# Brookesía



# Documentation

# Contents

1	Installation					
	1.1	Cantera	1			
	1.2 Brookesia					
		1.2.1 Through command line on Linux and Mac	1			
		1.2.2 By downloading the software on Github	1			
2	2 Basic usage					
	2.1	Input file creation through the Graphic User Interface	2			
	2.2	Input file modification on a text editor and tips	4			
	2.3	Running Brookesia from command line	4			
	2.4	Focus on reduction and optimization options	5			
3	Output files		6			
4	First examples					
5	Арр	pendices	10			

### 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 and use it properly!

### 1.2.1 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

### 1.2.2 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!

# 2 Basic usage

Before using Brookesia, make sure your Cantera environment is activated. On linux, type on a terminal:

```
source \ 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. On 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

Example: C1 GRI30.cti

Note: It is possible to load a previous input file by clicking on load file button

2. Select the target species

Example: CH<sub>4</sub>/CO/CO<sub>2</sub>

3. Select the reduction methods you want to apply

 $\frac{\text{Example: DRGEP\_sp} + \text{SA\_r}}{\rightarrow \text{ then new tabs must appear}}$ 

- 4. Select the errors options (pts/QoI; max/mean)
- 5. On the **Conditions** tab:

Define the canonical configurations you want to run

Example: Reactor (H,p) CH<sub>4</sub>/air  $\Phi = 0.5/1/1.5 p = 10^5 \text{Pa}$ ; T = 1600 K

6. On the *reduction* tab:

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

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

define all the options you want to specify (see 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 Example: First example.inp  $\rightarrow$  then saved in the condition input folder
- <del>change the folder name</del>

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



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

### 2.2 Input file modification on a text editor and tips

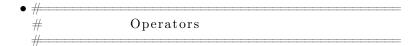
Input files (presented in appendices) are usually stored in the \_condition\_input folder. They are composed in three steps :



Corresponds to the informations 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 informations 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 retranscribed and applied to target species. Thus, if you want to define a tolerance threshold 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 dictionnary are presented in appendices

### 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 Focus on reduction and optimization options

### • Reduction options :

For all reduction methods, you can specify:

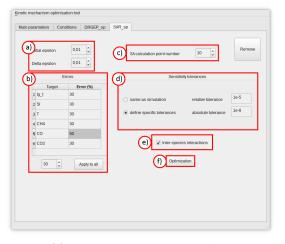
- a) The starting epsilon,
- b) The starting delta epsilon that will be applied between each iteration (subject to change during the reduction process)
- c) The number of calculation points distributed in each simulation
- d) The target tolerances
- e) The Inter Species Interactions loop
- f) The optimization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

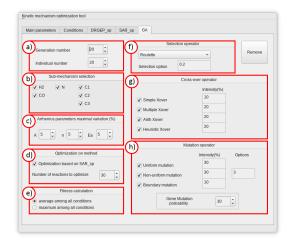
To facilitate the sensitivity analyses, it is possible to modify the tolerances (in the present example, relative/absolute tolerances are fixed at  $10^{-5}/10^{-8}$ , respectively)

### • Optimization options:

On the genetic algorithm tab, you can specify:

- 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 contrain 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 SAR

(b) Genetic algorithm tab

Figure 1: Results file main sections composition

# 3 Output files

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 (see figure 2. a).

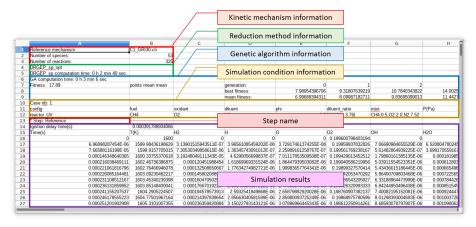
One the reduction is finished, you can check the results on the new folder [date\_time\_name\_of\_the\_folder], (here: 191225 1200 First example folder). It contains the following elements:

- File. Conditions redopt.inp: the input file of the reduction
- File. \*.cti: the reference mechanism (here: C1 GRI30.cti)
- File. red\_info.txt: contains informations 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 follows: 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.

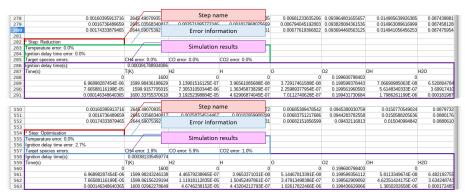
In the present example, the kinetic mechanism created are:

- 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 organized on 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

# 4 First examples

Five input files are provided for a gentle start with Brookesia software. Input conditions are summarized in Table 2.

Input file name	$1$ _reactor.inp	$2_{\mathrm{JSR.inp}}$	$3$ _Free_Flame.inp	$4_{\rm diff.inp}$	$5_{pp.inp}$
kinetic mechanism	C1_GRI30	C1_GRI30	C1_GRI30	C0_H2_Law	C1_GRI30
Species (reaction)	53 (325)	53 (325)	53 (325)	11 (32)	53 (325)
	Reactor (U,V)	JSR	Free flame	Diffusion flame	Partially-premixed flame
conditions	$\Phi$ =0.5, 1, 1.5	$\Phi = 0.5, 1, 1.5$	$\Phi = 0.5, 1, 1.5$		$\Phi = 1/0.5,  1.5/0.5$
	$p = 10^5 \text{ Pa}$	$p = 10^5 \text{ Pa}$	$p = 10^5 \text{ Pa}$	$p = 10^5 \text{ Pa}$	$p = 10^5 \text{ Pa}$
	$T=1600~\mathrm{K}$	T = 600 - 1200  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)	$CO_2(30)$
	T(30)	T(30)	T(30)	T(30)	T(30)
	Igt(30)		Sl(30)	K(30)	
Error method	points	points	QoI	QoI	points
Reduction	$DRGEP\_sp + GA$	DRGEP_sp	DRGEP_sp	DRGEP_sp	DRG_sp
method	$SAR\_sp + GA$	$DRG_r + GA$	$SARGEP\_sp + GA$	$DRG_r + GA$	$SAR_r + GA$
Final Species (reaction)	15 (57)	22 (114)	25 (133)	8 (12)	24 (86)
Computation time	7 min	5 min	2 h 08 min	35 min	40 min

Table 2: 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

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.

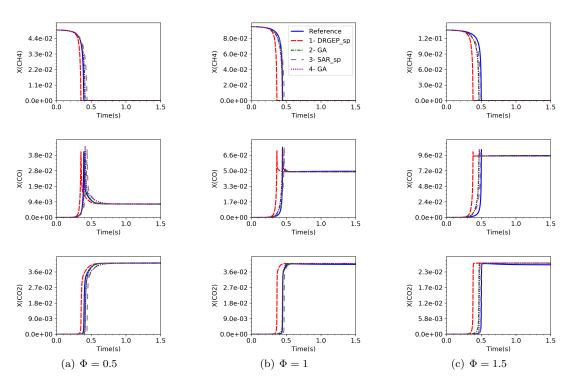


Figure 3: Simulation results obtained during the reduction process defined in the example  $$1_{\rm reactor.inp}$$ 

# 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
\operatorname{mut} \operatorname{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
                     = 10, 20, 30, 20
Xover_pct
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 dictionnary

Main parameters keywords		
main_path	name of the folder containing all results (to this will be added the date	
	and the hour of reduction)	
mech	reference mechanism name	
verbose	rules the amoung of information displayed during the reduction process	
	(range between 0 and 10)	
$show\_plots$	for spyder essentially, select to display or not the simulation results during	
	the reduction process	
$\operatorname{tspc}$	name of target species	
$T_{check}$	add (True) or not (False) the temperature as target	
$\mathrm{sp}_{-}\mathrm{T}$	temperature associated species to manage reduction with DRG methods	
Sl_check	add (True) or not (False) the flame speed as target	
$\mathrm{sp}_{-}\mathrm{Sl}$	flame speed associated species to manage reduction with DRG methods	
ig check	add (True) or not (False) the ignition delay time as target	
sp ig	ignition delay time associated species to manage reduction with reduction	
	methods	
$K_{check}$	add (True) or not (False) the extinction stretch rate as target	
$\mathrm{sp}_{-}\mathrm{K}$	extinction stretch rate associated species to manage reduction with	
error_calculation	reductions methods error method (point / QoI)	
error_coupling	error interpretation (max / mean)	

# Configuration keywords

	g y
config	configuration (reactor_UV, reactor_HP, free_flame, diff_flame,
	pp_flame, tp_flame)
${ m reactor\_UV}$	adiabatic, constant volume reactor
JSR	Jet-stirred reactor
PFR	Plug-flow reactor (!) beta version
$reactor\_HP$	adiabatic, constant pressure reactor
$free\_flame$	freely propagative adiabatic flame
$\operatorname{diff}_{-}\operatorname{flame}$	counterflow diffusion flame
$pp_flame$	partially-premixed flame
${ m tp\_flame}$	twin-premixed flames
$\operatorname{mixt}$	initial mixture composition (e.g. $mixt = CH4:0.1, O2:0.1, N2:0.8$ )
fuel	fuel species
oxidant	oxidant species
$\operatorname{diluent}$	diluent species
$\operatorname{diluent}$ 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)
$Scal\_ref$	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)

# Configuration keywords

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
$\mathrm{Ts}\_1$	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
$diluent_2$	for counterflow flames: top burner diluent species
$diluent_ratio_2$	for counterflow flames: top burner diluent ratio
$\mathrm{Ts}\_2$	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 <sup>2</sup> /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 $\epsilon$
$delta\_eps$	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 speciesis
	lower to the number of target species, only the first value will be retranscribed
	and applied to target species
$\max\_error\_T$	temperature tolerances
$\max\_error\_ig$	ignition delay time tolerances
$\max\_error\_Sl$	flame speed tolerances
$\max_{\text{error}} K$	extinction stretch rate tolerances
inter_sp_inter	application of the Target Species Interaction loop (True/False)
ttol_sensi	sensitivity analyses relative/absolute tolerances

## Genetic Algorithm keywords

denetic Higorithm key words			
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)		
$mut\_operator$	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		
$\operatorname{sub\_mech\_sel}$	sub-mechanism to optimize		