

CAABA/MECCA-3.0

User Manual

*Chemistry As A Boxmodel Application /
Module Efficiently Calculating the
Chemistry of the Atmosphere*

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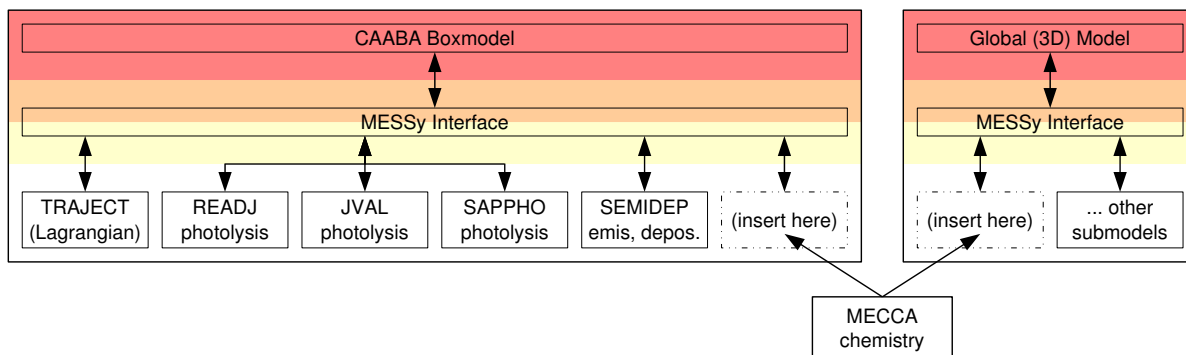


Figure 1: Diagram showing MECCA as part of the CAABA box model or of a global model.

1 Introduction

MECCA (Module Efficiently Calculating the Chemistry of the Atmosphere) is an atmospheric chemistry module that contains a comprehensive chemical mechanism with tropospheric and stratospheric chemistry of both the gas and the aqueous phase (Sander et al., 2005). For the numerical integration, MECCA uses the KPP software (Sandu and Sander, 2006).

To apply the MECCA chemistry to atmospheric conditions, MECCA must be connected to a base model. As shown in Fig. 1, the base model can be a complex, 3-dimensional model (e.g. Jöckel et al., 2006) but it can also be a simple box model. The connection is established via the MESSy interface (<http://www.messy-interface.org>) developed by Jöckel et al. (2005).

This manual describes how to install and work with MECCA when it is connected to the box model CAABA (Chemistry As A Boxmodel Application). This combination will be referred to as “CAABA/MECCA”. The main features of the CAABA box model are shown in Fig. 2. In addition to MECCA chemistry, CAABA also contains several other submodels, e.g. JVAL for calculating J-values, SAPPHO for simplified and parameterized photolysis rates, and SEMIDEP for simplified emission and deposition.

2 Installation

This section can be skipped if CAABA/MECCA is already installed on your computer.

2.1 System Requirements

2.1.1 Linux/Unix

CAABA/MECCA has been tested successfully on several UNIX-like operating systems. The easiest installation is probably on a Linux PC since several auxiliary

programs are already included in a typical Linux distribution.

2.1.2 MAC OS X

CAABA/MECCA does not work with the version of the `sed` program that is shipped with MAC OS X. Instead, it is necessary to install the GNU version of `sed`, called `gsed`. This can be done using the MacPorts (<http://www.macports.org/>). To ensure that `gsed` is always executed when `sed` is called, a symbolic link from `sed` to `gsed` can be created, e.g.:

```
sudo ln -s /opt/local/bin/gsed
/opt/local/bin/sed
```

Also, there may be problems executing the command “`echo -n`” under OS X. If this is the case, the script `xmecca` needs to be adjusted.

2.1.3 Windows

A native installation under Windows is neither recommended nor supported. However, it is possible to execute the model in a virtual machine running Linux on a Windows PC. The VMware Player, which is needed to run the virtual machine, can be obtained from <http://www.VMware.com>. Information how to obtain the Ubuntu Linux image file with the CAABA/MECCA model (about 8 GB) from our ftp site is given on the MECCA web page at <http://www.mecca.messy-interface.org>.

2.2 Prerequisites

A Fortran95 compiler (mandatory): Several compilers have been tested successfully: `g95` (for Linux), Lahey/Fujitsu (for Linux), Intel (for Linux), Compaq (Alpha UNIX). Other compilers can be used as well, if they accept standard Fortran95 code. It should be noted that the `g95` compiler for Linux is free and can be downloaded from <http://www.g95.org/>.

The Kinetic PreProcessor KPP (mandatory):

This flexible numerical integration package by Sandu and Sander (2006) transforms the chemistry mechanism into a set of ordinary differential equations (ODEs) in Fortran95 syntax. MECCA needs the KPP version that is provided in the `mecca/kpp/` directory. Follow the instructions in `mecca/kpp/readme` to install KPP.

Perl, tcsh, gawk, sed, and gmake (mandatory):

These UNIX tools are standard on Linux systems. Check that recent versions of them are installed. Especially gawk may lead to strange error messages. To test gawk, type:

```
gawk 'BEGIN {print match("X", "[^a-z]")}'
```

The result should be "1". However, you may get "0" as the result on your system. Supposedly, this is not a bug in gawk but a feature. You can solve the problem by setting the environment variable `LC_ALL` to "C":

```
export LC_ALL=C      (if you use bash)
setenv LC_ALL C      (if you use tcsh)
```

When you try the gawk test again, it should work fine.

LaTeX (optional): If you have LaTeX installed on your computer, you can print a table (including rate coefficients and references) of the currently selected mechanism (see Sect. 7.3.3 for details).

netCDF library (strongly recommended): The netCDF library is needed to create model output in netCDF format. It can be obtained from <http://www.unidata.ucar.edu/software/netcdf/>. Note that the *.mod files in the netCDF library are compiler-specific. Thus, it is necessary to create a netCDF library for each Fortran95 compiler and maybe also for each Fortran95 compiler version.

Software for manipulating or displaying netCDF data is listed at: <http://www.unidata.ucar.edu/software/netcdf/software.html>. If you don't have the netCDF library, you can still run the model but produce only ASCII output.

netCDF tools (optional): Several tools are used to analyse the netCDF output when the model is run in the multirun (Sect. 6.1) or Monte-Carlo (Sect. 6.2) mode. Specifically, the NCO programs `ncpdq`, `ncrcat`, and `ncks` from <http://nco.sourceforge.net>, the program `ncdump`, and the program `ncclump` from <http://ncclump.sourceforge.net> are needed.

ferret (optional): The ferret plotting program is needed to plot the contents of the netCDF output using the ferret scripts in the `jnl/` directory (see Sect. 5 for details). To ensure that ferret finds all necessary files, you have to add `./tools` to the `FER_GO` environment variable. The `ferret_paths*template` files show how to

do this. For example, when using the tcsh, type:
`setenv FER_GO "$FER_GO ./tools"`

graphviz (optional): The graphviz program can be used to create graphical visualizations of the reaction mechanism like Fig. 6.

fpc Pascal compiler (optional): To use the tagging diagnostics and isotope modeling features (see Sect. 6.4 for details), version 2.2.0 or higher of the free pascal compiler `fpc` from <http://www.freepascal.org/> is needed.

2.3 Installation

Once all prerequisites are fulfilled, you can install CAABA/MECCA by simply unpacking the zip archive:

```
unzip caaba_3.0.zip
```

Next, you have to check that all settings in `Makefile` are correct. If necessary, edit the file: Choose a Fortran95 compiler (`COMPILER`), enter its name (`F90`) and the compiler options (`F90FLAGS`). If you add a new compiler, check if you need to activate the C-preprocessor option. To activate netCDF output, you also have to edit the `Makefile`:

- Check that the variable `OUTPUT` is set to `NETCDF` (not to `ASCII`).
- Enter the correct netCDF library information in `NETCDF_INCLUDE` and `NETCDF_LIB`.

2.4 Troubleshooting

Should there be any problems with the CAABA/MECCA installation, please check the following:

- Confirm that all prerequisites (see above) are fulfilled!
- Confirm that the perl path in the first line of `sfmakedepend` is correct. It should be the same as the output of the command:
`which perl`
- Confirm that the tcsh paths in the first lines of `xcaaba` and `xmecca` are correct.
- Confirm that the model code was unzipped successfully from the zip archive. Check for potential problems during the unzipping process:
 - Make sure that the directory structure has not changed. Unfortunately, some unzipping programs seem to put all files into one directory, ignoring the original directory structure.

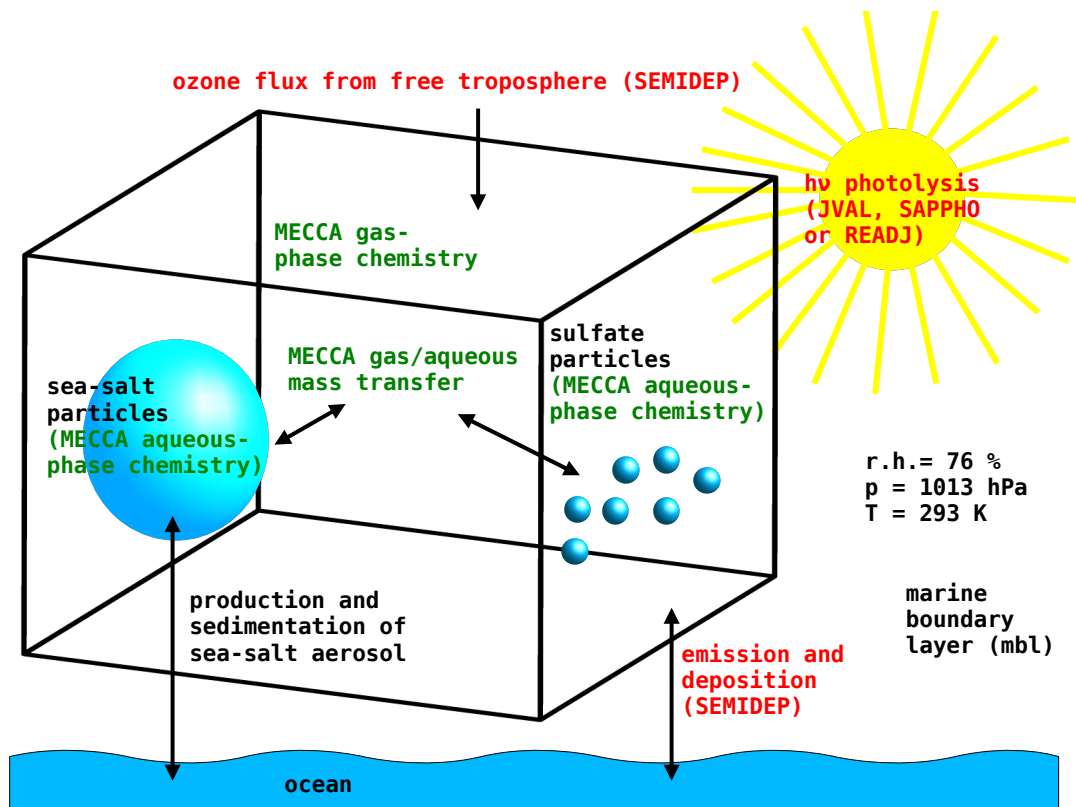


Figure 2: The CAABA box model

- Make sure that links have not been converted to files. For example, the output of the command “file caaba.nml” should tell you that caaba.nml is a symbolic link to nml/simple/caaba.nml.

3 Compiling and running the CAABA/MECCA box model with the shell script xcaaba

First, go to the base directory of the model code (note that all path names given in this manual are relative to this base directory):

```
cd caaba_3.0
```

Next, the tcsh script xcaaba will guide you through the process of running the box model, as illustrated in Fig. 4. To execute xcaaba, type:

```
./xcaaba
```

xcaaba will ask several questions, and recommended answers are given below. If you only press the Return key, you select the default.

```
Start xmecca?
```

If you answer “y”, you can create a new chemical mechanism with xmecca as described in detail in Sect. 4. However, for the first tests with CAABA/MECCA it is recommended to answer “n” and use the simple default mechanism.

Choose an option:

```
s = Start from scratch
c = Compile
r = Run existing executable
h = Help
q = Quit
```

Choose “c” to compile the Fortran95 code. After a successful compilation, xcaaba asks you to choose a namelist file:

```
Choose a namelist file from
the nml/ directory:
...
```

Nameliists control the behaviour of CAABA/MECCA during run-time, and editing them allows to define the model setup at run-time (see Sect. 7.1). The default is to use the same namelist as last time. For the first tests, the file caaba_simple.nml can be chosen. The active contents of the chosen namelist will be shown. Next, xcaaba asks if you want to run the model:

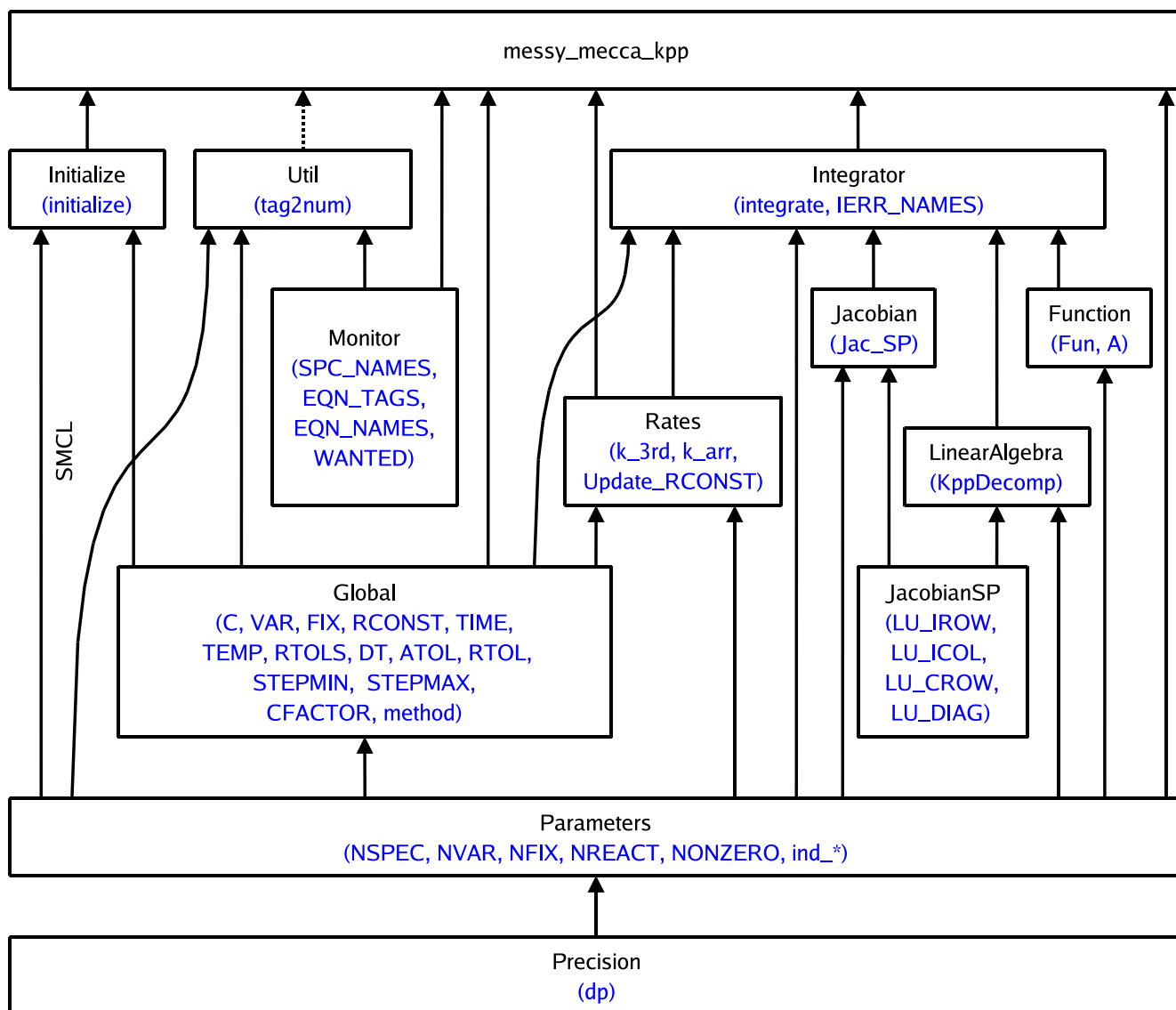


Figure 3: Module structure of KPP-produced Fortran95 files. The arrows start at the module which is exporting the PUBLIC variables and subroutines (which are shown in blue). They point to the module importing them via the Fortran95 USE instruction. A dotted line represents an optional connection.

```
Run CAABA boxmodel with MECCA chemistry?
y = Yes (default)
n = No
q = Quit
```

Answer “y”, and the CAABA/MECCA model simulation will start. The flow control is illustrated in Fig. 5. The model day and the current solar zenith angle (sza) are printed on the screen during the model simulation. The default is to integrate 8 days.

```
Save the output and model code
in output/ directory?
```

Answer “y”, and xcaaba will put the files into a subdirectory with a name based on the date and time of the model simulation, e.g.

output/2011-04-14-12:43:35/. It is recommended to rename the subdirectory to a more descriptive name.

4 Selecting a chemical mechanism with the shell script xmecca

MECCA contains a very comprehensive set of chemical reactions in both the gas phase and the aqueous phase. For many applications, using the complete mechanism will consume too much CPU time. Therefore, the shell script xmecca has been written which allows to create a custom-made subset of the chemical mechanism interactively. Normally, xmecca is called via xcaaba.

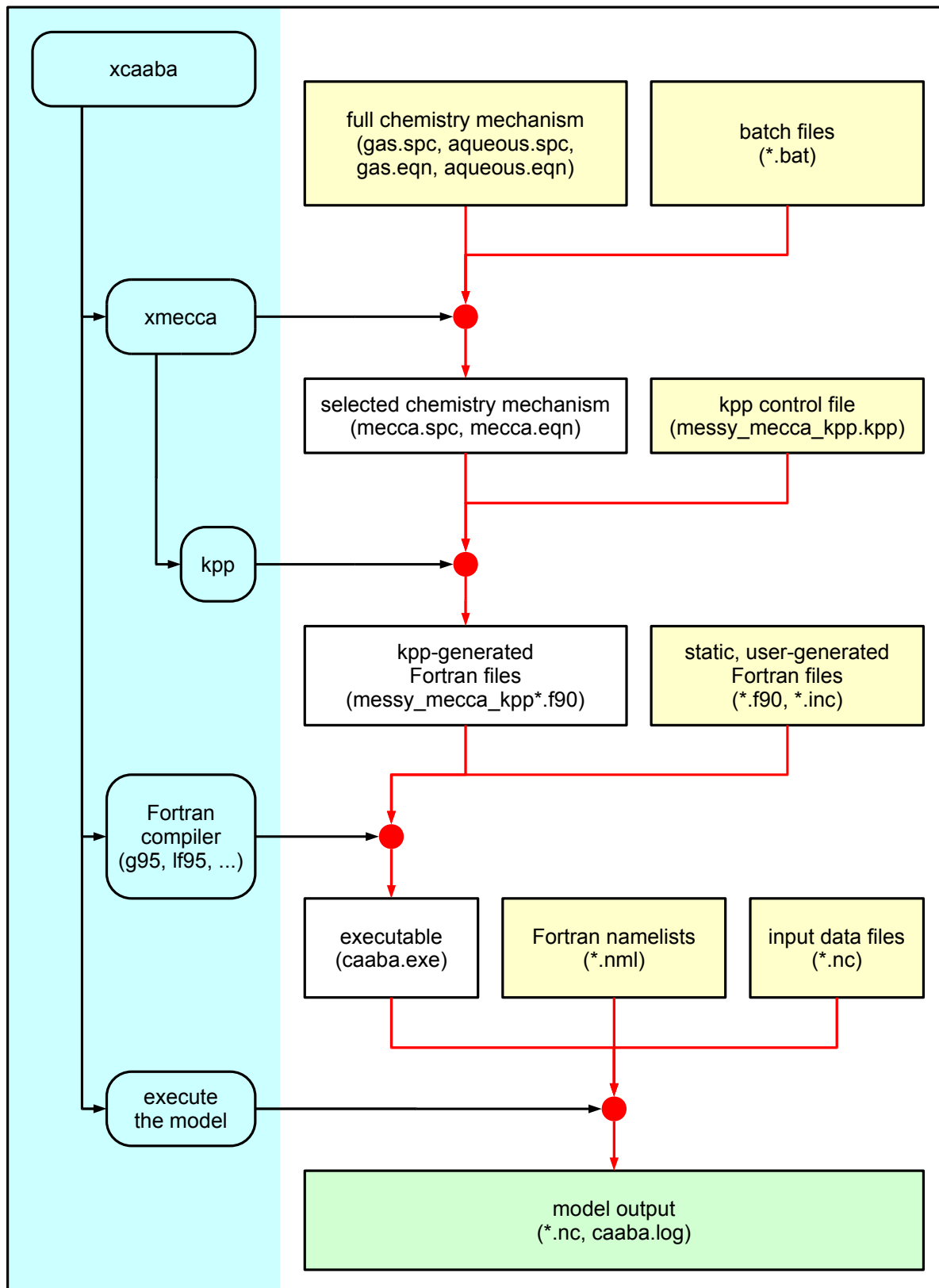


Figure 4: Illustration of the tasks performed by `xcaaba`. `xcaaba` and all scripts called by `xcaaba` are shown on a blue background. User-generated (static) input files are shown on a yellow background whereas automatically generated temporary files are shown on a white background.

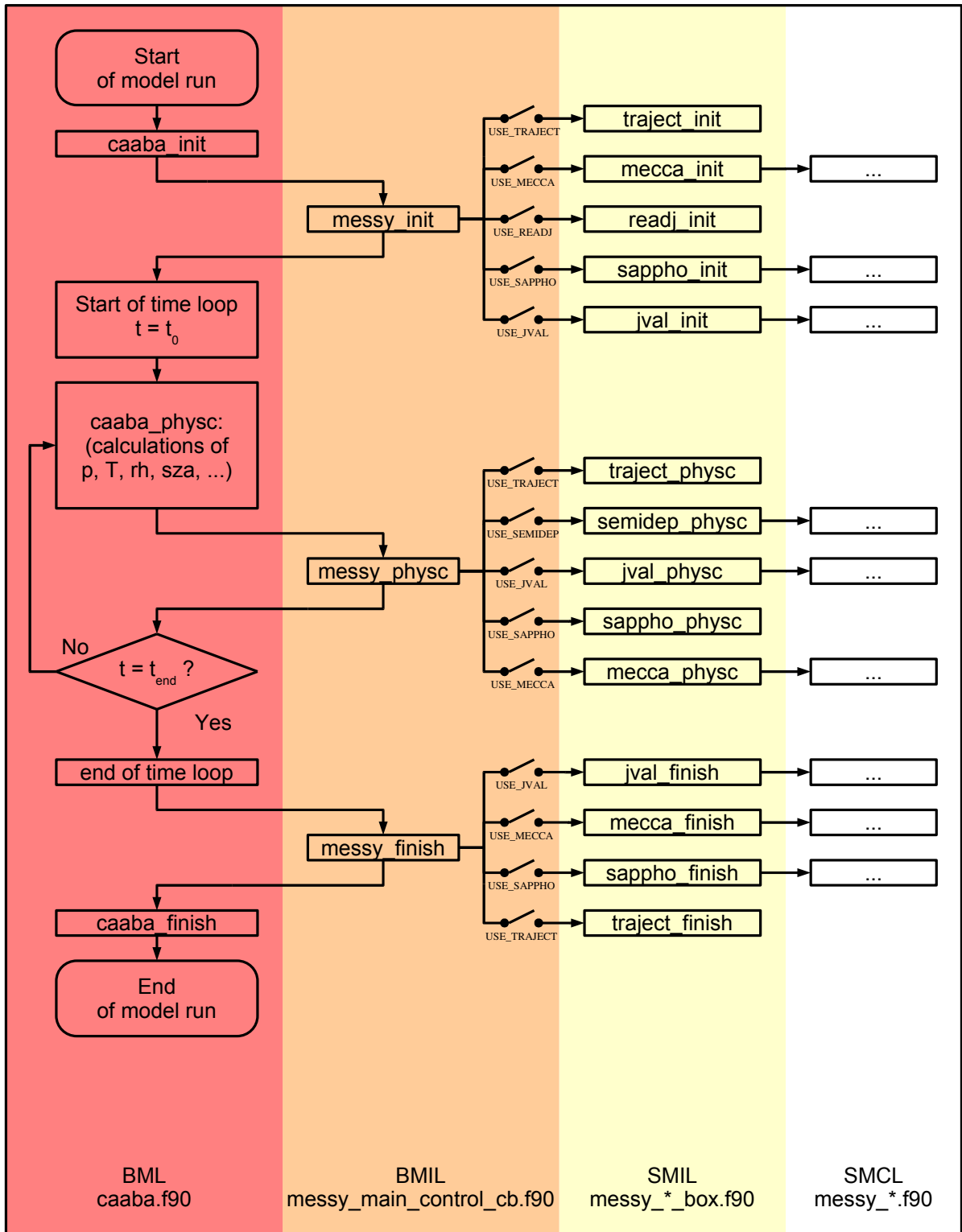


Figure 5: Flow control of a CAABA box model simulation

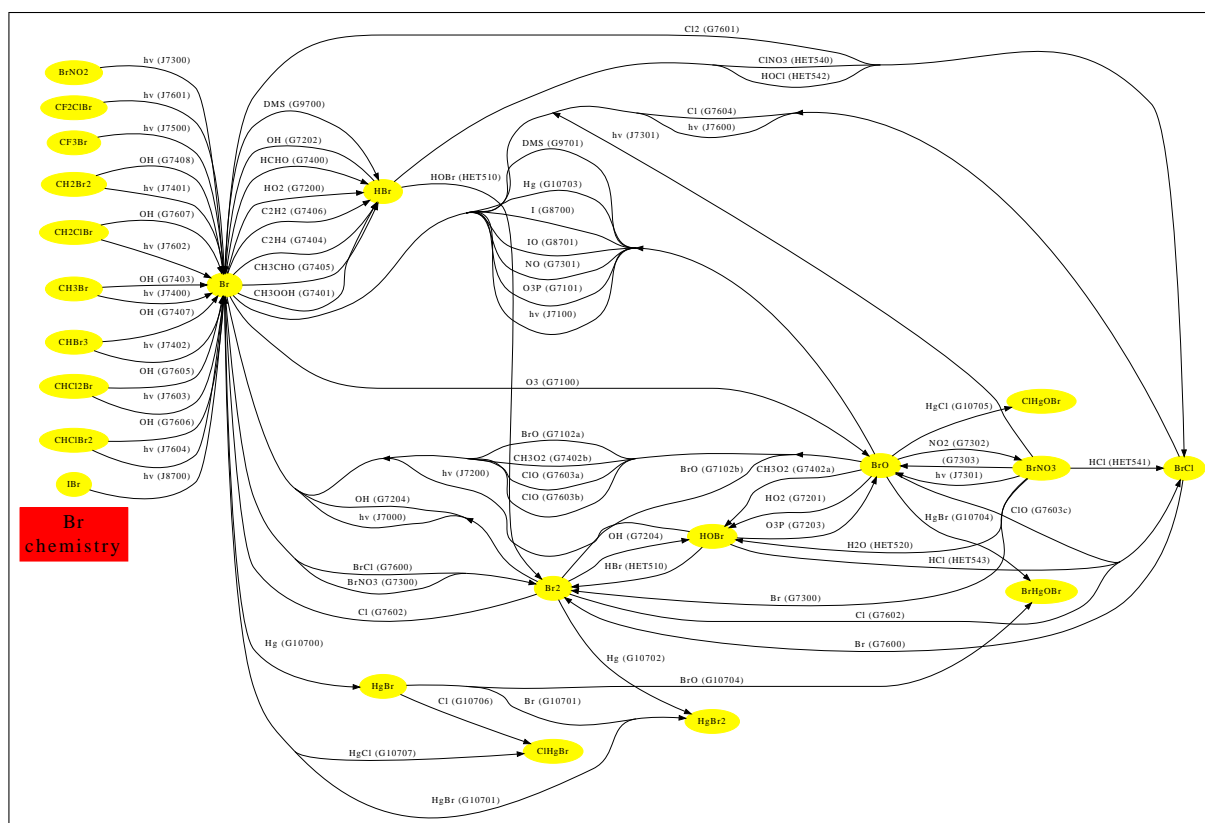


Figure 6: Visualization of the MECCA gas-phase bromine chemistry generated with the graphviz software.

However, you can also start it manually:

```
cd mecca
./xmecca
```

xmecca will ask several questions, and recommended answers are given below. If you only press the Return key, you select the default.

Select a batch file which defines the chemistry mechanism that you want to generate.

It is strongly recommended that you select a batch file here. Batch files contain all the information that xmecca needs to create a chemical mechanism. Several batch files are available already, and it is also possible to add your own batch files as explained at the end of this section. If you do not select a valid batch file, you can continue and answer all questions interactively as described here.

How many aerosol phases?

For a gas-phase only mechanism, type “0”. For a mechanism with aqueous-phase chemistry in seasalt and in sulfate particles, type “2”. Other values are possible if they have been defined in subroutine `define_aerosol` in `messy_mecca_box.f90`.

Modify gas.eqn with a replacement file?

Answer “0” unless you have written your own replacement file. More information about the replacement feature can be found in the file `rpl/gas.rpl-example`.

Choose a selection number or type a boolean expression:

Now you can choose a subset of chemical reactions. A few predefined standard selections are available. For all other purposes, a batch file should be created, as explained at the end of this section. Some of the predefined selections are:

EVAL: A mechanism that was used for the evaluation of the MECCA chemistry in the global model ECHAM5/MESSy (Jöckel et al., 2006).

Minimum tropospheric chemistry: A very small tropospheric mechanism.

Minimum MBL chemistry: A small mechanism that contains aqueous-phase chemistry and should only be used if the number of aerosol phases is > 0 .

For details about the selection, see Sect. 4.1.

Add Monte-Carlo factor to all rate coefficients? [y/n/q, default=n]

Answer “n” here unless you want to perform Monte-Carlo calculations, as described in Sect. 6.2.

Add diagnostic tracers to gas.eqn?
[q/0/?, default=0]

Answer “0”. Diagnostic tracers are usually only used for 3-dimensional model runs.

Calculate accumulated reaction rates
of all equations? [y/n/q, default=n]

Answer “y” if you want to have all accumulated reaction rates in the model output. Otherwise, answer “n”.

Tagging, doubling, both, or
none? [t/d/b/n/q, default=n]

Please use the default “n” here. The recommended way to test tagging diagnostics and isotope modeling is described in Sect. 6.4.

Run KPP?

Answer “y”.

Choose an integrator [q=quit,
default=rosenbrock_posdef]:

The default integrator is strongly recommended (see Sect. 4.2 for details). Next, KPP will create several Fortran95 files.

Remove indirect indexing with decomp?
[y/n/q, default=n]

If this question shows up, answer “n”.

Create LaTeX listing of selected mechanism?
[y/n/q, default=n]

If you answer “y” here, a table of the current reaction mechanism will be produced. Only the selected reactions will be listed. The table also contains the rate coefficients and their references, as described in Sect. 7.3.3.

Create graphviz plots of selected
mechanism? [y/n/q, default=n]

If you have the “dot” program from the graphviz software installed, you can create graphical visualizations of the reaction mechanism. As an example, the graphviz-generated plot of gas-phase bromine chemistry is shown in Fig. 6. For more information, look at the files `xgraphvizall`, `xgraphviz`, and `spc_extract.awk` in the `mecca/graphviz/` directory.

Do you want to delete the temporary
`xmecca` files?

It is okay to delete these temporary files unless you need them for debugging purposes.

When `xmecca` finishes successfully, the Fortran95 code of your selected mechanism has been created. The KPP-produced Fortran95 files (Tab. 2) are moved into the `mecca/smc1/` directory (with lower-case names). An exception is `messy_mecca_kpp_Model.f90`, which is produced by KPP but not needed for MECCA. The modular structure of the KPP-produced Fortran95 files is shown in Fig. 3.

If you need to create a chemical mechanism very often, it is quite tedious to answer all questions every time. To make this easier, you can copy the template `batch/example.bat` to a new name (e.g. `batch/myfile.bat`) and then enter your answers into that batch file. Now you can create a new chemical mechanism in batch mode with

```
./xmecca myfile
```

It is also possible to add the name of the batch file to the `xcaaba` command:

```
./xcaaba myfile
```

4.1 Selecting a set of chemical reactions

All chemical reactions are marked. Each marker consists of several labels, which contain information about the domain (troposphere/stratosphere), the phase where the reaction occurs (gas/aqueous), its relevant chemical elements, and more. See Sect. 7.3.2 for a complete list of labels. To define a set of chemical reactions, you can either choose a pre-defined selection by number or enter a boolean expression based on the labels. Boolean expressions are typed in gawk syntax. The most important operators and expressions are:

```
&& = AND
|| = OR
! = NOT
() = parentheses
1 = TRUE
0 = FALSE
```

For example, to select all gas-phase reactions (G) except for those including halogens (Cl, Br, I), type:

```
G && !Cl && !Br && !I.
```

It is important to understand the logic behind this selection mechanism. The expression “Cl && Br” selects only those reactions that contain chlorine *and* bromine. Similarly, the expression “G && Het” selects only those reactions that occur in the gas phase *and* are heterogeneous. However, since no reaction has both the “G” *and* the “Het” label, this results in an empty mechanism. If you want a mechanism that contains both gas-phase and heterogeneous reactions, you must select all reactions that contain either the label “G” *or* the label “Het”, i.e. you must use the expression “G || Het”.

4.2 Selecting a numerical integrator

Several numerical integrators are defined in the subdirectory `mecca/kpp/int/` and can be used with KPP. The default is the positive definite Rosenbrock solver with automatic time-step control (`rosenbrock_posdef`). It is very robust and capable of integrating very stiff sets of equations (e.g. chemical mechanisms including both gas- and aqueous-phase chemistry). Although a Rosenbrock solver with manual time-step control (`ros2_manual`) is also available, it is strongly recommended not to use it for stiff sets of equations. If you choose it, you do so at your own risk!

5 Plotting the model results with the ferret software

If you have chosen netCDF output, you can plot the model results with the ferret program (<http://ferret.wrc.noaa.gov/Ferret/>). Change into the `jnl/` directory, then start the program by typing “ferret”. When ferret has started, you can plot the gas-phase species of the latest model simulation with the ferret script `xxxg.jnl` by typing:

```
go xxxg.jnl
```

Similarly, `xxxa.jnl` can be used to plot aqueous-phase species:

```
go xxxa.jnl
```

The file `xxxa.jnl` accepts several parameters to modify the plots. The first parameter should be “0d” for plotting box model results. The second parameter can be set to “mpl” or “mpm” in order to plot either aqueous-phase concentrations in mole per liter or mixing ratios in mole per mole, respectively. The third parameter defines the aerosol bin. With two aerosol bins, “A01” refers to sulfate particles, and “A02” to sea-salt particles. For example, type:

```
go xxxa.jnl 0d mpl A02
```

Photolysis rate coefficients can be plotted with `jval.jnl`:

```
go jval.jnl
```

If the calculation of accumulated reaction rates had been switched on in `xmecca` (see Sect. 4), plots of the reaction rates can be made. One possibility is to plot all reactions with:

```
go rxnrates.jnl
```

Alternatively, it is possible to plot only the production and destruction rates for a certain species, e.g. for OH:

```
go rxnrates_scaled.jnl OH
```

To plot results from previous simulations which are saved in the `output/` directory, edit the file `setmodelrun.jnl` and enter the paths of the directories in the “GO _define_sensi” command. To compare model simulations, you can enter two or more “GO _define_sensi” commands in `setmodelrun.jnl`. To plot the difference between model simulations, activate the line “DEFINE SYMBOL diffplot TRUE” in `setmodelrun.jnl`.

6 Run CAABA/MECCA in special modes

In the base configuration described so far, CAABA/MECCA calculates the temporal evolution of the chemistry inside an air parcel. This is ideal for sensitivity studies analyzing the effect of individual reactions inside a large chemical mechanism. For other applications, some special modes exist as described below.

6.1 Multiple model simulations and steady-state

The so-called “multirun” mode performs multiple model simulations, each of them terminating when a steady-state has been reached. This is useful to calculate the steady-state concentrations of short-lived species when the concentrations of longer-lived species (e.g. non-methane hydrocarbons) are known from measurements. The default termination condition is that the relative change of OH and HO₂ between two model time steps is less than 10⁻⁶ s⁻¹. If necessary, this can be changed in the function `steady_state_reached` in `messy_mecca.f90`. To avoid that the concentrations of long-lived species change from their initial values, they can be fixed in the file `mecca/messy_mecca_kpp.kpp` by adding them to the “#SETFIX” line. A tracer initialization file (see Sect. 7.8.1) and a photolysis initialization file (see Sect. 7.8.2) must be available in the `multirun/input/` directory. As an example, the files `example_*.nc` are available. To create such input netCDF files from ASCII files, the script `asc2ferret4nc.tcsh` can be used. Finally, since the multirun mode needs “ncks” from the netCDF Operators (NCO) software, it must be ensured that this program is available. After these preparations, the multirun mode can be entered by running `xcaaba` and answering “Choose a namelist file” with “m”. The user can either select one input file or make model simulations for all input files in the `multirun/input/` directory. For each input netCDF file, the script `multirun.tcsh` is called. For each time step contained in the input file, `multirun.tcsh` first creates a suitable namelist file `caaba.nml` and

then performs a CAABA/MECCA model simulation. The namelist file contains values for temperature and pressure taken from the input netCDF file. In addition, the steady-state option is switched on with “`l_steady_state_stop = T`”, and the submodel READJ is activated and used with “`USE_READJ = T`” and “`phoratr_channel = 'readj'`”. After all model simulations have finished, a summary of the output is placed in the output directory. The name of the output directory will be based on the name of the input netCDF file, e.g. when the file `example_small.nc` is used, the output will be in `output/multirun/example_small/`.

6.2 Monte-Carlo

6.2.1 Performing Monte-Carlo simulations

In the Monte-Carlo mode, several CAABA/MECCA simulations are performed, with each individual simulation using slightly different rate coefficients. To activate it, you first have to create a new chemistry mechanism with `xmecca` (see Sect. 4) and answer the question “Add Monte-Carlo factor to all rate coefficients” with “y” (e.g. using the batch file `mcfct.bat`). This will start the `gawk` script `mcfct.awk`, which adds Monte-Carlo factors to the rate coefficients in the equation file. Next, the `xcaaba` script can be used to start the simulations. A suitable namelist for this purpose is `caaba_mcfct.nml`. The script `montecarlo.tcsh` in the directory `montecarlo/` will now perform the Monte-Carlo model simulations. The default is to make 100 model simulations. To choose another value (up to 9999), change the definition of `maxline` in `montecarlo.tcsh`.

6.2.2 Analyzing Monte-Carlo simulations

After performing the model simulations, the resulting netCDF files are merged (using the tools `ncpdq`, `ncclamp`, and `ncrcat`) and then stored in the output directory with a name based on the date and time of the model simulations, e.g. `$outputdir = output/montecarlo/2010-06-24-16:29:00`. The final concentrations and rate coefficients of all simulations are summarized in `caaba_mecca_c_end.nc` and `caaba_mecca_k_end.nc`. Results of the individual simulations can be found in the directories `$outputdir/runs/*`.

Time series

If the model is set up to run for a fixed length (e.g. using the default of `runtime_str = 8` days), the time series of all simulations can be plotted together with `ferret` by activating the lines for Monte-Carlo in `setmodelrun.jnl`. However, these plots become illegible if more than about 5 simulations are made.

Steady-state calculations

The most efficient way to analyze a large number of Monte-Carlo simulations is to use the steady-state option and only compare the final values of the different model simulations, not the individual time series. The `ferret` script `montecarlo.jnl` can be used to create scatter plots of concentrations vs rate coefficients. It also plots linear regression lines for all comparisons above a given threshold of the coefficient of determination (r^2). Note, however, that r^2 is only an indicator of the goodness of a *linear* correlation. It is also possible that the dependence of a species on a rate coefficient is *nonlinear*. For an exhaustive analysis of the model results, the threshold in the file `scatterplot_mc.jnl` can be set to zero, thus creating scatter plots of *all* species against *all* rate coefficients.

6.2.3 Variation of rate coefficients

In each individual Monte-Carlo simulation j , all rate coefficients k_i are varied by a Monte-Carlo factor:

$$k_{i,j}^{\text{MC}} = k_i \times f_i^{x_{i,j}} \quad (1)$$

Here, $k_{i,j}^{\text{MC}}$ is the rate coefficient of reaction i used in the Monte-Carlo simulation j . It is defined as the product of the recommended value k_i and the Monte-Carlo factor $f_i^{x_{i,j}}$. This Monte-Carlo factor consists of two parts, the uncertainty factor f_i and the exponent $x_{i,j}$:

The uncertainty factor f_i

The uncertainty factor f_i describes the uncertainty of the measured (or estimated) rate coefficient k_i . Its value can usually be found in publications of laboratory studies or summaries like the JPL evaluation (Sander et al., 2006).

The tables of the IUPAC evaluations (e.g. Atkinson et al., 2006) list the decadic logarithm $\lg(f_i)$ of the uncertainty factor, which they call “ $\Delta \log k$ ”.

Sometimes an absolute uncertainty is quoted instead of an uncertainty factor, e.g. $k = 2 \pm 0.2$ or $k = 2 \pm 10\%$. In this case we define f_i such that the upper limit is reached when multiplied with k_i , i.e. in the current example $f_i = (2 + 0.2)/2 = 1.1$.

The uncertainty factor is defined in the equation files (`*.eqn`) in a comment starting with the paragraph symbol. Three different syntax types are possible:

- If there is just one \S sign, (e.g. “`{§1.1}`”), the value inside the curly braces is the uncertainty factor f_i .
- With two \S signs, (e.g. “`{§§0.04}`”), the value inside the curly braces equals $\lg(f_i)$.
- If there is only a \S sign (“`{§}`”) but no number, the uncertainty factor is set to the default value of $f_i = 1.25$.

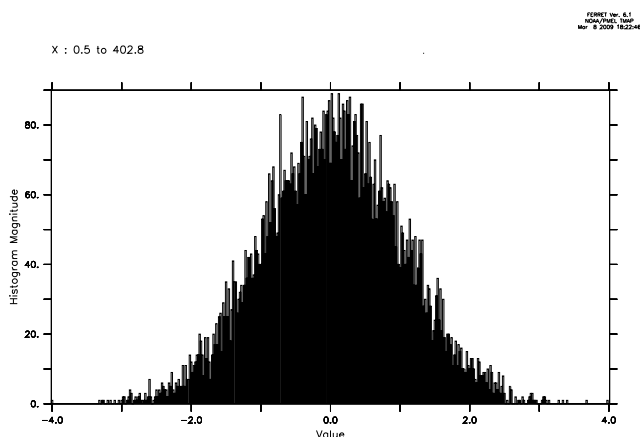


Figure 7: Example histogram of normally-distributed random numbers.

The Monte-Carlo exponent $x_{i,j}$

There is one Monte-Carlo exponent $x_{i,j}$ (variable “`mexp`” in the code) for each rate coefficient k_i and for each individual Monte-Carlo simulation j . The values of $x_{i,j}$ are normally-distributed random numbers centered around zero (see Fig. 7), and produced with the Marsaglia polar method (http://en.wikipedia.org/wiki/Marsaglia_polar_method). As input for the Marsaglia polar method, uniformly distributed random numbers between 0 and 1 calculated with either the standard Fortran95 function `RANDOM_NUMBER` or the Mersenne Twister algorithm (Matsumoto and Nishimura, 1998) are used.

6.2.4 Changing the uncertainty factors

The uncertainty factors can be changed by modifying the equation files, as shown in Sect. 7.3. Note that predefined rate coefficients (e.g. `k_HO2_HO2`) already contain an uncertainty factor and there must not be an additional factor in the reaction where they are used.

In some cases, it may be useful to vary only one or a few rate coefficients. To do this, it is first necessary to find the correct indices of `mexp(...)` in `mecca.eqn` (note that these indices may change when creating a new mechanism with `xmecca`). As an example, to vary only the rate coefficients that use `mexp(40)` and `mexp(50)`, the following lines can be added to subroutine `mecca_init` in `messy_mecca_box.f90` after `CALL define_mexp`:

```
DO i=1, MAX_MCEXP
  IF ((i/=40).OR.(i/=50)) mexp(i) = 0.
ENDDO
```

To verify that the rate coefficients are modified in the Monte-Carlo simulations, it is possible to temporarily activate the subroutine `montecarlo_check` in `template_messy_mecca_kpp.f90` and check

the output in `caaba.log`. After these tests, `montecarlo_check` must be switched off again to allow normal model simulations.

6.3 Lagrangian trajectories

CAABA can be used as a Lagrangian trajectory box model (Riede et al., 2009). The usual combination of submodels for this purpose includes the CAABA submodel `TRAJECT` for the processing of trajectory information, `MECCA` for atmospheric chemistry, and `JVAL` for photolysis rate calculation. All important settings for trajectory calculations can be made via the namelist file plus a few external files.

6.3.1 Namelist parameters

A namelist template can be found in `nml/caaba_trajectory_example.nml`. After copying the namelist file to a new name in the same directory and altering the settings, it will be available when running CAABA via `xcaaba`. There are standard and trajectory-exclusive namelist parameters to be set:

- **Submodel switches (mandatory):** The trajectory mode of CAABA requires that `USE_TRAJECT = T`, `USE_MECCA = T`, and `USE_JVAL = T` and/or `USE_SAPPHO = T`. One of the two photolysis rate models is sufficient, but it is also possible to run them in parallel (see also `photrat_channel`). If the use of external photolysis rates is desired, `USE_JVAL = T` is mandatory since the scaling of photolysis rate coefficients is currently only implemented for `JVAL`. For the application in Riede et al. (2009), the submodel `SEMIDEP` was switched off.
- **Scenarios (optional):** The use of scenarios is optional in trajectory mode. When using external input for chemical initialization and photolysis rates, they can be used to supplement default values for unspecified photolysis rate coefficients or initial mixing ratios.
- **Photolysis rate channel:** Since the scaling of photolysis rate coefficients is currently only implemented for `JVAL`, choose `photrat_channel = 'jval'` when planning to prescribe photolysis rates.
- **Trajectory input (mandatory):** The path to the netCDF file containing trajectory waypoints should be specified as `input_physc = 'trajectory/example_traj.nc'`. For its structure, see section 6.3.2.
- **Tracer initialization (optional):** Tracer mixing ratios can be initialized with an external netCDF file by specifying the path to it: `init_spec = 'trajectory/example_init.nc'`. For its structure, please refer to section 7.8.1.

Without an external file for tracer initialization, tracers mixing ratios are initialized by box model default or by the chosen scenario.

- **Photolysis rates (optional):** To scale photolysis rates to prescribed $J(\text{NO}_2)$ values, specify the path to the respective file as `input_jval = 'traject/example_jval.nc'`. For its structure, see 6.3.3.
- **Variable names (partly mandatory):** There are default trajectory variable names designated in CAABA. They can be selectively changed by providing alternative variable names. Here is a list of trajectory variables, their default name, and respective examples how to specify an alternative variable name:

quantity	default	alternative
longitude	LON	vlon = 'LON_TR'
latitude	LAT	vlat = 'LAT_TR'
pressure	PRESS	vpress = 'P'
temperature	TEMP	vtemp = 'TM1'
rel. humidity	RELHUM	vrelhum = 'rh'
spec. humidity		vspechum = 'sh'

For only one of the two humidity variables, an alternate name may be active in the namelist. This is the variable that is subsequently used as humidity and that is internally converted to relative humidity if necessary. When specific humidity is provided, then both specific humidity and relative humidity are written to output `caaba_physc.nc`, since CAABA uses relative humidity internally. When relative humidity is provided, only relative humidity will be written to output.

- **Humidity definitions (optional):** To switch from the traditional relative humidity definition to the WMO definition, `l_relhum_wmo = T` can be selected (see also Sect. 6.3.4).
- **Use relative humidity? (optional):** By default, the relative humidity is used to calculate the concentration of water vapor $c(\text{H}_2\text{O})$. If `l_ignore_relhum = T`, then the relative humidity is ignored, and $c(\text{H}_2\text{O})$ must be initialized in SUBROUTINE `x0` (either directly or via external chemical initialization).
- **Water vapor saturation pressure (optional):** By default, the parameterizations from Murphy and Koop (2005) for both, vapor pressure over liquid and over ice are used. To use the saturation vapor pressure parameterizations from EMAC, choose the namelist entry `l_psat_emac = T`,
- **Integration time (optional):** `timesteplen_str` sets the integration and output time step. See also Sect. 7.1.1.
- **Selecting trajectory parts (optional):** Two namelist parameters allow flexible selection of the

model runtime along the trajectory. `runlast` defines the start of the CAABA simulation counted backwards in time from the trajectory end, i.e. `runlast = 4.5` means “calculate the last 4.5 days of the trajectory”. The unit is days. The parameter `runtime_str` defines the overall model simulation time. Thus, `runlast` and `runtime_str` combined select any desired part of the trajectory.

6.3.2 Trajectory input file

The trajectory information is provided to CAABA via an external netCDF file specified in the namelist by `input_physc`. A sample file is available at `traject/example_traj.nc`. The file should contain a time origin in 'seconds/minutes/hours/days since yyyy-mm-dd hh:mm:ss', where the seconds in the time string are optional, for example: "MINUTES since 2000-01-19 08:00:00". The file must contain at least two trajectory waypoints and the following time-dependent variables:

quantity	default name	unit
longitude	LON	degrees east
latitude	LAT	degrees north
pressure	PRESS	Pascal
temperature	TEMP	Kelvin
(rel. humidity)		1
(spec. humidity)		kg/kg

Of the two humidity quantities, only one needs to be present. If specific humidity is given, it is converted to relative humidity (RH) within CAABA. Depending on the namelist parameter `l_relhum_wmo`, either the traditional definition of relative humidity

$$\text{RH} = \frac{p_{\text{H}_2\text{O}}(T)}{p_{\text{sat}}(T)}, \quad (2)$$

or the WMO definition (Jacobson, 1999)

$$\text{RH} = \frac{\omega_v}{\omega_{vs}} = \frac{p_{\text{H}_2\text{O}}(T)}{p - p_{\text{H}_2\text{O}}(T)} \times \frac{p - p_{\text{sat}}(T)}{p_{\text{sat}}(T)} \quad (3)$$

is assumed, with p = atmospheric pressure, $p_{\text{H}_2\text{O}}$ = water vapor partial pressure, p_{sat} = water vapor saturation pressure, ω_v = water vapor mass mixing ratio, and ω_{vs} = saturation water vapor mass mixing ratio in dry air. We calculate the latter two as:

$$\omega_v = \frac{q}{1 - q} \quad (4)$$

$$\omega_{vs} = \frac{M(\text{H}_2\text{O})}{M(\text{air})} \times \frac{p_{\text{sat}}(T)}{p - p_{\text{sat}}(T)}, \quad (5)$$

using the temperature-dependent saturation water vapor pressure $p_{\text{sat}}(T)$, and the molar masses M of water and dry air. There are two parameterization schemes available for the water vapor saturation pressure, which can be selected by namelist (see Sect. 6.3.1).

6.3.3 Photolysis rate file

It is possible to scale photolysis rate coefficients via prescribed $J(\text{NO}_2)$ values from a netCDF file. An example is available at `traject/example_jval.nc`. The name in the netCDF file must be `J_N02`. The files specified in `input_jval` (e.g. `example_jval.nc`) and `input_physc` (e.g. `example_traj.nc`) must both refer to exactly the same trajectory because the J values are read into the model at the same times as other trajectory information.

6.3.4 Trajectory mode output

Output along the trajectory is written to `caaba_messy.nc`. There are some special variables written out in addition to the default `caaba_messy.nc` output. They are listed in the second part of Tab. 1.

Specific humidity (q) is only written to output if it was provided as input.

6.4 Tagging diagnostics and isotope modeling

Before using the tagging feature, please make sure that version 2.2.0 or higher of `fpc` (Free Pascal compiler, <http://www.freepascal.org/>) is installed and configured on your system. To create an isotopically tagged chemical mechanism with `xmecca`, the batch file `iso_example.bat` can be used. Note that `tagdbl` is set to “d” (doubling) here. The alternative option “t” (tagging) is not intended to be used in box-model simulations and thus currently disabled. Before running CAABA/MECCA, the execution of the doubling code has to be enabled by setting `l_dbl=T` in the `&CTRL` namelist in `mecca.nml`. In this configuration, the model simulation will produce additional files `caaba_mecca_dbl_*.nc` containing output from the doubling, e.g., concentrations of isotopologues and isotope ratios. The batch file `iso_example.bat` contains a simple example of the $^{12}\text{C}/^{13}\text{C}$ isotopes of methane tagging. Further tagging configurations can be found by running `xmecca` interactively (without using a batch file) and answering “d” to the question about doubling/tagging. To obtain further details, please contact Sergey Gromov <sergey.gromov@mpic.de>.

7 Modifying CAABA/MECCA

The CAABA/MECCA model simulation can be modified by changing the input files (`*.nc`), the namelist files (`*.nml`), the species files (`*.spc`), the equation files (`*.eqn`) and the Fortran95 files (`*.f90`). Frequently applied changes are:

- Change the model time (start, stop), location (lon, lat), and/or meteorology (p , T , RH) → Sect. 7.1.1

- Add, delete, and change individual chemical reactions → Sect. 7.5
- Create or change the set of photolysis rate coefficients → Sect. 7.6
- Create or change the set of emission fluxes → Sect. 7.6
- Create or change the set of deposition velocities → Sect. 7.6
- Create or change the set of initial mixing ratios → Sect. 7.6
- Change the model initialization using input files → Sect. 7.8

The following sections describe typical (mostly minor) changes to the model that are probably needed by many users. If you would like to make extensive changes/additions to the model, please follow also the general programming guidelines described in Sect. 7.10.

7.1 Namelist files

Fortran95 namelist files allow modifications of the model simulation without having to recompile the source code.

7.1.1 The CAABA namelist file `caaba.nml`

The file `caaba.nml` contains the namelist `&CAABA`. Here individual parts of the CAABA model (the so-called “MESSy submodels”) can be switched on or off. It is important that the following switches are set to “T” (=true):

```
USE_MECCA = T
USE_SAPPHO = T
USE_SEMIDEP = T
```

To use the photolysis rate coefficients from SAPPHO in MECCA, set:

```
photrat_channel = 'sappho'
```

Alternatively, you can switch on the JVAL submodel with `USE_JVAL = T` and then select `photrat_channel = 'jval'`. It is fine to switch on both the JVAL and the SAPPHO submodel, which can be useful for a comparison. However, only the values selected by `photrat_channel` are used for the MECCA chemistry.

You can define the model start, runtime, and time step, e.g.:

```
model_start_day = 90.
runtime_str = '10 days'
timesteplen_str = '15 minutes'
```

Table 1: List of trajectory mode output variables.

variable	unit	notes
lon	(dummy 3-D x-coordinate)	
lat	(dummy 3-D y-coordinate)	
lev	(dummy 3-D z-coordinate)	
time	<time unit> since <time origin>	UTC
lon_tr	degrees east	longitude
lat_tr	degrees north	latitude
press	Pa	pressure
temp	K	temperature
relhum	1	relative humidity (RH)
spechum	kg/kg	specific humidity (q)
sza	deg	solar zenith angle
J_N02_x	1/s	NO ₂ photolysis rate
localtime	(same as time)	local time at trajectory position
year_loc		year of local time
month_loc		month of local time
day_loc		day of local time
hour_loc		hour of local time
min_loc		minute of local time
sec_loc		second of local time

If you don't set these, the default is a model start on day-of-year ("Julian Day") 80, a model simulation duration of 8 days, and an output time step of 20 minutes. The `timesteplen_str` value can be given as any integer or floating point and in the units of `seconds`, `minutes`, or `hours`.

As an alternative, it is possible to stop the model simulation when a steady state has been reached. This is normally used in the "multirun" mode (Sect. 6.1):

```
l_steady_state_stop = T
```

The default location of the model simulation (latitude, longitude) is 45° N and 0° E. It can be changed with e.g.:

```
degree_lat = 82. ! Alert
degree_lon = 297. ! Canada
```

Changing the latitude only affects photolysis calculations (via the zenith angle calculations). The longitude is only used for Lagrangian trajectory calculations.

The values of temperature (`temp`), pressure (`press`), relative humidity (`relhum`), and the height of the boundary layer (`zdbl`) can be defined, e.g.:

```
temp = 293. ! [K]
press = 101325. ! [Pa]
relhum = 0.81 ! [1]
zdbl = 1000. ! [m]
```

The values shown here are the default values as defined in `caaba_mem.f90`.

In the submodel SEMIDEP, emissions are distributed evenly into the well-mixed boundary layer of height

`zdbl`. Note that CAABA is a box model, and changing `zdbl` has no other effects than this.

It is possible to initialize chemical species from a netCDF file (see Sect. 7.8.1). To activate this feature, define a valid input file name, e.g.:

```
init_spec = 'traject/example_init.nc'
```

If the submodel READJ is switched on, a netCDF file containing J-values must be defined (see Sect. 7.8.2). In addition, an index can be defined, if the netCDF file contains data for more than one time step, e.g.:

```
init_j = 'multirun/input/example_small.nc'
init_j_index = 25
```

To facilitate running CAABA under different boundary conditions, so-called "scenarios" can be defined. Currently, there are scenarios for photolysis (`photo_scenario`), initialization (`init_scenario`), emission (`emission_scenario`), and dry deposition (`drydep_scenario`):

```
photo_scenario = 'MBL'
init_scenario = 'MBL'
emission_scenario = 'MBL'
drydep_scenario = 'MBL'
```

Possible values ("MBL" is used here as an example) for the scenarios can be found in the variable `list_of_scenarios` in `caaba.f90`. Note that values have not yet been assigned for all scenarios. See Sect. 7.6 for details about scenarios.

Finally, it is possible to skip the chemistry calculations with KPP completely. This is only useful for debugging:

```
l_skipkpp = T
```


Table 2: List of CAABA/MECCA Fortran95 files

CAABA box model related files	
caaba.f90	main box model file
caaba_io.f90	input/output
caaba_io_netcdf.inc	netCDF input/output
caaba_io_ascii.inc	ASCII input/output
caaba_mem.f90	declaration of CAABA variables
messy_main_control_cb.f90	flow control
messy_jval_box.f90	connection of JVAL to CAABA
messy_mecca_box.f90	connection of MECCA to CAABA
messy_mecca_dbl_box.f90	for isotope modeling
messy_mecca_tag_box.f90	for isotope modeling
messy_readj_box.f90	connection of READJ to CAABA
messy_sappho_box.f90	connection of SAPPHO to CAABA
messy_semidep_box.f90	simplified emission and deposition, including connection of SEMIDEP to CAABA
messy_traject_box.f90	trajectory calculations
static core files (generic)	
messy_cm_n_gasaq.f90	common definitions for gas/aqueous mass transfer
messy_cm_n_photol_mem.f90	common definitions for photolysis
messy_main_blather.f90	print utilities
messy_main_constants_mem.f90	physical constants
messy_main_rnd.f90	random number generation
messy_main_rnd_lux.f90	(file exists but is not used with CAABA)
messy_main_rnd_mtw.f90	Mersenne-Twister random numbers
messy_main_timer.f90	timer
messy_main_tools.f90	auxiliary functions
messy_main_tools_kp4_compress.f90	(file exists but is not used with CAABA)
static core files (submodel-specific)	
messy_jval.f90	calculation of J-values
messy_jval_jvpp.inc	include file for JVAL
messy_readj.f90	read J-values
messy_sappho.f90	simplified and parameterized photolysis rate coefficients
static MECCA core files	
messy_mecca.f90	MECCA core
messy_mecca_aero.f90	aerosol chemistry
messy_mecca_khet.f90	(file exists but is not used with CAABA)
messy_mecca_dbl_parameters.inc	for isotope modeling
messy_mecca_tag_parameters.inc	for isotope modeling
KPP- and xmecca-produced files	
messy_mecca_kpp.f90	a wrapper for the KPP files
messy_mecca_kpp_function.f90	ODE function
messy_mecca_kpp_global.f90	global data headers
messy_mecca_kpp_initialize.f90	initialization
messy_mecca_kpp_integrator.f90	numerical integration
messy_mecca_kpp_jacobian.f90	ODE Jacobian
messy_mecca_kpp_jacobiansp.f90	Jacobian sparsity
messy_mecca_kpp_linearalgebra.f90	sparse linear algebra
messy_mecca_kpp_monitor.f90	equation info
messy_mecca_kpp_parameters.f90	model parameters
messy_mecca_kpp_precision.f90	arithmetic precision
messy_mecca_kpp_rates.f90	user-defined rate laws
messy_mecca_kpp_util.f90	utility input-output

7.1.2 The MECCA namelist file `mecca.nml`

The file `mecca.nml` contains the namelists `&CTRL_KPP` and `&CTRL` (the namelist `&CPL` is not used in connection with CAABA). `&CTRL_KPP` is used for fine-tuning the numerical integration. The default selection `icntrl(3) = 2` should normally be suitable.

7.1.3 The JVAL namelist file `jval.nml`

The file `jval.nml` contains several namelists. When JVAL is run as a submodel for CAABA, only the control namelist (`&CTRL`) is used. Normally, there is no need to change the default settings.

7.2 The species files `gas.spc` and `aqueous.spc`

The files `*.spc` declare chemical species for KPP. All species that may occur in an equation must be declared here. Additional dummy species may also be declared here.

Gas-phase species are declared in `gas.spc`. Examples for gas-phase species are O2, O1D, and NO2. The names of lumped species start with “L”. The names of species with two or more carbon atoms are taken from the master chemical mechanism (MCM).

MECCA also includes aqueous species which are declared in `aqueous.spc`. The names of cations end with “p” for plus. The names of single-charge anions end with “m” for minus. Doubly-charged anions end with “mm”. Examples for aqueous species are “H2O2” (H₂O₂), “Hp” (H⁺), “NO3m” (NO₃⁻), and “SO4mm” (SO₄²⁻).

All aqueous-phase species have the suffix “_a##”, which is a placeholder for the aerosol phase. `xmecca` replaces it by a two-digit number, e.g., “_a01” for the accumulation or “_a02” for the coarse mode. This allows separate chemistry calculations for aerosol particles of different size and composition.

All species are defined here with `#DEFVAR`, i.e. KPP considers them as prognostic variables. To treat a species as a constant (e.g. CO₂), it can be added to the `#SETFIX` command in the file `messy_mecca_kpp.kpp`. The declarations in `#DEFVAR` can and should remain unchanged when altering `#SETFIX`.

7.3 The equation files `gas.eqn` and `aqueous.eqn`

The equation files `*.eqn` define the chemical reaction mechanism for KPP. After making any changes to the equation files, it is always necessary to execute KPP via `xmecca` again. Each reaction occupies one line in this file. An example is:

```
<G1000> O2 + O1D = O3P + O2 : {%StTrG}
3.3E-11*EXP(55./temp); {%1945}{§1.1}
```

Note that, although split here in this manual, this is only 1 line in the equation file. The line starts with the reaction number, which is enclosed in angle brackets “<...>” (see Sect. 7.3.1). The second part (up to the colon) defines the reaction, and the third part (between the colon and the semicolon) defines the rate coefficient. The lines may also contain comments. Comments in equation files are either enclosed in curly braces, or the comment line starts with “//”. When using `xmecca`, some comments have a special meaning. Comments starting with the percent symbol “{%...}” are markers (see Sect. 7.3.2). Comments starting with the ampersand “{%...}”, the “at”-symbol “{@...}”, or the dollar “{\$. . .}” are used to store information for the listing of reactions, as explained in Sect. 7.3.3. Comments starting with the paragraph symbol “{§...}” are defining uncertainties of the rate coefficients for Monte-Carlo calculations (see Sect. 6.2).

If the definition of a rate coefficient is very complex, it can be stored in a Fortran95 variable and the variable is put into the `gas.eqn` file. For example, the rate of the self reaction of HO₂ is quite complex since it depends on humidity. It is predefined and the reaction line can be simplified to:

```
H02 + H02 = H2O2 : k_H02_H02;
```

The declaration and definition of `k_H02_H02` are also in the `gas.eqn` file. They can be found in the so-called KPP “inline types” `F90_GLOBAL` and `F90_RCONST`, e.g.:

```
#INLINE F90_GLOBAL
REAL :: k_H02_H02
#ENDINLINE

#INLINE F90_RCONST
k_H02_H02 = (1.5E-12*EXP(19./temp)+ &
1.7E-33*EXP(1000./temp)*cair)* &
(1.+1.4E-21* &
EXP(2200./temp)*C(KPP_H2O))
#ENDINLINE
```

Another method to add reaction rates with complex dependencies are Fortran95 functions. This is done for example for the oxidation of S(IV) by H₂O₂ (`k_SIV_H2O2`). A function call is given as the rate expression in the `*.eqn` file. These functions are defined with the “inline type” `F90_RATES`:

```
#INLINE F90_RATES
ELEMENTAL REAL(dp) FUNCTION k_SIV_H2O2 &
(k_298,tdep,cHp,temp)
...
END FUNCTION k_SIV_H2O2
#ENDINLINE
```

7.3.1 Reaction numbers

Each reaction in an equation file has a unique reaction “number” (number is not quite correct, since letters are included as well), which is enclosed in angle brackets, e.g.: “<G1000>”. The reaction number starts with one or more upper case letters denoting the type of reaction. The following types exist:

A	aqueous-phase reactions
H	Henry’s law (dissolution and evaporation)
EQ	equilibria in the aqueous phase (forward and backward reactions of acid/base and other equilibria)
G	gas-phase reactions
J	J-values of photolysis reactions
HET	heterogeneous reactions (e.g. on polar stratospheric clouds)

The type is followed by a sequence of 3 or 4 digits. The first digit is the number of the main element of the reaction. The following numbers are used:

1)	O	Oxygen
2)	H	Hydrogen
3)	N	Nitrogen
4)	C	Carbon
5)	F	Fluorine
6)	Cl	Chlorine
7)	Br	Bromine
8)	I	Iodine
9)	S	Sulfur
10)	Hg	Mercury

Out of those elements that occur in a reaction, the one with the highest number is called the main element. Accordingly, the second digit is determined by the element with the second highest number (or set to zero if there is no second element in the reaction). There is one exception in this numbering scheme: For the carbon group, the second digit is the number of C atoms in the largest organic molecule.

The following digits have no special meaning. If a reaction branches into several pathways, a suffix “a”, “b”, “c”, ... is added.

7.3.2 Markers and labels

Each reaction must contain a marker. A marker contains several case-sensitive labels. The syntax is “{%. . .}” where the dots represent the labels. Labels are used to select specific reactions, as described above (Sect. 4.1). The labels are placed in the marker without separators. The following labels are available and should appear in this order:

1. the domain, i.e. altitudes at which the reaction occurs (mandatory, include at least one)
 - St = Reactions relevant in the stratosphere
 - Tr = Reactions relevant in the troposphere

2. phase (mandatory, include exactly one)
 - Aa## = Aqueous, aerosol (## is a placeholder for the 2-digit aerosol phase number)
 - Ara = Aqueous, rain (not used for the box model)
 - G = Gas phase reactions
 - Het = heterogeneous reactions (e.g. on polar stratospheric clouds)
3. elements (include all elements that occur in the reaction, except for H and O)
 - N = Nitrogen
 - C = Carbon with > 1 C atom (only used for C,N,O species but not for halogenated or sulfur-containing organics)
 - F = Fluorine
 - Cl = Chlorine
 - Br = Bromine
 - I = Iodine
 - S = Sulfur
 - Hg = Mercury
4. other
 - J = Photolysis reactions
 - Mbl = Minimum reaction mechanism for MBL chemistry
 - Sc = Scavenging chemistry mechanism
 - Scm = Scavenging chemistry mechanism, minimum selection

See Sect. 7.5.8 for a description how to add new labels to `xmecca`.

7.3.3 Creating a table of the chemical mechanism

To ensure that the documentation of the chemical mechanism is always up to date, the necessary information is contained inside the species and equation files. If you have the programs `pdfLaTeX` and `BibTeX` installed on your system, you can generate a table of the chemical mechanism in pdf format.

The gawk scripts `spc2tex.awk` and `eqn2tex.awk` convert information from the selected reactions into a LaTeX table. BibTeX citations are included in comments starting with an ampersand “{&. . .}”. If there is a second ampersand “{&&. . .}”, additional information about reactions can be found in `meccanism.tex` as a footnote to the tables. Comments starting with the “at” symbol “{@. . .}” or the dollar “{\$. . .}” can be used to put LaTeX commands directly into the *.eqn files. `eqn2tex.awk` produces several *.tex files which are included into `meccanism.tex`.

7.4 Fortran95 files

The CAABA/MECCA simulations can be modified by changing the Fortran95 files (see Tab. 2 for a list of files). The modular structure of the Fortran95 files is

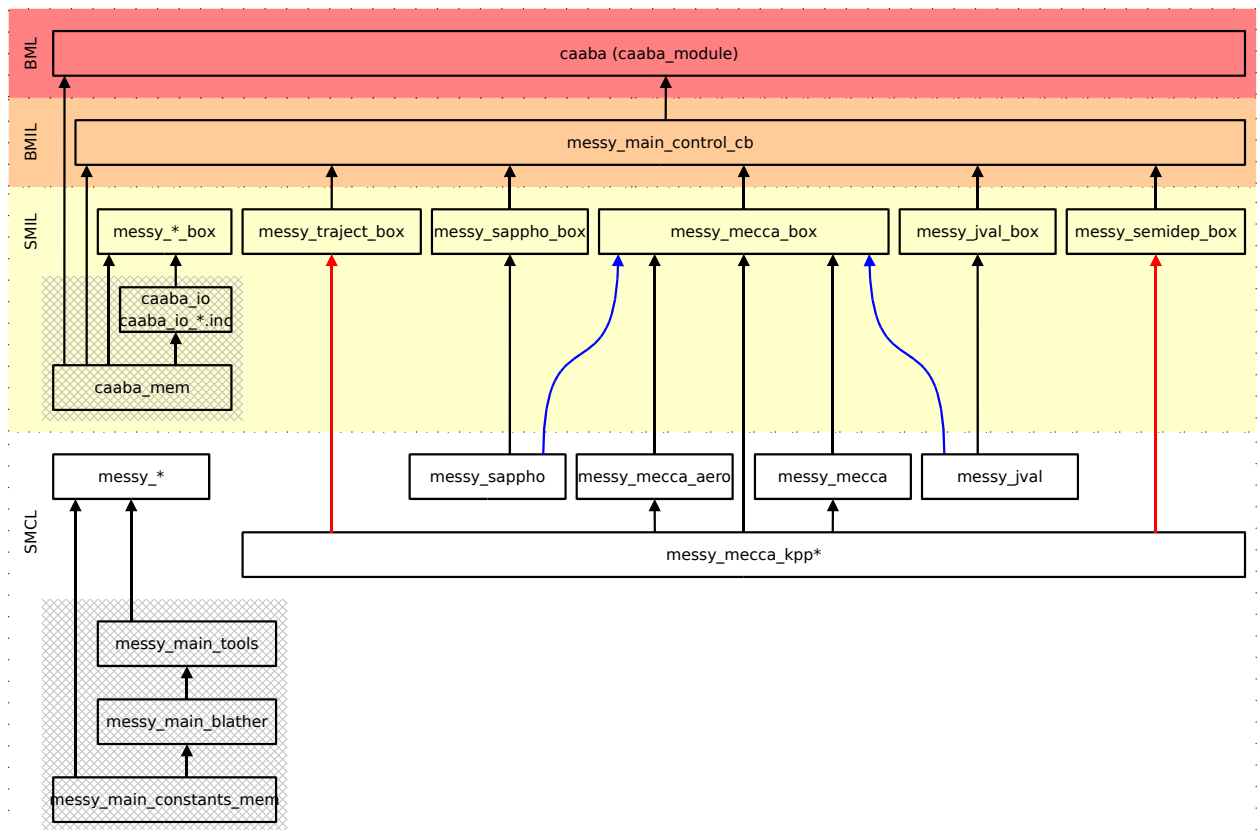


Figure 8: Module structure of MECCA when it is connected to the CAABA box model. The box-model related files are in the colored layers marked with BML, BMIL, and SMIL. The submodel core layer (SMCL) of MECCA is independent of the box model (see Jöckel et al. (2005) for details about the MESSy layers). The arrows start at the module which is exporting the variables and subroutines. They point to the module importing them via the Fortran95 USE instruction. Here, the box `messy_mecca_kpp*` represents all KPP-generated files. The KPP-internal structure is shown in Fig. 3.

shown in Fig. 8. Most of the files need only be changed by model developers. Those that are also interesting for model users, are briefly explained below.

7.4.1 caaba.f90

This file contains the main Fortran95 program (“PROGRAM caaba”).

7.4.2 caaba_mem.f90

This file contains variable declarations which are needed by several CAABA files.

7.4.3 messy_main_control_cb.f90

Flow control. Editing this file is only necessary when a new submodel is added.

7.4.4 messy_jval_box.f90

This file contains the connection of JVAL to CAABA.

7.4.5 messy_jval.f90 and messy_jval_jvpp.inc

These are the core files of JVAL, which calculate the J-values.

7.4.6 messy_mecca_box.f90

This file contains the connection of MECCA to CAABA. The chemical composition of seawater is defined in SUBROUTINE `mecca_init`.

Aerosol properties (radius, liquid water content (LWC), and their chemical composition) are defined in SUBROUTINE `define_aerosol`. In addition, the factor `cvfac` is defined here, which converts the aqueous-phase unit mol/L (referring to the volume of the liquid)

to the gas-phase unit molecules/cm³ (referring to the gas-phase volume).

Initial mixing ratios of chemical species are defined in SUBROUTINE `x0`. Depending on which scenario was chosen in the CAABA namelist file (see Sect. 7.1.1), one of the initialization subroutines `x0_*` will be used.

7.4.7 `messy_sappho_box.f90`

This file contains the connection of SAPPHO to CAABA.

7.4.8 `messy_sappho.f90`

This is the core file of SAPPHO, which defines simplified parameterized photolysis rate coefficients.

7.4.9 `messy_semidep_box.f90`

This file contains the connection of SEMIDEP to CAABA. Simplified emission fluxes and deposition velocities are defined here.

7.4.10 `messy_cmn_gasaq.f90`

This file contains gas- and aqueous-phase data of the chemicals: molar masses (`M`), Henry's law coefficients (`Henry_T0`, `Henry_Tdep`), and accommodation coefficients (`alpha_T0`, `alpha_Tdep`).

7.4.11 `messy_mecca_aero.f90`

Several variables needed to calculate multiphase rate coefficients are defined in `messy_mecca_aero.f90`. The accommodation coefficients from `messy_cmn_gasaq.f90` are used for the calculation of the mass transfer coefficients (`kmt`). Together with the Henry's law coefficients (also from `messy_cmn_gasaq.f90`), they are needed to calculate equilibria between the gas and the aqueous phase. Heterogeneous reactions are described with the forward (`k_exf`) and backward (`k_exb`) rate coefficients. The variable `xaer` is set to 1 or 0 to switch aqueous-phase chemistry on or off, respectively.

7.5 How to expand the chemical mechanism

Small changes to the chemical mechanism can be made using "replacement files". More information about this feature can be found in the file `mecca/rpl/gas.rpl-example`. This section contains brief descriptions for experienced model developers explaining where to make changes to the code for certain model expansions. In the descriptions, "xyz" is used as an example for the name of the addition.

7.5.1 Adding a new gas-phase species

- `gas.spc`:
Add the new species, its elemental composition, the name in LaTeX syntax, and a comment, e.g.:
`NC4H10 = 4C + 10H ; {@C_4H_<10>} {n-butane}`
Note that curly brackets needed by LaTeX must be entered as angle brackets.
- `jnl/xxxg.jnl`:
Add one line per new species. Check if the new species is part of an existing family, e.g. add new reactive bromine species to `Brx`.
- `jnl/tools/_kppvarg.jnl`:
Add one line per new species.

7.5.2 Adding a new aqueous-phase species

- `aqueous.spc`:
Add the new species, the name in LaTeX syntax, and a comment, e.g.:
`S04mm_a## = IGNORE; {@SO_4^<2->\aq} {sulfate}`
The suffix `_a##` is mandatory. The elemental composition is currently ignored. Note that curly brackets needed by LaTeX must be entered as angle brackets.
- `jnl/xxxa.jnl`:
Add one line per new species.
- `jnl/_families_a.jnl`:
Check if the new species is part of an existing family, e.g. add new bromine species to `Brtot`.
- `jnl/tools/_kppvara.jnl`:
Add one line per new species.

7.5.3 Adding a new gas-phase reaction

First, choose an appropriate reaction number. To avoid that several developers assign the same number to different new reactions, it is strongly recommended that a preliminary reaction number is used initially. This can be done by adding the developer's initials as a suffix, e.g. John Doe would use `G0001JD`, `G0002JD`, `G0003JD`, and so on. When the new code is merged with other development branches, the final reaction numbers will be assigned.

- `gas.eqn`:
 - Add one line per new reaction.
 - Add Monte-Carlo uncertainty factor. If unknown, only add "{`$`"}.
- `latex/meccanism.tex`:
If necessary, add a footnote about the new reaction here.

7.5.4 Adding a new gas-phase photolysis reaction

First, add the reaction, as explained in Sect. 7.5.3.

In addition, check if the necessary photolysis rate coefficient is already provided by SAPPHO, READJ, and/or JVAL. If not, add it:

- `messy_cmn_photol_mem.f90`:
 - Add a new index of photolysis `ip_XYZ` at the end of the list.
 - Increase `IP_MAX`.
 - Add the name to `jname`.
- `messy_sappho_box.f90`:
Add `XYZ` to `CALL open_output_file` and `CALL write_output_file`.
- `messy_sappho.f90`:
Add a simple definition for `jx(ip_XYZ)`.
- `messy_jval_box.f90`:
Add one line.
- `messy_jval_jvpp.inc`:
Calculate the definition with `jvpp` or add it manually here.

7.5.5 Adding a new aqueous-phase reaction

First, choose an appropriate reaction number, as explained in Sect. 7.5.3.

- `aqueous.eqn`:
 - Add one line per new reaction.
 - Add Monte-Carlo uncertainty factor. If unknown, only add “`{}`”.
- `latex/meccanism.tex`:
If necessary, add a footnote about the new reaction here.

7.5.6 Adding a new Henry’s law equilibrium

First, choose an appropriate reaction number, as explained in Sect. 7.5.3.

- `aqueous.eqn`:
 - Add two lines per new equilibrium, one for the forward and one for the backward reaction.
 - Add Monte-Carlo uncertainty factors. If unknown, only add “`{}`”.
- `messy_cmn_gasaq.f90`:
 - Add molar mass:
`CALL add_species('XYZ', ...)`

- Add the Henry’s law coefficient:
`CALL add_henry('XYZ', ...)`
- Add the accommodation coefficient:
`CALL add_alpha('XYZ', ...)`

Using these data, the subroutines `mecca_aero_trans_coeff`, `mecca_aero_henry`, and `mecca_aero_calc_k_ex` in `messy_mecca_aero.f90` will automatically calculate the rate coefficients `k_exf` and `k_exb` for `aqueous.eqn`.

- `latex/meccanism.tex`:
If necessary, add a footnote about the new equilibrium here.

7.5.7 Adding a new acid-base equilibrium

First, choose an appropriate reaction number, as explained in Sect. 7.5.3.

- `aqueous.eqn`:
 - Add two lines per new equilibrium, one for the forward and one for the backward reaction.
 - Add Monte-Carlo uncertainty factors. If unknown, only add “`{}`”.
- `latex/meccanism.tex`:
If necessary, add a footnote about the new equilibrium here.

7.5.8 Adding a new label

First, choose a name for the new label. The name must start with an upper case letter and can be followed by one or more lower case letters or numbers. Element symbols must not be used because they are reserved for reactions of that element. For example, since S is sulfur, the symbol S could not be used for the stratosphere. To avoid that several developers introduce new labels with the same name for different purposes, it is strongly recommended that a preliminary label is used initially. This can be done by adding the developer’s initials as a prefix, e.g. John Doe would use `Jd1`, `Jd2`, `Jd3`, and so on. When the new code is merged with other development branches, a final label name can be assigned.

- `xmecca`:
In the generation of `awkfile1`, add another `locate` function, and print the new label to the logfile.

7.5.9 Adding a new emission

- `messy_semidep_box.f90`:
Add one line to `emission_default` (or one of the other `emission_*` subroutines).

7.5.10 Adding a new deposition

- `messy_semidep_box.f90`:
Add one line to `drydep_default` (or one of the other `drydep_*` subroutines).

7.5.11 Enlarging KPP

If the selected chemistry mechanism has too many reactions, it may become necessary to increase some limits of KPP. The main changes are listed here:

- Increase `MAX_EQN` and `MAX_SPECIES` in `gdata.h`.
- With a large mechanism, some lines of the generated Fortran95 code become very long. The variable `MAX_NO_OF_LINES` in `code_f90.c` defines the maximum number of continuation lines that KPP will create. Unfortunately, if `MAX_NO_OF_LINES` is too small, KPP may incorrectly split commands into two parts. Therefore, a large value of `MAX_NO_OF_LINES` is needed for large mechanisms. Currently, `MAX_NO_OF_LINES` is set to 100. For very large mechanisms, it may be necessary to increase it even further. Note, however, that the Fortran95 standard only allows a maximum of 39 continuation lines and that you need a compiler that allows to exceed this limit.
- To increase the maximum size of inlined code (`F90_GLOBAL` etc.), change `MAX_INLINE` in `scan.h`.

To allow longer Fortran95 expressions for the rate coefficients in the `*.eqn` file, change consistently:

- `crtToken`, `nextToken`, `crtFile`, and `crt_rate` in `scan.l`
- `MAX_K` in `gdata.h` (note that `MAX_EQNLEN` here only determines how long the printout of the equation in the monitor file will be)
- `union` in `scan.y`

After each change in the source code, run `gmake` again.

7.6 How to modify and add new scenarios

The photolysis (`photo_scenario`), initialization (`init_scenario`), emission (`emission_scenario`), and dry deposition (`drydep_scenario`) can be modified for the different scenarios by entering appropriate values into the following subroutines:

scenario	subroutine	file
photo	<code>jvalues</code>	<code>messy_sappho.f90</code>
	<code>jval_init</code>	<code>messy_jval_box.f90</code>
init	<code>x0</code>	<code>messy_mecca_box.f90</code>
emission	<code>emission</code>	<code>messy_semidep_box.f90</code>
drydep	<code>drydep</code>	<code>messy_semidep_box.f90</code>

To define a new scenario, it is also necessary to add its name to the `list_of_scenarios` in `caaba.f90` and increase the value of `MAX_SCENARIOS` accordingly.

7.7 How to modify the aerosol modes

Aerosol properties are defined in SUBROUTINE `define_aerosol` in the file `messy_mecca_box.f90`. Depending on the total number of aerosol phases (`APN`), different setups are defined. For example, if `APN = 2`, then an accumulation mode with sulfate (index 1) and a coarse mode with sea salt are defined (index 2). For each aerosol phase, the following properties must be defined inside the appropriate `CASE` section:

variable	definition	unit
<code>xaer</code>	off/on (0. or 1.)	
<code>radius</code>	radius	m
<code>lwc</code>	liquid water content	m^3/m^3
<code>csalt</code>	total salt concentration	$\text{mcl}/\text{cm}^3(\text{air})$
<code>c0_NH4p</code>	$c(\text{NH}_4^+)$	$\text{mcl}/\text{cm}^3(\text{air})$
<code>c0_HCO3m</code>	$c(\text{HCO}_3^-)$	$\text{mcl}/\text{cm}^3(\text{air})$
<code>c0_NO3m</code>	$c(\text{NO}_3^-)$	$\text{mcl}/\text{cm}^3(\text{air})$
<code>c0_Cl1m</code>	$c(\text{Cl}^-)$	$\text{mcl}/\text{cm}^3(\text{air})$
<code>c0_Brm</code>	$c(\text{Br}^-)$	$\text{mcl}/\text{cm}^3(\text{air})$
<code>c0_Im</code>	$c(\text{I}^-)$	$\text{mcl}/\text{cm}^3(\text{air})$
<code>c0_IO3m</code>	$c(\text{IO}_3^-)$	$\text{mcl}/\text{cm}^3(\text{air})$
<code>c0_SO4mm</code>	$c(\text{SO}_4^{2-})$	$\text{mcl}/\text{cm}^3(\text{air})$
<code>c0_HSO4m</code>	$c(\text{HSO}_4^-)$	$\text{mcl}/\text{cm}^3(\text{air})$
<code>exchgng</code>	$1/\tau = \text{exchange}$	1/s

These values can be changed to modify the properties (including the initial chemical composition) of fresh aerosols. To add a new aerosol mode, another `CASE` section can be added. If a definition for the chosen value of `APN` exists already, the original code needs to be deactivated. Otherwise, a block defining a new total number of aerosol phases can simply be added.

Note that `APN = 3` is a special case where the third mode represents sea water at the ocean surface (not aerosol particles). This is under construction and not further described here.

7.8 Input files

Data in netCDF files can be used to initialize chemical tracers and photolysis rates as described below. In addition, time-dependent photolysis rates of NO_2 from a netCDF input file can be used to scale all other photolysis rates from the JVAL submodel. This has already been described in Sect. 6.3.3.

7.8.1 Tracer initialization file

MECCA provides several initialization scenarios for a variety of species and simulation aims (see

`init_scenario` in Sect. 7.6). However, for several consecutive simulations with changing initialization, the possibility to define an initialization file using `init_spec` is convenient. The tracer initialization file is a netCDF file with one point in time, at which selected species' mixing ratios are defined in mol/mol. The point in time itself is not important and not checked when reading the file. All tracers that are not specified in the input file are initialized according to default or a chosen `init_scenario`. An example for the initialization file can be found at `traject/example_init.nc`.

7.8.2 Photolysis initialization file

The submodel READJ reads J-values from a netCDF file. These values are used throughout the whole model run. Thus, READJ is normally only used when the model should run into steady-state (see Sect. 6.1). It is possible to use one comprehensive netCDF file containing values for both the tracer initialization (Sect. 7.8.1) and the photolysis initialization.

7.9 How to add a new MESSy submodel

Below you can find a brief description how to add a new MESSy submodel. For more detailed information about programming in the MESSy system, please refer to Jöckel et al. (2010).

- Choose a name (up to 7 lowercase alphanumerical characters, starting with a letter). Here, “xyz” is used as an example.
- `caaba_mem.f90`:
LOGICAL :: USE_XYZ = .FALSE.
- `messy_xyz.f90`:
Put all generic subroutines here, i.e. all subroutines that are used for the CAABA boxmodel as well as for a global model.
- `messy_xyz_box.f90`:
Put CAABA-specific code here. Generic code is not included directly here. Instead, the generic subroutines in `messy_xyz.f90` are called from here. This file contains up to four subroutines:
 - If the submodel needs an initialization, put subroutine `xyz_init` here.
 - If the submodel performs calculations during the time loop, put subroutine `xyz_physc` here.
 - If the submodel prints results to the screen or netCDF files, put subroutine `xyz_result` here.

- If the submodel needs to close any open files at the end of the model simulation, put subroutine `xyz_finish` here.
- `messy_main_control_cb.f90`:
 - Add “USE_XYZ” to “USE caaba_mem”
 - If subroutine `xyz_init` exists, add:
USE messy_xyz_box, ONLY: xyz_init
IF (USE_XYZ) CALL xyz_init
to subroutine `messy_init`.
 - If subroutine `xyz_physc` exists, add:
USE messy_xyz_box, ONLY: xyz_physc
IF (USE_XYZ) CALL xyz_physc
to subroutine `messy_physc`.
 - If subroutine `xyz_result` exists, add:
USE messy_xyz_box, ONLY: xyz_result
IF (USE_XYZ) CALL xyz_result
to subroutine `messy_result`.
 - If subroutine `xyz_finish` exists, add:
USE messy_xyz_box, ONLY: xyz_finish
IF (USE_XYZ) CALL xyz_finish
to subroutine `messy_finish`.
- `caaba.f90`:
Edit subroutine `caaba_read_nml`:
 - Add “USE_XYZ” to “USE caaba_mem”.
 - Add “USE_XYZ” to namelist /CAABA/.
 - Print value of USE_XYZ (see “selected MESSy submodels”)
 - If applicable, perform consistency checks for interaction of new submodel with other submodels.
- `xyz.nml`:
Add sensible default values for controlling the new submodel (optional).
- `manual/caaba_mecca_manual.tex`:
Mention new submodel in this user manual (Sect. 7.4, Tab. 2, and Fig. 5).

7.10 General programming guidelines

To achieve some consistency of the model code, the following guidelines should be adhered to when writing new code for the CAABA/MECCA modeling system:

- All Fortran code must be compatible with the Fortran95 standard. Compiler-specific extensions should not be used.
- Shell scripts should be written in `tcsh` syntax unless there is a specific reason for using `bash`, `ksh`, or any other shell.
- The file names of shell scripts should start with the letter `x` for all scripts that are executed directly by the model user.

- The file names of shell scripts should start with the underscore character (“_”) if the script is called via another script but not executed directly by the user.
- The names of temporary files should start with the prefix tmp_.

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