Brookesía



Tutorial for starting with Brookesia

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1 Installation

Brookesia is developed under the informatic language Python 3. It can be used on Linux, macOS, and Windows.

The necessary computations for the reduction procedure are done with the open-source Cantera software toolkit. The first step is thus to install it.

1.1 Cantera

Every necessary information for the installation of Cantera are provided on Cantera website:

https://www.cantera.org/install/conda-install.html

1.2 Brookesia

At the moment, Brookesia do not need installation. The only thing you need to do is to download the source files, install the required modules and use it properly!

1.2.1 Necessary python modules for proper use of Brookesia

To use Brokesia, the modules Pandas (https://pandas.pydata.org/) and Scipy (https://www.scipy.org/) must be installed. On a terminal ¹, go to your future reduction working folder then type:

```
conda activate <name_of_your_environment>
conda install pandas
conda install scipy
conda install matplotlib
conda install numpy
```

1.2.2 Through command line on Linux and Mac

On a terminal, go to your future reduction working folder then type:

```
git clone https://github.com/Brookesia-py/Brookesia
```

1.2.3 By downloading the software on Github

- 1. Go to the following webpage https://github.com/Brookesia-py/Brookesia
- 2. click on Clone or download button then Download zip
- 3. unzip the downloaded file on your future working folder

After that, all source files shall be on your working folder and you can directly start to work!

 $^{^1}$ On Windows, start Anaconda then click on: Environment \to Name_of_your_environment \to \blacktriangleright \to Open Terminal

2 Basic for reduction and subsequent optimization of detailed mechanisms

Before using Brookesia, make sure your Cantera environment is activated. On Anaconda: click on Environments tab then on your environment name. On a terminal, type:

```
conda activate <path to cantera environment>
```

2.1 Input file creation through the Graphic User Interface

On **Spyder** (normally installed with the Anaconda suite), load the file GUI_red_mech.py and run it. By command line, on Brookesia folder, just type:

```
python GUI_red_mech.py
```

Then, proceed to the following steps to operate a mechanism reduction (see the screen shots in Table 1):

On the **Main parameters** tab:

- 1. Load the kinetic mechanism
 - Table 1 example: C1 GRI30.cti

Note: It is possible to skip all the following steps by loading a previous input file by clicking on **load** file button

- 2. Select the target species
 - Table 1 example: CH₄/CO/CO₂
- 3. Select the reduction methods you want to apply

```
\underline{\text{Table 1 example: DRGEP\_sp} + \text{SA\_r}}
```

- \rightarrow then new tabs must appear
- 4. Select the errors options (pts/QoI; max/mean)
- 5. On the **Conditions** tab:

```
define the canonical configurations you want to run
```

```
Table 1 example: Reactor (H,p) CH<sub>4</sub>/air \Phi = 0.5/1/1.5 p = 10^5 Pa; T = 1600 K
```

6. On the *reduction* tab:

define all the options you want to specify (see section 2.4 for details)

7. On the **GA** tab (if so):

define all the options you want to specify (see section 2.4 for details)

- 8. On the **Main parameters** tab:
 - If necessary:
 - change the condition name and save it by clicking on the button Save current conditions
 Table 1 example: First example.inp → then saved in the condition input folder
 - change the folder name

```
Table 1 example: First example folder
```

Note: to this will be added the date and the hour of reduction (i.e. here 20191225_1200_First example folder)

- change the amount of outputs during the reduction process (verbose /show plot during reductions)

Run the reduction by clicking on **RUN** button

The reduction shall now take place. If the calculations are operated on Spyder and the option *Show plots during reduction* has been selected, you can follow the accuracy of the reduced models on the graphs displayed on the Spyder console.

2.2 Input file modification on a text editor

Saved input files (presented in appendices) are stored in an ASCII file, in the _condition_input folder. It may sometimes be more convenient to modify this text file directly than resorting to the GUI. Those input files can be then run by command line from a terminal (see next section).

They are composed in three parts:

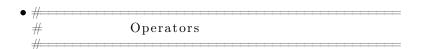


Corresponds to the information displayed in "Main parameters" tab in GUI.

Note: several species can be associated to the global data T, igt, Sl, and K. To do that just separate the associated species by a coma, i.e.:

Note: instead of entering fuel, oxidant, diluent, options, you can enter the mixture in the Cantera format using "mixt" option (and "mixt2" for counterflow burner configurations), i.e.:

$$mixt = CH4:0.1, O2:0.1, N2:0.8$$



Corresponds to the information displayed in " $Reduction\ operator$ " and "GA" tabs in GUI.

Note: if the number of values provided for the tolerance limit of target species is lower than the number of target species, only the first value will be transcribed and applied to target species. Thus, if you want to define a tolerance limit of 30% for all target species, you only need to enter the value 30 after the max_error_sp keyword, i.e.:

$$\max \text{ error sp} = 30$$

An example of input file and the corresponding keyword dictionary are presented in appendices

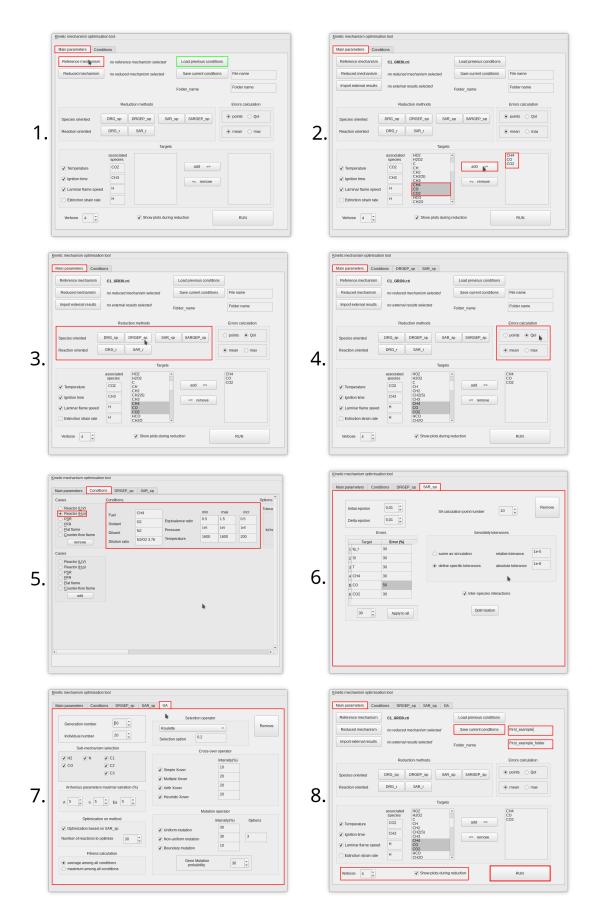


Table 1: Successive usual steps for the reduction and optimization of a kinetic mechanism

2.3 Running Brookesia from command line

From the head of the working folder, type:

```
python\ main\_reduction.py\ \_conditions\_input/< name\_of\_the\_input\_file>
```

The argument "_conditions_input/<name_of_the_input_file>" is the path toward the reduction condition input file.

2.4 Reduction and optimization options

• Reduction options :

Seven reduction methods are implemented in Brookesia:

- DRG oriented species (DRG_sp)
- DRGEP oriented species (DRGEP_sp)
- Sensitivity analysis oriented species (SAR_sp)
- Sensitivity analysis with graph search oriented species (SARGEP_sp)
- DRG oriented reactions (DRG_r)
- Sensitivity analysis oriented reactions (SAR r)
- Computational Singular Perturbation QSSA candidate identification and oriented reactions reduction (CSP)

For all reduction methods, you can specify (Figure 1 a.):

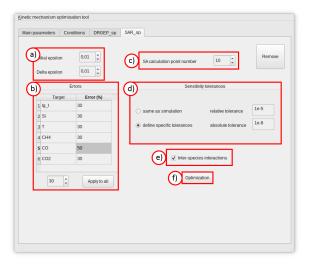
- a) The starting epsilon,
- b) The starting delta epsilon that will be applied between each iteration (subject to change during the reduction process)
- c) The number of calculation points distributed in each simulation
- d) The target tolerances
- e) The Inter Species Interactions loop
- f) The optimization after the reduction, if so, a new tab will appear

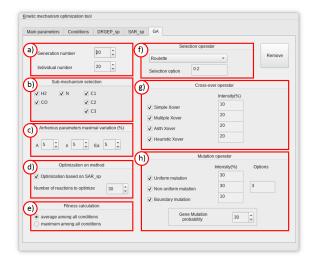
To facilitate the sensitivity analyses, it is possible to modify the tolerances (in the present example, relative/absolute tolerances are fixed at $10^{-5}/10^{-8}$, respectively)

• Optimization options:

On the genetic algorithm tab, you can specify (Figure 1 b.):

- a) the number of generation, of individuals,
- b) the sub-mechanism to optimize
- c) the variation range of reaction rate coefficients B, n and C
- d) to constrain the reduction method to the important reactions identified during the reduction
- e) to define the fitness computation depending on the average error or the maximal error (among all targets and conditions)
- f) the selection method
- g) the cross-over method and corresponding intensity
- h) the mutation method and corresponding intensity. The gene mutation probability define the reaction probability to get its reaction rate coefficients modified





(a) Reduction tab, example of Sensitivity Analysis based Reduction

(b) Genetic algorithm tab

Figure 1: Composition of the operator tabs (description in section 2.4)

2.5 Output files

Ones the reduction is finished, you can check the results on the new folder [Date_Time_<name of the folder>], (here: 191225_1200_First_example_folder). It contains the following elements:

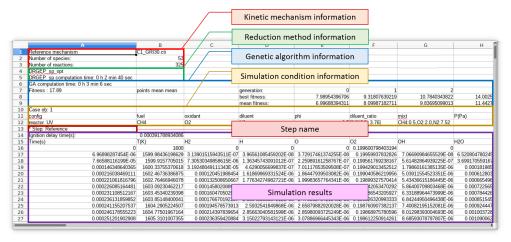
- File. Conditions_redopt.inp: input file of the reduction
- File. *.cti: reference mechanism (here: C1 GRI30.cti)
- File. red info.txt: contains information of the reduction process
- File. X_reduction_results.csv: contains the simulation results of the X reduction step (here, 0_reduction_result.csv for the DRGEP_sp step and 1_reduction_result.csv for the SA_r step). See details, hereafter.
- Folder. Flame_ref_results (if so): store the *.xml reference flame results used for restore Cantera option to accelerate the new mechanism simulations
- Folder. Red_mech: contains the reduced and optimized step named as follow: X(opt) B.cti

where X represent the step number, (opt) is a character string added for the optimized kinetic mechanism, B is the reference mechanism name.

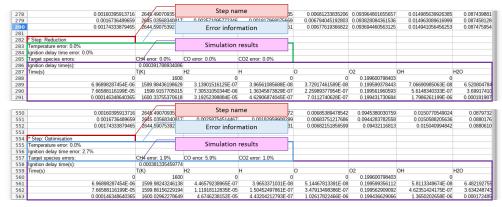
In the present example, the kinetic mechanism created are:

- 1 C1 GRI30.cti: reduced mechanism after DRGEP sp step
- 2 C1 GRI30.cti: reduced mechanism after SAR sp step
- 2opt_C1_GRI30.cti: optimized mechanism after genetic algorithm step

Simulation results are written in a *.csv file as presented in Figures 2. The first part of the file (a) indicate information concerning the reference mechanism, the reduction method and, if so, the genetic algorithm. The main information concerning the conditions of the simulation cases (canonical configuration, mixture composition, pressure, temperature, simulation tolerances, etc.) are reminded and the results of the reference simulation are provided. As indicated, in the Figure 2 b), after the reference results, the simulation results obtained with the reduced mechanism and, if so, the optimized mechanism are given. Error information are also provided.



(a) Reference result part



(b) Reduction/optimization results part

Figure 2: Results file main sections composition

3 Data importation

3.1 Start from a previously reduced kinetic mechanism

It is possible to continue a reduction/optimization process previously started while keeping the initial data (i.e. i.e. simulation reference results and reaction rate constants) of the detailed baseline mechanism. To do this, you must import the reference mechanism and specify the reduced mechanism from which you wish to start.

Procedure for specifying the reduced mechanism:

- from the GUI: click on the Reduced mechanism button on Main parameter tab.
- in an input file: in the Main parameters section, use the keyword mech_prev_red, e.g.: mech_prev_red = red_mech.cti

3.2 Import results file

In section 2.1, the reference results are calculated at the beginning of the reduction process from the detailed mechanism. It is also possible to conduct the reduction/optimization process from imported reference

column	reactor_HP reactor_UV	JSR	free_flame	burner_flame	diff_flame	pp_flame
1			config			
2	fuel (*)					
3			oxidant (*)			
4			diluent (*)			
5			phi (*)			
6			diluent ratio	(*)		
7			mixt (*)			
8			P (Pa)			
9	Ti (K)	time (s)	Γ	Ti (K)	fuel	2 (*)
10	rtol_ts		oxidant2 (*)			
11	atol ts		diluent2 (*)			
12	ig_time (s) rtol_ss		phi2			
13	atol_ss			ratio2 (*)		
14			transport_model			xt2
15	m Sl~(m/s)~~mdot~(kg/m2/s)~~mdo		ot2			
16					Ti	(K)
17						_ts
18						l_ts
19					rtol	_ss
20			·			l_ss
21				transpor	t_model	
22					K_ma	$\overline{\mathrm{x}(1/\mathrm{s})}$

Table 2: Simulation condition information layout in the imported result files

data. It allows, for instance, to use data simulated by another kinetic mechanisms than the one to be reduced/optimized as references, or also to define experimental data as references.

The input file for external results has to be filled in the same way than the output file provided by Brookesia (see figure 2). Thus, the easiest way to fill a new input result file is probably to start from a former output result file. If the value of a target for optimization or reduction is not provided in the input file, it is simply skipped for the evaluation of the simulation quality. For instance, it is possible to include in the experimental data panel experiments containing only ignition delay times while the optimization targets include ignition delay time as well as the evolution of CH₄, CO, and NO species. In the same way, flame structure experimental measurements containing only the profile of NO can be included even if the targets are CH₄, CH, and NO.

Results input files must be csv semicolon-separated file. Comments must be preceded by the hash symbol (#). The key-word "Case" is used to separate the different input conditions. This line is followed by the conditions specification, constituted, themselves in two lines. The first is a headline and the second contains the condition information. The column order must respect the arrangement presented in Table 2.

Important: when reference data are imported, the simulation conditions are only defined by those provided in the data file. In GUI, the **Conditions** tab is removed.

Procedure for importing a results file:

- from the GUI: after defining the reference kinetic mechanism, click on the buttaon import external results. Then, a window will appear to specify the units of the data (molar concentrations / molar fractions).
- in an input file: in the Main parameters section, use the keyword ext_results_file, e.g.: ext_results_file = red_mech.cti then specify the nature of the imported data with the keywords conc_units, e.g.:

4 First examples

Five input files are provided for a gentle start with Brookesia software. Input conditions are summarized in Table 3.

As an example, the results obtained with the successive kinetic mechanisms simulation of the reduction procedure given in 1_reactor.inp are presented in Figure 3.

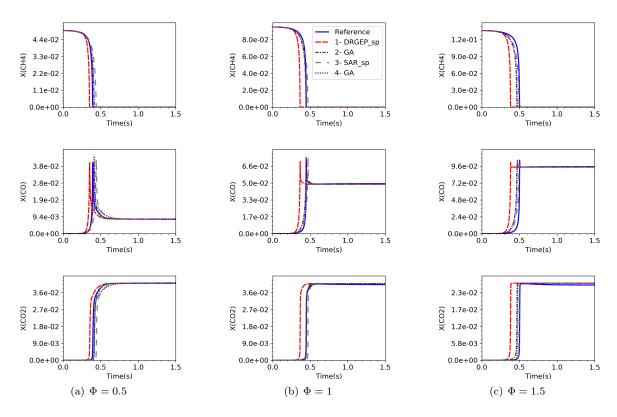


Figure 3: Simulation results obtained during the reduction process defined in the example 1 reactor.inp

Input file name	1 _reactor.inp	$2_{\mathrm{JSR.inp}}$	3 _Free_Flame.inp	4 _diff.inp	5 _pp.inp	$6_\mathrm{import}_\mathrm{Sl}$
kinetic mechanism	C1_GRI30	C1_GRI30	C1_GRI30	C0_H2_Law	C1_GRI30	C3_Gong_red_a
Species (reaction)	53 (325)	53 (325)	53 (325)	11 (32)	53 (325)	28 (118)
	Reactor (U,V)	JSR	Free flame	Diffusion flame	Partially-premixed flame	Free flame
oon ditions	$ m CH_4/air$	$\mathrm{CH_4/air}$	$ m H_2/air$	$\mathrm{CH_4/air}$	$\mathrm{CH_4/air}$	$\mathrm{C_2H_6/air}$
conditions	Φ =0.5, 1, 1.5	$\Phi=0.5,1,1.5$	$\Phi=0.5,1,1.5$		$\Phi = 1/0.5, 1.5/0.5$	$\Phi=0.6$ - 1.8
	$p = 10^5 \text{ Pa}$	$p = 10^5 \text{ Pa}$	$p = 10^5 \text{ Pa}$	$p = 10^5 \text{ Pa}$	$p = 10^5 \text{ Pa}$	$p = 10^5 \text{ Pa}$
	T = 1600 K	T = 600 - 1200 K	T = 300 K	T = 300 K	T = 300 K	T = 300 K
	$CH_4(30)$	$CH_4(30)$	$CH_4(30)$	$H_2(30)$	$CH_4(30)$	
	CO(30)	OH(30)	CO(30)	$H_2O(30)$	CO(30)	
Target(error)	$CO_4(30)$	$CO_2(30)$	$CO_2(30)$	H(30)	$CO_2(30)$	Sl
	T(30)	T(30)	T(30)	T(30)	T(30)	
	Igt(30)		Sl(30)	K(30)		
Error method	points	points	QoI	QoI	points	points
Reduction	$DRGEP_sp + GA$	DRGEP_sp	DRGEP_sp	DRGEP_sp	DRG_sp	GA
method	$SAR_sp + GA$	$DRG_r + GA$	$SARGEP_sp + GA$	$DRG_r + GA$	$SAR_r + GA$	GA
Final Species (reaction)	15 (57)	23 (114)	20 (100)	8 (11)	26 (87)	28 (118)
Computation time	7 min	5 min	2 h 08 min	35 min	40 min	23 min
Computation time	7 min	5 min	2 h 08 min	35 min	40 min	23 min

Table 3: Summary presentation of the five input files provided as examples targets symbols: T: temperature, igt: ignition delay time, Sl: laminar flame speed, K: Extinction stretch rate

5 Appendices

Input file example

```
Main parameters
#
#
main_path
                   = TEST_1_reactor
mech
                   = C1_GRI30.cti
                  = 4
verbose
show_plots
                  = True
tspc
                   = CH4, CO, CO2
T_check
sp_T
Sl_check
                   = True
                   = CO2
                   = False
sp_Sl
                   = H
                  = True
ig_check
sp_ig
K_check
                   = CH3
                   = False
\mathrm{sp}_{\mathrm{K}}
                   = H
error calculation = points
error_coupling = mean
             Simulation cases
#------- Case 1
config
                   = reactor UV
                   = 100000.0
Ps
                   = CH4
fuel
                   = O2
oxidant
                   = N2
diluent
                 = N2/O2 3.76
diluent_ratio
                   = 1600.0
Ts
Ps
                   = 100000.0
                   = 0.5, 1.0, 1.5
phis
                  = 250.0
n_{pts}
delta npts
                  = 20.0
t_{max}_coeff
                   = 5.0
Scal_ref
grad_curv_ratio
                   = H2O
                  = 0.5
                   = 130.0
tign_nPoints
tign_dt
                   = 1e-09
tol_ts
                   = 1e-06, 1e-12
             Operators
# Op: DRGEP_sp
                = DRGEP_sp
operator
                 = 0.02
eps
                = 0.01
delta_eps
n_points
                = 10.0
                = 30, 30, 30
max_error_sp
max_error_ig = 30
max_error_ig = 30
inter_sp_inter = True
optim
# Optimization
n_{gen}
n_indiv
```

```
error_fitness
                     = mean
nb_r2opt
                     = 30
selection\_operator = Roulette
selection\_options = 0.2
                     = simple\_Xover \,, \ multiple\_Xover \,, \ arith\_Xover \,, \ heuristic\_Xover
Xover_operator
Xover_pct
Xover_opt
                     = 10, 20, 20, 20
mut_operator
                     = uniform_mutation, non_uniform_mutation, boundary_mutation
mut\_pct
                     = 30, 30, 10
mut_opt
mut_intensity
                     = , 3, 
 = 20
sub_mech_sel
                     = H2, CO, C1, C2, C3, N
# Op: SAR sp
                 = SAR_sp
operator
                 = 0.02
eps
delta eps
                 = 0.01
                 = 10.0
n_{points}
max_error_sp
max_error_T
                 = 30.0, 30.0, 30.0
                 = 30.0
max_error_ig
                 = 30.0
inter\_sp\_inter = True
                 = True
optim
ttol_sensi
                 = [1e-05, 1e-08]
# Optimization
n_{gen}
n_{indiv}
                     = 5
error_fitness
                     = mean
Arrh_max_variation = 8, 3, 3 optim_on_meth = False
nb r2opt
                     = 30
selection\_operator = Roulette
selection\_options = 0.2
Xover_operator
                     = simple_Xover, multiple_Xover, arith_Xover, heuristic_Xover
Xover_pct
                     = 10, 20, 30, 20
Xover\_opt
                     = uniform\_mutation \,, \ non\_uniform\_mutation \,, \ boundary\_mutation
\operatorname{mut\_operator}
                     =\ 10\,,\ 70\,,\ 40
\operatorname{mut}\operatorname{\_pct}
mut\_opt
                     = , 3,
mut_intensity
                     = 30
sub_mech_sel
                     = H2, CO
```

Input file keyword dictionary

Main parameters keywords

main nath	name of the folder containing all results (to this will be added the date and the
$\operatorname{main}_{-}\operatorname{path}$	- ,
	hour of reduction)
mech	reference mechanism name
$\operatorname{mech_prev_red}$	starting reduced mechanism name
$ext_results_file$	name of the external file containing reference conditions and corresponding
•.	results
conc_units	concentration unit of the imported external data (Molar_fraction/mol_m3)
$show_plots$	for Spyder essentially, select to display or not the simulation results during the
	reduction process
verbose	rules the amoung of information displayed during the reduction process (range
	between 0 and 10)
tspc	name of target species
ig_check	add (True) or not (False) the ignition delay time as target
K_{check}	add (True) or not (False) the extinction stretch rate as target
Sl_check	add (True) or not (False) the flame speed as target
T_{check}	add (True) or not (False) the temperature as target
$\mathrm{sp}\mathrm{_ig}$	ignition delay time associated species to manage reduction with reduction
**	methods
$\mathrm{sp}_{-}\mathrm{K}$	extinction stretch rate associated species to manage reduction with reductions
$\mathrm{sp}_{-}\mathrm{Sl}$	methods flame speed associated species to manage reduction with DRG methods
	temperature associated species to manage reduction with DRG methods
sp_T	
$error_calculation$	error method (point/QoI)
$\operatorname{error_coupling}$	error interpretation (max/mean)

${\bf Configuration\ keywords}$

_		<u> </u>
	config	configuration (reactor_UV, reactor_HP, free_flame, diff_flame, pp_flame,
		tp_flame)
	$reactor_UV$	adiabatic, constant volume reactor
	JSR	Jet-stirred reactor
	PFR	Plug-flow reactor (!) beta version
	${ m reactor_HP}$	adiabatic, constant pressure reactor
	free_flame	freely propagative adiabatic flame
	diff_flame	counterflow diffusion flame
	pp_flame	partially-premixed flame
	tp_flame	twin-premixed flames
	mixt	initial mixture composition (e.g. mixt = CH4:0.1, O2:0.1, N2:0.8)
	fuel	fuel species
	oxidant	oxidant species
	diluent	diluent species
	$diluent_ratio$	dilution ratio (%)
	Ts	initial temperature(s) (K)
	Ps	initial pressure(s) (Pa)
	phis	equivalent ratio(s)
	tol_ts	simulation transient tolerances
	n_{pts}	for reactors: simulation point number (for reactors)
	$delta_npts$	for reactors: tolerance in simulation point number
	t_{max}_{coeff}	for reactors: final time of the simulations (multiple of ignition delay time)

Configuration keywords

Configuration keywords			
Scal_ref	for reactors: reference scalar for grad and curve interpretation		
$\operatorname{grad} \operatorname{_curv} \operatorname{_ratio}$	for reactors: grad/curv options for time discretization		
t_{max}	for JSR: residence time on the reactor (s)		
xmax	for free_flames: dimension of the computational domain (m)		
tol_ss	for flames: simulation steady-state tolerances		
$transport_model$	for flames: transport model (Mix/Mult)		
$pts_scatter$	for flames: initial grid		
slope	for flames: Cantera refining criteria		
	normalized maximum difference in value between two adjacent points		
curve	for flames: Cantera refining criteria		
	normalized maximum difference in slope between two adjacent intervals		
ratio	for flames: Cantera refining criteria		
	add points if the ratio of the spacing on either side of a grid point exceeds this value		
prune	for flames: Cantera refining criteria		
	remove point if the slope or curve criteria are satisfied to the level of "prune"		
xmax	for free_flames: dimension of the computational domain (m)		
$fuel_1$	for counterflow flames: bottom burner fuel species		
$\operatorname{oxidant}_{1}$	for counterflow flames: bottom burner oxidant species		
$\operatorname{diluent}_{1}$	for counterflow flames: bottom burner diluent species		
$diluent_ratio_1$	for counterflow flames: bottom burner diluent species		
Ts_1	for counterflow flames: bottom burner initial temperature(s) (K)		
$phis_1$	for counterflow flames: bottom burner equivalent ratio(s)		
$mdots_1$	for counterflow flames: bottom burner mass flux $(kg/m^2/s)$		
$fuel_2$	for counterflow flames: top burner fuel species		
$\operatorname{oxidant}_2$	for counterflow flames: top burner oxidant species		
$\operatorname{diluent}_2$	for counterflow flames: top burner diluent species		
$diluent_ratio_2$	for counterflow flames: top burner diluent ratio		
Ts_2	for counterflow flames: top burner temperature(s) (K)		
phis_1	for counterflow flames: top burner equivalent ratio(s)		
$mdots_2$	for counterflow flames: top burner mass flux $(kg/m^2/s)$		
width	for counterflow flames: interval between the bottom and the top burner (m)		

${\bf Reduction\ method\ keywords}$

operator	reduction operator (DRG_sp, DRGEP_sp, DRG_r, SAR_sp, SAR_r,
	SARGEP_sp)
eps	starting cut-off threshold ϵ
delta eps	starting delta epsilon (subject to change during the reduction process)
n points	number of calculation points distributed in each simulation
max_error_sp	target tolerances
	Note: if the number of values provided for the tolerance limit of target species is lower
	to the number of target species, only the first value will be transcribed and applied to
	target species
$\max_{\text{error}} T$	temperature tolerances
max_error_ig	ignition delay time tolerances
$\max_{\text{error}} Sl$	flame speed tolerances
max error K	extinction stretch rate tolerances
inter sp inter	application of the Target Species Interaction loop (True/False)
ttol sensi	sensitivity analyses relative/absolute tolerances
	l ·

Genetic Algorithm keywords

Genetic Algorithm keywords				
optim	genetic algorithm optimization (True/False)			
n_gen	generation number			
n_indiv	individual number			
$\operatorname{error_fitness}$	fitness computation option			
	mean: computation based on the average error / max: computation based on the			
	maximal error among all targets and conditions on all /max			
Arrh_max_variation	variation range of reaction rate coefficients B, n and C			
$optim_on_meth$	optimization method constrained to the important reactions identified by			
	reduction methods (True/False/DRG/SA)			
nb_r2opt	number of reaction to optimize			
selection_operator	selection operator			
selection_options	selection operator option			
Xover_operator	cross-over operator			
$Xover_pct$	cross-over operator use rate (% of the number of individuals)			
$\operatorname{mut}_{\operatorname{operator}}$	mutation operator			
$\operatorname{mut} \operatorname{pct}$	mutation operator use rate (% of the number of individuals)			
$\operatorname{mut}\operatorname{_opt}$	mutation options 'leave empty if not necessary			
$\operatorname{mut_intensity}$	probability of a reaction to get its reaction rate coefficients modified by mutation			
	operator			
sub_mech_sel	sub-mechanism to optimize			