruning

- `toleranceKeepInEdge`

Any edge species to prune should have peak flux along the whole conversion course lower than `toleranceKeepInEdge * characteristic flux`. Thus, larger values will lead to smaller edge mechanisms.

- `toleranceMoveToCore`

Any edge species to enter core model should have flux at some point larger than `toleranceMoveToCore * characteristic flux`. Thus, in general, smaller values will lead to larger core mechanisms.

- `toleranceInterruptSimulation`

Once flux of any edge species exceeds `toleranceInterruptSimulation * characteristic flux`, dynamic simulation will be stopped. Usually this tolerance will be set a very high value so that any flux's exceeding that means mechanism is too incomplete to continue dynamic simulation.

- `maximumEdgeSpecies`

If dynamic simulation isn't interrupted in half way and total number of the edge species whose peak fluxes are higher than `toleranceKeepInEdge * characteristic flux` exceeds `maximumEdgeSpecies`, such excessive amount of edge species with lowest peak fluxes will be pruned.

- `minCoreSizeForPrune`

Ensures that a minimum number of species are in the core before pruning occurs, in order to avoid pruning the model when it is far away from completeness. The default value is set to 50 species.

- `minSpeciesExistIterationsForPrune`

Set the number of iterations an edge species must stay in the job before it can be pruned. The default value is 2 iterations.

## How Pruning Works

### 3.1.3 Dynamics Criterion

When dealing with more complex chemical mechanisms the standard RMG flux criterion has trouble picking up key chain branching reactions and has limited guarantees that it accurately represents the concentrations of all species. The dynamics criterion is a measure of how much a given reaction affects core concentrations. This allows it to pick up key low-flux chain branching reactions and better represent species concentrations.

#### Calculating the Dynamics Criterion

Let us define rates of production  $P_i(t)$  and consumption  $L_i(t)$  for a given species  $\frac{dc_i}{dt} = P_i(t) - L_i(t)$

Let us define a dimensionless concentration variable we will refer to as the accumulation number  $Ac$  for a given species

$$Ac_{spc,i} = \frac{P_i}{L_i} \approx \frac{\bar{c}_i}{c_{i0}}$$

where  $\bar{c}_i$  is the steady state concentration or more specifically the concentration at which  $P_i = L_i$  assuming  $L_i$  scales with  $c_i$  and  $c_{i0}$  is the current concentration.

This species accumulation number is a measure of how far species  $i$  is from steady state.

Since this number can only be calculated for core species, by itself it is only a measure of the behavior of species  $i$  within the reaction network.

However if we consider models with and without some edge reaction  $j$  we can define

$$\Pi_{Ac,i,j} = \frac{Ac_{spc,i,withj}}{Ac_{spc,i,withoutj}}$$

Which is a measure of how much the concentration of species  $i$  is impacted by reaction  $j$ .

In order to directly compare multiple reactions we can then sum over all core species involved in reaction  $j$  to get our criterion the dynamics number.

$$\sum_{i \in core} |Ln(\Pi_{Ac,i,j})| = Dy > \epsilon$$

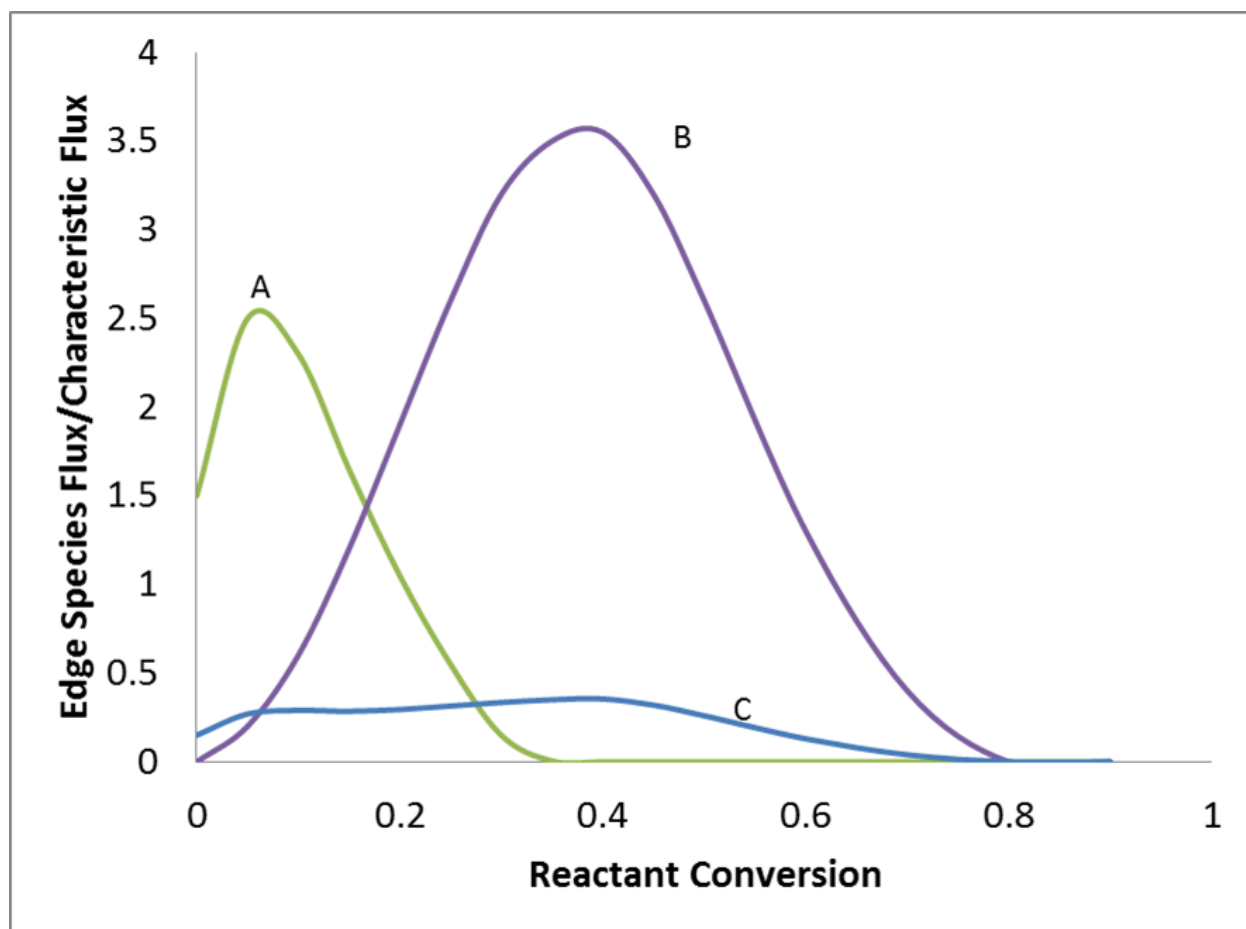


Fig. 1: The goal of pruning is to delete those “useless” edge species. So “usefulness” should be defined and it’s natural to have flux as a criterion for “usefulness”. Since flux changes with reactant conversion, peak flux is chosen here to make decision of pruning or not. Every time pruning is triggered, edge species with peak flux lower than  $\text{toleranceKeepInEdge} * \text{characteristic flux}$  will be deleted.

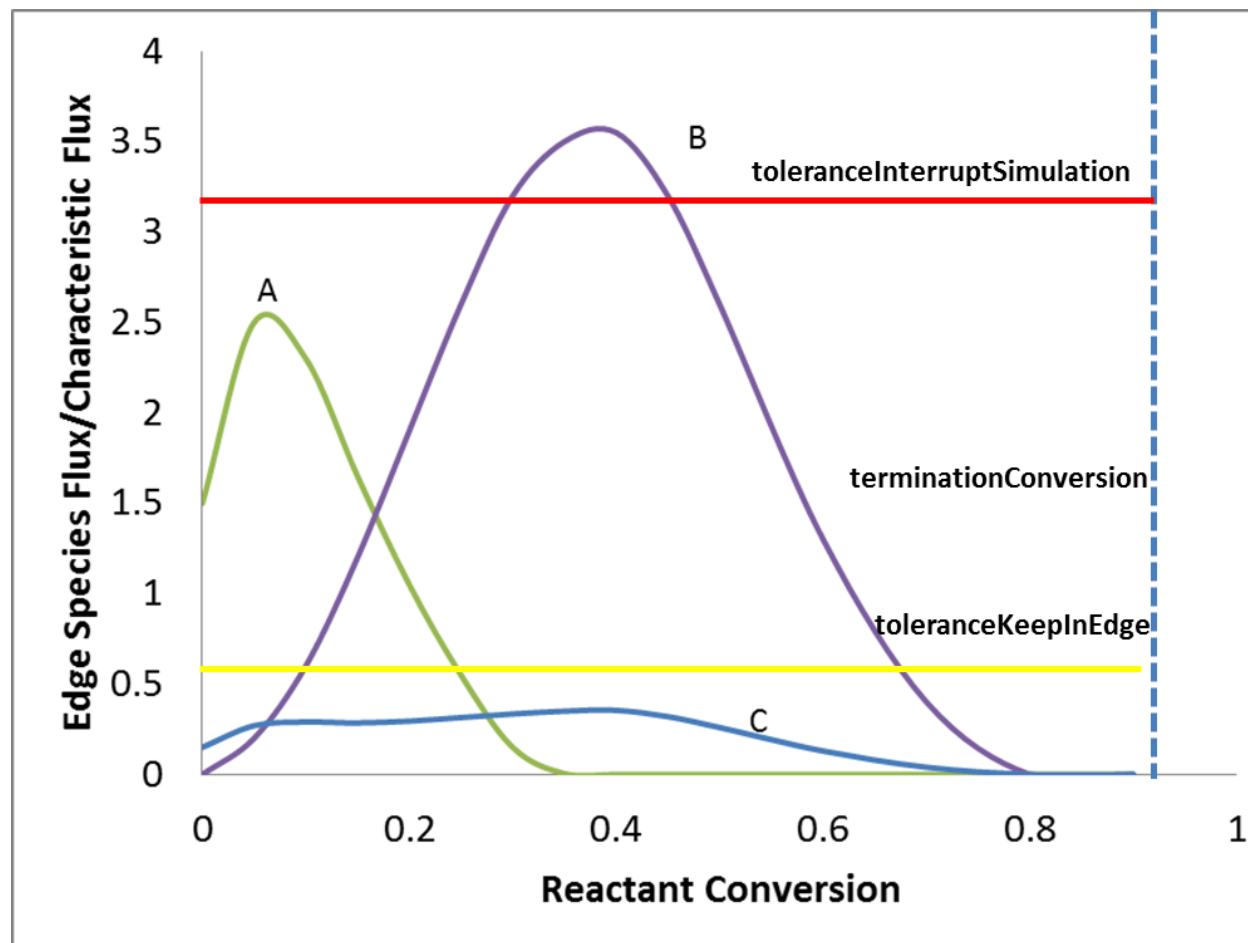


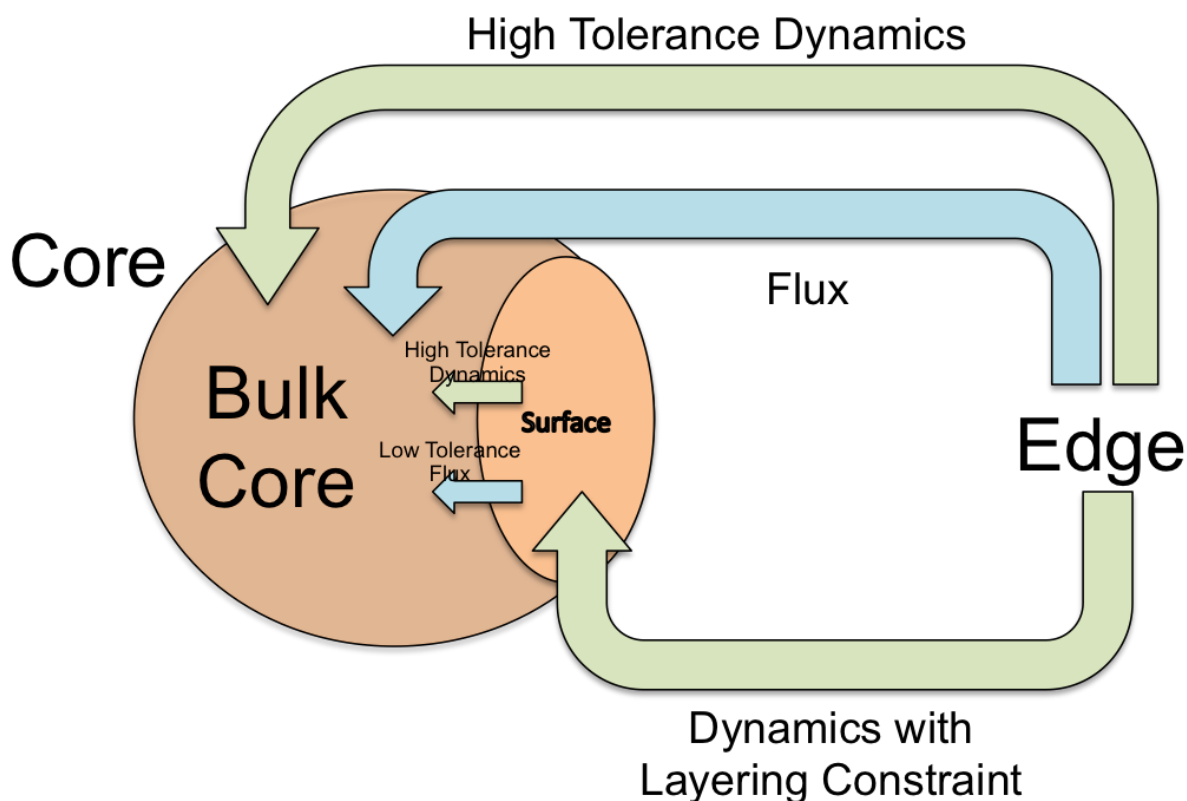
Fig. 2: However, pruning is not always triggered because of `toleranceInterruptSimulation`. As mentioned above, in order to prune, RMG needs to figure out the peak flux of each edge species, which requires dynamic simulation to complete. If some run of dynamic simulation is terminated in half way by `toleranceInterruptSimulation`, pruning is rejected although there might be some edge species with peak fluxes lower than `toleranceKeepInEdge * characteristic flux`. Since pruning requires to complete dynamic simulation, setting `toleranceInterruptSimulation` to be positive infinity, as an extreme case, means always enabling pruning. Another extreme case would be that it has same value as `toleranceMoveToCore` where no pruning occurs.

In summary, each run of dynamic simulation will proceed towards `terminationConversion` unless some flux exceeds `toleranceInterruptSimulation * characteristic flux`. Following complete simulation is the pruning of edge species whose flux is not high enough to be kept in the edge, which is followed by pruning of excessive amount of edge species to make sure total edge species number is no greater than `maximumEdgeSpecies`.



## Surface Algorithm

One common issue with the dynamics criterion is that it treats all core species equally. Because of this, if the dynamics criterion is set too low it enters a feedback loop where it adds species and then since it can't get those species' concentrations right it adds more species and so on. In order to avoid this feedback loop the surface algorithm was developed. It creates a new partition called the *surface* that is considered part of the core. We will refer to the part of the core that is not part of the surface as the *bulk core*. When operating without the dynamics criterion everything moves from edge to the bulk core as usual; however the dynamics criterion is managed differently. When using the surface algorithm most reactions pulled in by the dynamics criterion enter the surface instead of the bulk core. However, unlike movement to bulk core a constraint is placed on movement to the surface. Any reaction moved to the surface must have either both reactants or both products in the bulk core. This prevents the dynamics criterion from pulling in reactions to get the concentrations of species in the surface right avoiding the feedback loop. To avoid important species being trapped in the surface we also add criteria for movement from surface to bulk core based on flux or dynamics criterion. However, to avoid important species being trapped in the surface we also add criteria for movement from surface to bulk core based on flux or dynamics criterion.



## Key Parameters for Dynamics Criterion and Surface Algorithm

- **toleranceMoveEdgeReactionToCore**

An edge reaction will be pulled directly into the bulk core if its dynamics number ever exceeds this value.

- **toleranceMoveEdgeReactionToSurface**

An edge reaction will be pulled into the surface if its dynamics number ever exceeds this value.

- **toleranceMoveEdgeReactionToCoreInterrupt**

When any reaction's dynamics number exceeds this value the simulation will be interrupted.

- **toleranceMoveEdgeReactionToSurfaceInterrupt**

When the dynamics number of any reaction that would be valid for movement to the surface exceeds this value the simulation will be interrupted

- **toleranceMoveSurfaceReactionToCore**

A surface reaction will be pulled into the bulk core if its dynamics number ever exceeds this value. Note this is done on the fly during simulation.

- **toleranceMoveSurfaceSpeciesToCore**

A surface species will be pulled into the bulk core if it's rate ratio ever exceeds this value. Note this is done on the fly during simulation.

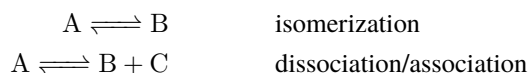
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## 3.2 Pressure-Dependence Theory Guide

### 3.2.1 Introduction

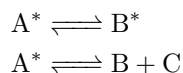
#### Unimolecular Reactions

Unimolecular reactions are those that involve a single reactant or product molecule, the union of isomerization and dissociation/association reactions:



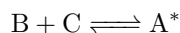
Gas-phase chemical reactions occur as the result of bimolecular collisions between two reactant molecules. This presents a problem when there is only one participating reactant molecule! The conclusion is that the above reactions cannot be elementary as written; another step must be involved.

For a unimolecular reaction to proceed, the reactant molecule A must first be excited to an energy that exceeds the barrier for reaction. A molecule that is sufficiently excited to react is called an *activated species* and often labeled with an asterisk A\*. If we replace the stable species with the activated species in the reactions above, the reactions become elementary again:

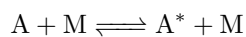


There are a number of ways that an activated species A\* can be produced:

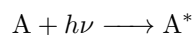
- **Chemical activation.** A\* is produced as the adduct of an association reaction:



- **Thermal activation.** A\* is produced via transfer of energy from an otherwise inert species M via bimolecular collision:



- **Photoactivation.**  $A^*$  is produced as a result of absorption of a photon:



Once an activated molecule has been produced, multiple isomerization and dissociation reactions may become competitive with one another and with collisional stabilization (thermal deactivation); these combine to form a network of unimolecular reactions. The major pathway will depend on the relative rates of collision and reaction, which in turn is a function of both temperature and pressure. At high pressure the collision rate will be fast, and activated molecules will tend to be collisionally stabilized before reactive events can occur; this is called the *high-pressure limit*. At low pressures the collision rate will be slow, and activated molecules will tend to isomerize and dissociate, often traversing multiple reactive events before collisional stabilization can occur.

The onset of the pressure-dependent regime varies with both temperature and molecular size. The figure below shows the approximate pressure at which pressure-dependence becomes important as a function of temperature and molecular size. The parameter  $m \equiv N_{\text{vib}} + \frac{1}{2}N_{\text{rot}}$  represents a count of the internal degrees of freedom (vibrations and hindered rotors, respectively). The ranges of the x-axis and y-axis suggest that pressure dependence is in fact important over a wide regime of conditions of practical interest, particularly in high-temperature processes such as pyrolysis and combustion [Wong2003].

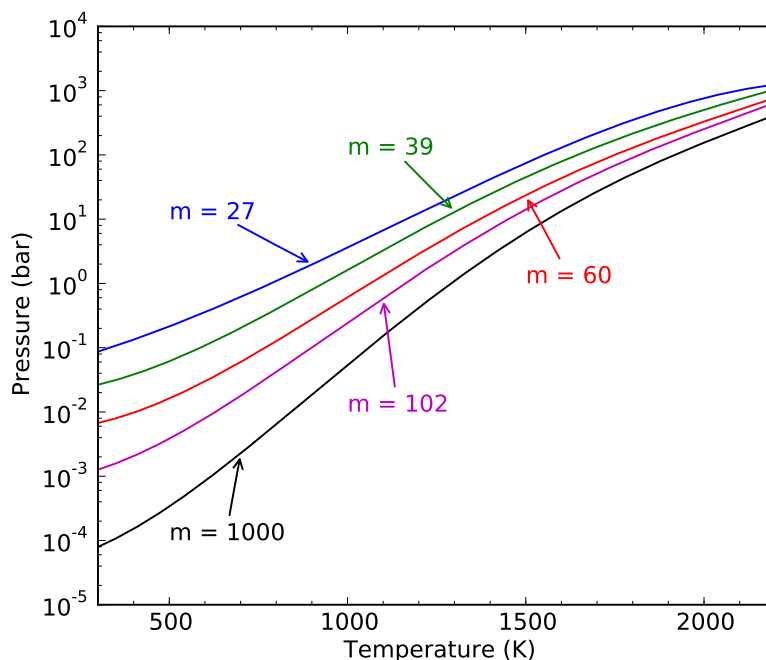


Fig. 3: Plot of the switchover pressure – indicating the onset of pressure dependence – as a function of temperature and molecular size. The value  $m \equiv N_{\text{vib}} + \frac{1}{2}N_{\text{rot}}$  represents a count of the internal degrees of freedom. Over a wide variety of conditions of practical interest, even very large molecules exhibit significant pressure dependence. Figure adapted from Wong, Matheu and Green (2003).

## Historical Context

The importance of bimolecular collisions in unimolecular reactions was first proposed by Lindemann in 1922 [Lindemann1922]. It was soon recognized by Hinshelwood and others that a rigorous treatment of these processes required consideration of molecular energy levels [Hinshelwood1926]. The RRKM expression for the microcanonical rate coefficient  $k(E)$  was derived in the early 1950s [Rice1927] [Kassel1928] [Marcus1951]. In the late 1950s master equation models of chemical systems began appearing [Siegert1949] [Bartholomay1958] [Montroll1958] [Krieger1960] [Gans1960], including an early linear integral-differential equation formulation by Widom [Widom1959]. Analytical solutions for a variety of simple models soon followed [Keck1965] [Troelike1967] [Troelike1973], as did the first numerical approaches [Tardy1966]. Numerical methods – which are required for complex unimolecular reaction networks – became much more attractive in the 1970s with the appearance of new algorithms, including Gear’s method for solving stiff systems of ordinary differential equations [Gear1971] and efficient algorithms for calculating the density of states [Beyer1973] [Stein1973] [Astholz1979]. In the 1990s computing power had increased to the point where it was practical to solve them numerically by discretizing the integrals over energy.

### 3.2.2 The Master Equation

A full treatment of the energy states of each molecule is unfeasible for molecules larger than diatomics, as there are simply too many states. To simplify things we apply the RRKM approximation, which leaves the state of a molecule as a function of two quantities: the total energy  $E$  and total angular momentum quantum number  $J$ . Frequently we will find that even this is too difficult, and will only keep the total energy  $E$  as an independent variable.

#### Isomers, Reactants, and Products

Throughout this document we will utilize the following terminology:

- An **isomer** is a unimolecular configuration on the potential energy surface.
- A **reactant channel** is a bimolecular configuration that associates to form an isomer. Dissociation from the isomer back to reactants is allowed.
- A **product channel** is a bimolecular configuration that is formed by dissociation of an isomer. Reassociation of products to the isomer is *not* allowed.

The isomers are the configurations for which we must model the energy states. We designate  $p_i(E, J, t)$  as the population of isomer  $i$  having total energy  $E$  and total angular momentum quantum number  $J$  at time  $t$ . At long times, statistical mechanics requires that the population of each isomer approach a Boltzmann distribution  $b_i(E, J)$ :

$$\lim_{t \rightarrow \infty} p_i(E, J, t) \propto b_i(E, J)$$

We can simplify by eliminating the angular momentum quantum number to get

$$p_i(E, t) = \sum_J p_i(E, J, t)$$

Let us also denote the (time-dependent) total population of isomer  $i$  by  $x_i(t)$ :

$$x_i(t) \equiv \sum_J \int_0^\infty p_i(E, J, t) dE$$

The two molecules of a reactant or product channel are free to move apart from one another and interact independently with other molecules in the system. Accordingly, we treat these channels as fully thermalized, leaving as the only variable the total concentrations  $y_{nA}(t)$  and  $y_{nB}(t)$  of the molecules  $A_n$  and  $B_n$  of reactant channel  $n$ . (Since the product channels act as infinite sinks, their populations do not need to be considered explicitly.)

Finally, we will use  $N_{\text{isom}}$ ,  $N_{\text{reac}}$ , and  $N_{\text{prod}}$  as the numbers of isomers, reactant channels, and product channels, respectively, in the system.

## Collision Models

Bimolecular collisions with an inert species M are the primary means by which an isomer molecule changes its energy. A reasonable estimate – although generally a bit of an underestimate – of the total rate of collisions  $k_{\text{coll},i}(T)$  for each isomer  $i$  comes from Lennard-Jones collision theory:

$$k_{\text{coll},i}(T) = \sqrt{\frac{8k_{\text{B}}T}{\pi\mu_i}} \pi d_i^2 \Omega_i^{(2,2)*}$$

Above,  $\mu_i$  is the reduced mass,  $d_i$  is the collision diameter, and  $k_{\text{B}}$  is the Boltzmann constant. The collision diameter is generally taken as  $d \approx \frac{1}{2}(\sigma_i + \sigma_{\text{M}})$ , the arithmetic average of the Lennard-Jones  $\sigma$  parameter for the isomer and the bath gas. The parameter  $\Omega_i^{(2,2)*}$  represents a configurational integral, which is well-approximated by the expression

$$\Omega_i^{(2,2)*} = 1.16145\tilde{T}^{-0.14874} + 0.52487e^{-0.7732\tilde{T}} + 2.16178e^{-2.437887\tilde{T}}$$

where  $\tilde{T} \equiv k_{\text{B}}T/\sqrt{\epsilon_i\epsilon_{\text{M}}}$  is a reduced temperature and  $\epsilon_i$  is the Lennard-Jones  $\epsilon$  parameter. Note that we have used a geometric average for the  $\epsilon$  parameters of the isomer and the bath gas in this expression. Assuming the total gas concentration to be constant and that the gas is ideal, we obtain an expression for the collision frequency  $\omega_i(T, P)$ , which makes explicit the pressure dependence:

$$\omega_i(T, P) = k_{\text{coll},i}(T) \frac{P}{k_{\text{B}}T}$$

Now that we have an estimate for the total rate of collisions, we need to develop a model of the effect that these collisions have on the state of the isomer distribution. To this end, we define  $P(E, J, E', J')$  as the probability of a collision resulting in a transfer of a molecule from state  $(E', J')$  to state  $(E, J)$ . There are two mathematical constraints on  $P(E, J, E', J')$ . The first of these is normalization:

$$\sum_{J'} (2J' + 1) \int_0^\infty P(E, J, E', J') dE' = 1$$

The second of these is detailed balance, required in order to obtain the Boltzmann distribution at long times:

$$P(E, J, E', J') b(E', J') = P(E', J', E, J) b(E, J)$$

$$P_i(E', J', E, J) = \frac{\rho_i(E', J')}{\rho_i(E, J)} \exp\left(-\frac{E' - E}{k_{\text{B}}T}\right) P_i(E, J, E', J') \quad E < E'$$

Rather than define models directly for  $P(E, J, E', J')$ , we usually eliminate the angular momentum contribution and instead define  $P(E, E')$ . This can be related to  $P(E, J, E', J')$  via

$$P(E, J, E', J') = P(E, E') \phi(E, J) = P(E, E') (2J + 1) \frac{\rho(E, J)}{\rho(E')}$$

where  $\rho(E) \equiv \sum_J (2J + 1) \rho(E, J)$ .

There are a variety of models used for  $P(E, E')$ . By far the most common is the single exponential down model

$$P(E, E') = C(E') \exp\left(-\frac{E' - E}{\alpha}\right) \quad E < E'$$

where  $C(E')$  is determined from the normalization constraint. Note that this function has been defined for the deactivating direction ( $E < E'$ ) only, as the activating direction ( $E > E'$ ) is then set from detailed balance. The parameter  $\alpha$  corresponds to the average energy transferred in a deactivating collision  $\langle \Delta E_{\text{d}} \rangle$ , which itself is a weak function of temperature.

Other models for  $P(E, J, E', J')$  include the Gaussian down

$$P(E, E') = C(E') \exp\left[-\frac{(E' - E)^2}{\alpha^2}\right] \quad E < E'$$

and the double exponential down

$$P(E, E') = C(E') \left[ (1 - f) \exp\left(-\frac{E' - E}{\alpha_1}\right) + f \exp\left(-\frac{E' - E}{\alpha_2}\right) \right] \quad E < E'$$

The parameters for these simple models generally contain so much uncertainty that more complex functional forms are generally not used.

## Reaction Models

Chemical reaction events cause a change in molecular configuration at constant energy. The rate coefficient for this process must be determined as a function of energy rather than the usual temperature. Such a quantity is called a *microcanonical rate coefficient* and written as  $k(E, J)$ . In the master equation we will differentiate between microcanonical rate coefficients for isomerization, dissociation, and association by using different letters:  $k_{ij}(E, J)$  for isomerization,  $g_{nj}(E, J)$  for dissociation, and  $f_{im}(E, J)$  for association. (By convention, we use indices  $i$  and  $j$  to refer to unimolecular isomers,  $m$  and  $n$  to refer to bimolecular reactant and product channels, and, later,  $r$  and  $s$  to refer to energy grains.)

As with collision models, the values of the microcanonical rate coefficients are constrained by detailed balance so that the proper equilibrium is obtained. The detailed balance expressions have the form

$$k_{ij}(E, J)\rho_j(E, J) = k_{ji}(E, J)\rho_i(E, J)$$

for isomerization and

$$f_{in}(E, J)\rho_n(E, J) = g_{ni}(E, J)\rho_i(E, J)$$

for association/dissociation, where  $\rho_i(E, J)$  is the density of states of the appropriate unimolecular or bimolecular configuration.

An alternative formulation incorporates the macroscopic equilibrium coefficient  $K_{\text{eq}}(T)$  and equilibrium distributions  $b_i(E, J, T)$  at each temperature:

$$k_{ij}(E, J)b_j(E, J, T) = K_{\text{eq}}(T)k_{ji}(E, J)b_i(E, J, T)$$

for isomerization and

$$f_{in}(E, J)b_n(E, J, T) = K_{\text{eq}}(T)g_{ni}(E, J)b_i(E, J, T)$$

for association/dissociation. Note that these two formulations are equivalent if the molecular degrees of freedom are consistent with the macroscopic thermodynamic parameters. There are multiple reasons to use the latter formulation:

- Only the density of states of the unimolecular isomers need be computed. This is a result of the assumption of thermalized bimolecular channels, which means that we only need to compute the product  $f_{in}b_n$ , and not the individual values of  $f_{in}$  and  $b_n$ .
- Only the reactive rovibrational modes need be included in the density of states. Missing modes will not affect the observed equilibrium because we are imposing the macroscopic equilibrium via  $K_{\text{eq}}(T)$ .
- Constants of proportionality in the density of states become unimportant, as they cancel when taking the ratio  $\rho(E, J)/Q(\beta)$ . For example, if the external rotational constants are unknown then we will include an active K-rotor in the density of states; this property means that the rotational constant of this active K-rotor cancels and is therefore arbitrary.

There are two common ways of determining values for  $k(E, J)$ : the inverse Laplace transform method and RRKM theory. The latter requires detailed information about the transition state, while the former only requires the high-pressure limit rate coefficient  $k_{\infty}(T)$ .

## Inverse Laplace Transform

The microcanonical rate coefficient  $k(E)$  is related to the canonical high-pressure limit rate coefficient  $k_\infty(T)$  via a Boltzmann averaging

$$k_\infty(T) = \frac{\sum_J \int_0^\infty k(E) \rho(E, J) e^{-\beta E} dE}{\sum_J \int_0^\infty \rho(E, J) e^{-\beta E} dE}$$

where  $\rho(E, J)$  is the rovibrational density of states for the reactants and  $\beta \equiv (k_B T)^{-1}$ . Neglecting the angular momentum dependence, the above can be written in terms of Laplace transforms as

$$k_\infty(T) = \frac{\mathcal{L}[k(E)\rho(E)]}{\mathcal{L}[\rho(E)]} = \frac{\mathcal{L}[k(E)\rho(E)]}{Q(\beta)}$$

where  $Q(\beta)$  is the rovibrational partition function for the reactants. The above implies that  $E$  and  $\beta$  are the transform variables. We can take an inverse Laplace transform in order to solve for  $k(E)$ :

$$k(E) = \frac{\mathcal{L}^{-1}[k_\infty(\beta)Q(\beta)]}{\rho(E)}$$

Hidden in the above manipulation is the assumption that  $k_\infty(\beta)$  is valid over a temperature range from zero to positive infinity.

The most common form of  $k_\infty(T)$  is the modified Arrhenius expression

$$k(T) = AT^n \exp\left(-\frac{E_a}{k_B T}\right)$$

where  $A$ ,  $n$ , and  $E_a$  are the Arrhenius preexponential, temperature exponent, and activation energy, respectively. For  $n = 0$  and  $E_a > 0$  the inverse Laplace transform can be easily evaluated to give

$$k(E) = A \frac{\rho(E - E_a)}{\rho(E)} \quad E > E_a$$

We can also determine an expression when  $n > 0$  and  $E_a > 0$  using a convolution integral:

$$k(E) = A \frac{\phi(E - E_a)}{\rho(E)} \quad E > E_a$$

$$\phi(E) = \mathcal{L}^{-1}[T^n Q(\beta)] = \frac{1}{k_B^n \Gamma(n)} \int_0^E (E - x)^{n-1} \rho(x) dx$$

Finally, for cases where  $n < 0$  and/or  $E_a < 0$  we obtain a rough estimate by lumping these contributions into the preexponential at the temperature we are working at. By redoing this at each temperature being considered we minimize the error introduced, at the expense of not being able to identify a single  $k(E)$ .

## RRKM Theory

RRKM theory – named for Rice, Ramsperger, Kassel, and Marcus – is a microcanonical transition state theory. Like canonical transition state theory, detailed information about the transition state and reactants are required, e.g. from a quantum chemistry calculation. If such information is available, then the microcanonical rate coefficient can be evaluated via the equation

$$k(E, J) = \frac{N^\ddagger(E, J)}{h \rho(E, J)}$$

where  $N^\ddagger(E, J)$  is the sum of states of the transition state,  $\rho(E, J)$  is the density of states of the reactant, and  $h$  is the Planck constant. Both the transition state and the reactants have been referenced to the same zero of energy. The sum of states is related to the density of states via

$$N(E, J) = \int_0^E \rho(x, J) dx$$

The angular momentum quantum number dependence can be removed via

$$k(E) = \sum_J (2J + 1) k(E, J)$$

## The Full Master Equation

The governing equation for the population distributions  $p_i(E, J, t)$  of each isomer  $i$  and the reactant concentrations  $y_{nA}(t)$  and  $y_{nB}(t)$  combines the collision and reaction models to give a linear integro-differential equation:

$$\begin{aligned} \frac{d}{dt} p_i(E, J, t) = & \omega_i(T, P) \sum_{J'} \int_0^\infty P_i(E, J, E', J') p_i(E', J', t) dE' - \omega_i(T, P) p_i(E, J, t) \\ & + \sum_{j \neq i}^{N_{\text{isom}}} k_{ij}(E, J) p_j(E, J, t) - \sum_{j \neq i}^{N_{\text{isom}}} k_{ji}(E, J) p_i(E, J, t) \\ & + \sum_{n=1}^{N_{\text{reac}}} y_{nA}(t) y_{nB}(t) f_{in}(E, J) b_n(E, J, t) - \sum_{n=1}^{N_{\text{reac}} + N_{\text{prod}}} g_{ni}(E, J) p_i(E, J, t) \\ \frac{d}{dt} y_{nA}(t) = & \frac{d}{dt} y_{nB}(t) = \sum_{i=1}^{N_{\text{isom}}} \int_0^\infty g_{ni}(E, J) p_i(E, J, t) dE \\ & - \sum_{i=1}^{N_{\text{isom}}} y_{nA}(t) y_{nB}(t) \int_0^\infty f_{in}(E, J) b_n(E, J, t) dE \end{aligned}$$

A summary of the variables is given below:

Variable	Meaning
$p_i(E, J, t)$	Population distribution of isomer $i$
$y_{nA}(t)$	Total population of species $A_n$ in reactant channel $n$
$\omega_i(T, P)$	Collision frequency of isomer $i$
$P_i(E, J, E', J')$	Collisional transfer probability from $(E', J')$ to $(E, J)$ for isomer $i$
$k_{ij}(E, J)$	Microcanonical rate coefficient for isomerization from isomer $j$ to isomer $i$
$f_{im}(E, J)$	Microcanonical rate coefficient for association from reactant channel $m$ to isomer $i$
$g_{nj}(E, J)$	Microcanonical rate coefficient for dissociation from isomer $j$ to reactant or product channel $n$
$b_n(E, J, t)$	Boltzmann distribution for reactant channel $n$
$N_{\text{isom}}$	Total number of isomers
$N_{\text{reac}}$	Total number of reactant channels
$N_{\text{prod}}$	Total number of product channels

The above is called the two-dimensional master equation because it contains two dimensions: total energy  $E$  and total angular momentum quantum number  $J$ . In the first equation (for isomers), the first pair of terms correspond to collision, the second pair to isomerization, and the final pair to association/dissociation. Similarly, in the second equation above (for reactant channels), the pair of terms refer to dissociation/association.



We can also simplify the above to the one-dimensional form, which only has  $E$  as a dimension:

$$\begin{aligned} \frac{d}{dt} p_i(E, t) &= \omega_i(T, P) \int_0^\infty P_i(E, E') p_i(E', t) dE' - \omega_i(T, P) p_i(E, t) \\ &+ \sum_{j \neq i}^{N_{\text{isom}}} k_{ij}(E) p_j(E, t) - \sum_{j \neq i}^{N_{\text{isom}}} k_{ji}(E) p_i(E, t) \\ &+ \sum_{n=1}^{N_{\text{reac}}} y_{nA}(t) y_{nB}(t) f_{in}(E) b_n(E, t) - \sum_{n=1}^{N_{\text{reac}} + N_{\text{prod}}} g_{ni}(E) p_i(E, t) \\ \frac{d}{dt} y_{nA}(t) &= \frac{d}{dt} y_{nB}(t) = \sum_{i=1}^{N_{\text{isom}}} \int_0^\infty g_{ni}(E) p_i(E, t) dE \\ &- \sum_{i=1}^{N_{\text{isom}}} y_{nA}(t) y_{nB}(t) \int_0^\infty f_{in}(E) b_n(E, t) dE \end{aligned}$$

The equations as given are nonlinear, both due to the presence of the bimolecular reactants and because both  $\omega_i$  and  $P_i(E, E')$  depend on the composition, which is changing with time. The rate coefficients can be derived from considering the pseudo-first-order situation where  $y_{nA}(t) \ll y_{nB}(t)$ , and all  $y(t)$  are negligible compared to the bath gas  $M$ . From these assumptions the changes in  $\omega_i$ ,  $P_i(E, E')$ , and all  $y_{nB}$  can be neglected, which yields a linear equation system.

### The Energy-Grained Master Equation

Except for the simplest of unimolecular reaction networks, both the one-dimensional and two-dimensional master equation must be solved numerically. To do this we must discretize and truncate the energy domain into a finite number of discrete bins called *grains*. This converts the linear integro-differential equation into a system of first-order ordinary differential equations:

$$\frac{d}{dt} \begin{bmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \\ \vdots \\ y_{1A} \\ y_{2A} \\ \vdots \end{bmatrix} = \begin{bmatrix} \mathbf{M}_1 & \mathbf{K}_{12} & \cdots & \mathbf{F}_{11} \mathbf{b}_1 y_{1B} & \mathbf{F}_{12} \mathbf{b}_2 y_{2B} & \cdots \\ \mathbf{K}_{21} & \mathbf{M}_2 & \cdots & \mathbf{F}_{21} \mathbf{b}_1 y_{1B} & \mathbf{F}_{22} \mathbf{b}_2 y_{2B} & \cdots \\ \vdots & \vdots & \ddots & \vdots & \vdots & \ddots \\ (\mathbf{g}_{11})^T & (\mathbf{g}_{12})^T & \cdots & h_1 & 0 & \cdots \\ (\mathbf{g}_{21})^T & (\mathbf{g}_{22})^T & \cdots & 0 & h_2 & \cdots \\ \vdots & \vdots & \ddots & \vdots & \vdots & \ddots \end{bmatrix} \begin{bmatrix} \mathbf{p}_1 \\ \mathbf{p}_2 \\ \vdots \\ y_{1A} \\ y_{2A} \\ \vdots \end{bmatrix}$$

The diagonal matrices  $\mathbf{K}_{ij}$  and  $\mathbf{F}_{in}$  and the vector  $\mathbf{g}_{ni}$  contain the microcanonical rate coefficients for isomerization, association, and dissociation, respectively:

$$\begin{aligned} (\mathbf{K}_{ij})_{rs} &= \begin{cases} \frac{1}{\Delta E_r} \int_{E_r - \Delta E_r/2}^{E_r + \Delta E_r/2} k_{ij}(E) dE & r = s \\ 0 & r \neq s \end{cases} \\ (\mathbf{F}_{in})_{rs} &= \begin{cases} \frac{1}{\Delta E_r} \int_{E_r - \Delta E_r/2}^{E_r + \Delta E_r/2} f_{in}(E) dE & r = s \\ 0 & r \neq s \end{cases} \\ (\mathbf{g}_{ni})_r &= \frac{1}{\Delta E_r} \int_{E_r - \Delta E_r/2}^{E_r + \Delta E_r/2} g_{ni}(E) dE \end{aligned}$$

The matrices  $\mathbf{M}_i$  represent the collisional transfer probabilities minus the rates of reactive loss to other isomers and to reactants and products:

$$(\mathbf{M}_i)_{rs} = \begin{cases} \omega_i [P_i(E_r, E_r) - 1] - \sum_{j \neq i}^{N_{\text{isom}}} k_{ij}(E_r) - \sum_{n=1}^{N_{\text{reac}} + N_{\text{prod}}} g_{ni}(E_r) & r = s \\ \omega_i P_i(E_r, E_s) & r \neq s \end{cases}$$

The scalars  $h_n$  are simply the total rate coefficient for loss of reactant channel  $n$  due to chemical reactions:

$$h_n = - \sum_{i=1}^{N_{\text{isom}}} \sum_{r=1}^{N_{\text{grains}}} y_{nB} f_{in}(E_r) b_n(E_r)$$

## Further Reading

The interested reader is referred to any of a variety of other sources for alternative presentations, of which an illustrative sampling is given here [Gilbert1990] [Baer1996] [Holbrook1996] [Forst2003] [Pilling2003].

## 3.2.3 Methods for Determining Phenomenological Rate Coefficients

Solving the energy-grained master equation is often prohibitively expensive for chemical reaction mechanisms of even modest size. Instead, we seek to reduce the master equation matrix down to a set of phenomenological rate coefficients  $k(T, P)$ . In particular, we need to replace the isomer population distributions  $p_i(E, t)$  with the corresponding time-dependent total isomer populations  $x_i(t)$ .

Three methods of varying rigor, computational cost, and robustness will be discussed in the upcoming sections. The modified strong collision (MSC) method is the fastest and most robust, but utilizes the least realistic approximations. The reservoir state (RS) method uses better approximations, which leads to increased accuracy, but requires more computational effort. Finally, the chemically-significant eigenvalues (CSE) method is the most theoretically sound, but is very computationally expensive and not very robust. Your choice of method will depend on the particular balance between expense, robustness, and rigor that is required for your intended application.

## A Common Formalism

All of the methods discussed here can be expressed in terms of a common formalism. Each method seeks to express the population distribution vector  $p_i(E, t)$  for each unimolecular isomer  $i$  as a linear combination of the total populations  $x_j(t)$  and  $y_{mA}(t)y_{mB}$  of unimolecular isomers  $A_j$  and reactant channels  $A_m + B_m$ :

$$p_i(E, t) = \sum_{j=1}^{N_{\text{isom}}} x_j(t) u_{ij}(E) + \sum_{m=1}^{N_{\text{reac}}} y_{mA}(t) y_{mB} v_{im}(E)$$

The function  $u_{ij}(E)$  represents the portion of the population distribution of unimolecular isomer  $i$  at energy  $E$  that tracks the population of isomer  $j$ . In the modified strong collision and reservoir state methods, this is because the energy levels of isomer  $i$  are in pseudo-steady-state relationships with isomer  $j$ . The interpretation is a bit different for the chemically-significant eigenvalues method, but the form of the equations is the same. Similarly, the function  $v_{im}(E)$  represents the population distribution of unimolecular isomer  $i$  at energy  $E$  that tracks the population of reactant channel  $m$ . Both functions  $u_{ij}(E)$  and  $v_{im}(E)$  are functions of energy only, and not of time.

After discretizing the energy domain, the above becomes

$$\mathbf{p}_i(t) = \sum_{j=1}^{N_{\text{isom}}} x_j(t) \mathbf{u}_{ij} + \sum_{m=1}^{N_{\text{reac}}} y_{mA}(t) y_{mB} \mathbf{v}_{im}$$

The phenomenological rate coefficients can be constructed from the energy-grained master equation matrix and the

vectors  $\mathbf{u}_{ij}$  and  $\mathbf{v}_{im}$ :

$$\begin{aligned}
 k_{ij}(T, P) &= \sum_{s=1}^{N_{\text{grains}}} (\mathbf{M}_i \mathbf{u}_{ij})_s + \sum_{\ell \neq i}^{N_{\text{isom}}} \sum_{s=1}^{N_{\text{grains}}} (\mathbf{K}_{i\ell} \mathbf{u}_{\ell j})_s \\
 k_{im}(T, P) &= \sum_{s=1}^{N_{\text{grains}}} (\mathbf{M}_i \mathbf{v}_{im})_s + \sum_{\ell \neq i}^{N_{\text{isom}}} \sum_{s=1}^{N_{\text{grains}}} (\mathbf{K}_{i\ell} \mathbf{v}_{\ell m})_s + \sum_{s=1}^{N_{\text{grains}}} (\mathbf{F}_{im} \mathbf{b}_m)_s \\
 k_{nj}(T, P) &= \sum_{\ell=1}^{N_{\text{isom}}} \mathbf{g}_{n\ell} \cdot \mathbf{u}_{\ell j} \\
 k_{nm}(T, P) &= \sum_{\ell=1}^{N_{\text{isom}}} \mathbf{g}_{n\ell} \cdot \mathbf{v}_{\ell m}
 \end{aligned}$$

Above, the indices  $i$  and  $j$  represent unimolecular isomers of the initial adduct,  $m$  represents bimolecular reactants,  $n$  represents bimolecular reactants and products, and  $s$  represents an energy grain. Thus, the rate coefficients above are for isomerization, association, dissociation, and bimolecular reactions, respectively.

The output from each of the three methods is a set of phenomenological rate coefficients  $k(T, P)$  and the vectors  $\mathbf{u}_{ij}$  and  $\mathbf{v}_{im}$  which can be used to construct the approximate population distribution predicted by that method.

### The Modified Strong Collision Method

### The Reservoir State Method

### The Chemically-Significant Eigenvalues Method

- genindex
- modindex
- search



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