PCP cleaned data

April 24, 2021

1 PCP case study

1.1 No chl prime

1.1.1 Notebook helper function for pretty output

```
[1]: from IPython.display import Markdown, display

def print_md(markdown_printable):
    """Pretty render Markdown."""
    display(Markdown(str(markdown_printable)))

def print_yaml_file(file_path):
    """Pretty render yaml file."""
    with open(file_path) as f:
        print_md(f"```yaml\n{f.read()}\n```")
```

1.1.2 Plotting functions (pyglotaran_extras + matplotlib)

```
[2]: import matplotlib.pyplot as plt
from pyglotaran_extras.plotting.plot_overview import plot_overview
from pyglotaran_extras.plotting.plot_svd import plot_svd
from pyglotaran_extras.plotting.style import PlotStyle

plot_style = PlotStyle()
plt.rc("axes", prop_cycle=plot_style.cycler)
plt.rcParams["figure.figsize"] = (10, 7)
```

1.1.3 Analysis functions

```
[3]: from glotaran.analysis.optimize import optimize from glotaran.io import load_dataset, load_model, load_parameters from glotaran.project.scheme import Scheme
```

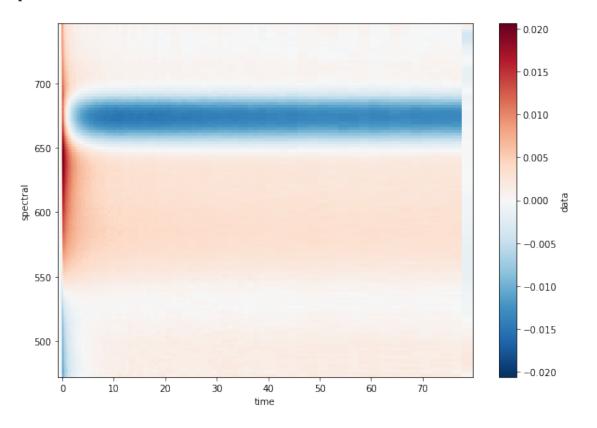
1.1.4 Read data

```
[4]: dataset = load dataset("PCP490.ascii")
     dataset
[4]: <xarray.Dataset>
                                       (left_singular_value_index: 127,
     Dimensions:
     right_singular_value_index: 127, singular_value_index: 127, spectral: 127, time:
     198)
     Coordinates:
       * time
                                       (time) float64 -0.825 -0.725 \dots 76.7 78.7
                                       (spectral) float64 473.2 475.3 ... 743.2 745.3
       * spectral
     Dimensions without coordinates: left_singular_value_index,
     right_singular_value_index, singular_value_index
     Data variables:
         data
                                       (time, spectral) float64 0.0002336 ... 0.000...
         data_left_singular_vectors
                                       (time, left_singular_value_index) float64 -0...
         data_singular_values
                                       (singular_value_index) float64 0.7069 ... 0...
         data_right_singular_vectors
                                      (right_singular_value_index, spectral) float64
```

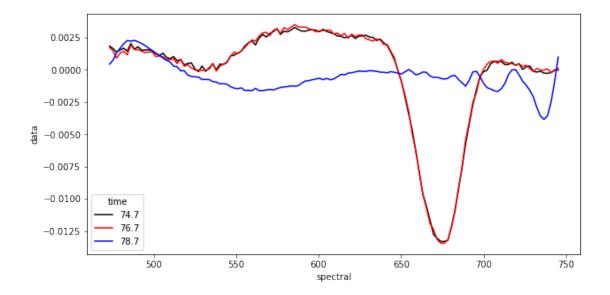
1.2 Investigating the original data

```
[5]: dataset.data.plot(x="time", y="spectral")
```

[5]: <matplotlib.collections.QuadMesh at 0x1dd3a52ad60>



```
[6]: last_traces = dataset.data.isel(
          time=slice(-3, None),
)
last_traces.plot.line(x="spectral", aspect=2, size=5)
```



As can be seen in the two plots above, the last spectral value appears to be erroneous and thus should be removed from the dataset.

1.3 Removing data

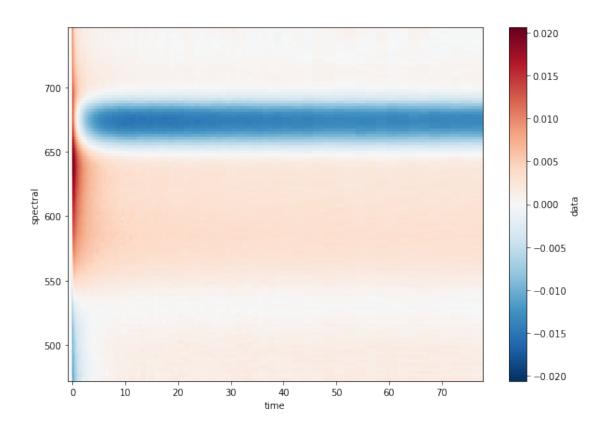
To remove data in an index based manner the isel method together with slice can be used on the Dataset to select only the wanted data and the resulting Dataset can be assigned to a new variable. The keywords in isel are the names of the axes that the selection should be applied on and slice is the index based selection interval.

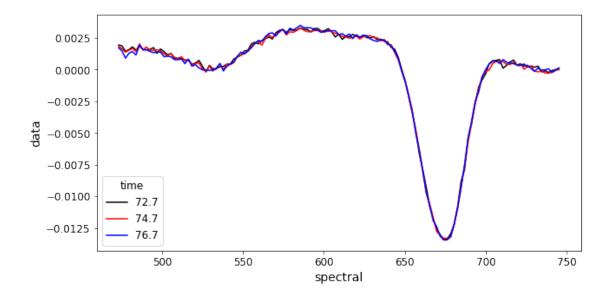
1.3.1 slice usage examples

```
slice(-i)
will select all but the last i values
slice(i)
will select all values up to i
slice(i, None)
will select all values from index i until the end
slice(i, j)
will select all values from index i until index j
```

```
[7]: dataset_cleaned = dataset.isel(time=slice(-1)) # drop the last spectral values dataset_cleaned.data.plot(x="time", y="spectral")
```

[7]: <matplotlib.collections.QuadMesh at 0x1dd3a639790>





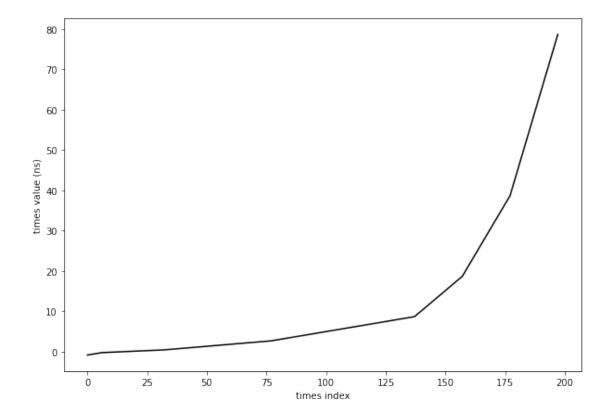
1.4 None linear time axis

To understand why the heatmap of the data appears to be unevenly spaced we can have a look at the time axis's values over their index.

```
[9]: import numpy as np

plt.plot(np.arange(len(dataset.time)), dataset.time)
plt.xlabel("times index")
plt.ylabel("times value (ns)")
```

[9]: Text(0, 0.5, 'times value (ns)')



The exponential values of the times long their index explains the "mistery" of the unevenly spaced heatmap.

1.4.1 Load model and parameters

```
[10]: PCP_model = load_model("models/PCP-model.yml")
PCP_parameters = load_parameters("models/PCP-parameters.yml")
print_md(PCP_model.validate(parameters=PCP_parameters))
```

Your model is valid.

```
[11]: print_md(PCP_model)
```

2 Model

Type: kinetic-spectrum

2.1 Initial Concentration

- input1:
 - Label: input1
 - Compartments: ['s1', 's2', 's3', 's4', 's5']
 - Parameters: [input.1, input.0, input.0, input.0, input.0]

- Exclude From Normalize: []

2.2 K Matrix

- km1:
 - Label: km1
 - Matrix:
 - * ('s1', 's1'): kinetic.9
 - * ('s2', 's1'): kinetic.1
 - * ('s5', 's1'): kinetic.2
 - * ('s2', 's2'): kinetic.9
 - * ('s3', 's2'): kinetic.3
 - * ('s4', 's2'): kinetic.4
 - * ('s5', 's2'): kinetic.8
 - * ('s3', 's3'): kinetic.9
 - * ('s5', 's3'): kinetic.5
 - * ('s4', 's4'): kinetic.9
 - * ('s5', 's4'): kinetic.6

 - * ('s5', 's5'): kinetic.7

2.3 Irf

- irf1 (gaussian):
 - Label: irf1
 - Type: gaussian
 - Center: irf.center
 - Width: irf.width
 - Normalize: True
 - Backsweep: False

2.4 Dataset

- dataset1:
 - Label: dataset1
 - Megacomplex: ['mc1']
 - Initial Concentration: input1
 - Irf: irf1

2.5 Megacomplex

- mc1:
 - Label: mc1
 - *K Matrix*: ['km1']

2.5.1 Create scheme and optimize it

[12]: PCP_scheme = Scheme(PCP_model, PCP_parameters, {"dataset1": dataset_cleaned})
PCP_result = optimize(PCP_scheme)

Iteration	Total nfev	Cost	Cost reduction	Step norm
$\mathtt{Optimality}$				
0	1	9.2376e-04		
3.59e-02				
1	2	5.5506e-04	3.69e-04	1.57e-02
4.15e-03				
2	3	5.4022e-04	1.48e-05	6.52e-03
8.85e-04				
3	4	5.3898e-04	1.23e-06	2.03e-03
2.55e-04				
4	5	5.3889e-04	9.12e-08	5.50e-04
6.87e-05				
5	6	5.3889e-04	6.64e-09	1.49e-04
1.85e-05				
6	7	5.3889e-04	4.81e-10	4.00e-05
4.98e-06				
7	8	5.3889e-04	3.48e-11	1.08e-05
1.34e-06				
8	9	5.3889e-04	2.52e-12	2.89e-06
3.60e-07				

[`]ftol` termination condition is satisfied.

Function evaluations 9, initial cost 9.2376e-04, final cost 5.3889e-04, first-order optimality 3.60e-07.

[13]: PCP_result.data["dataset1"]

[13]: <xarray.Dataset>

Dimensions: (clp_label: 5, component: 5, from_species: 5, left_singular_value_index: 127, right_singular_value_index: 127, singular_value_index: 127, species: 5, spectral: 127, time: 197, to_species: 5)

Coordinates:

* time	(time) float64 -0.825 76.7
* spectral	(spectral) float64 473.2 745.3
* clp_label	(clp_label) <u2 's1'="" 's2'="" 's5'<="" th=""></u2>
* species	(species) <u2 's1'="" 's2'="" 's5'<="" th=""></u2>
rate	(component) float64 -15.14
lifetime	(component) float64 -0.06605
* to_species	(to_species) <u2 's1'="" 's5'<="" th=""></u2>
* from_species	(from_species) <u2 's1'="" 's5'<="" th=""></u2>

Dimensions without coordinates: component, left_singular_value_index, right_singular_value_index, singular_value_index

Data variables: (12/24)

```
float64 ...
          data_singular_values
                                                      (singular_value_index) float64 ...
          data_right_singular_vectors
                                                      (right_singular_value_index,
      spectral) float64 ...
          matrix
                                                      (time, clp_label) float64 1.259...
          clp
                                                      (spectral, clp_label) float64 -...
                                                      (component, species) float64 1...
          a matrix
                                                      (to species, from species) float64
          k matrix
          k_matrix_reduced
                                                      (to species, from species) float64
                                                      float64 0.009177
          irf_center
          irf_width
                                                      float64 0.06631
                                                      (time) float64 4.309e-35 ... 0.0
          irf
      Attributes:
          root_mean_square_error:
                                             0.0002075526312040566
          weighted_root_mean_square_error: 0.0002075526312040566
     2.5.2 Result plots
[14]: PCP result.data["dataset1"]
[14]: <xarray.Dataset>
      Dimensions:
                                                      (clp_label: 5, component: 5,
      from species: 5, left singular value index: 127, right singular value index:
      127, singular_value_index: 127, species: 5, spectral: 127, time: 197,
      to species: 5)
      Coordinates:
        * time
                                                      (time) float64 -0.825 ... 76.7
                                                      (spectral) float64 473.2 ... 745.3
        * spectral
        * clp_label
                                                      (clp_label) <U2 's1' 's2' ... 's5'
        * species
                                                      (species) <U2 's1' 's2' ... 's5'
          rate
                                                      (component) float64 -15.14 ... ...
          lifetime
                                                      (component) float64 -0.06605 ...
        * to_species
                                                      (to_species) <U2 's1' ... 's5'
        * from_species
                                                      (from_species) <U2 's1' ... 's5'
      Dimensions without coordinates: component, left_singular_value_index,
      right_singular_value_index, singular_value_index
      Data variables: (12/24)
                                                      (time, spectral) float64 0.0002...
          data_left_singular_vectors
                                                      (time, left_singular_value_index)
      float64 ...
                                                      (singular_value_index) float64 ...
          data_singular_values
          data_right_singular_vectors
                                                      (right_singular_value_index,
```

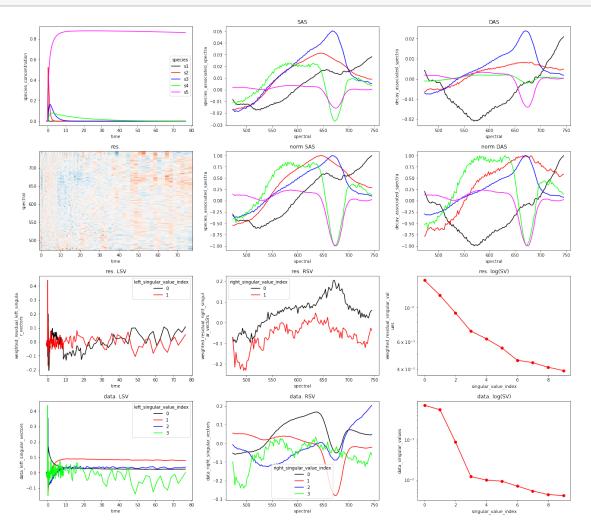
(time, spectral) float64 0.0002...
(time, left_singular_value_index)

data

data_left_singular_vectors

```
spectral) float64 ...
    matrix
                                                (time, clp_label) float64 1.259...
                                                (spectral, clp_label) float64 -...
    clp
                                                (component, species) float64 1...
    a_matrix
                                                (to_species, from_species) float64
    k_matrix
    k_matrix_reduced
                                                (to_species, from_species) float64
    irf_center
                                                float64 0.009177
                                                float64 0.06631
    irf_width
    irf
                                                (time) float64 4.309e-35 \dots 0.0
Attributes:
                                       0.0002075526312040566
    root_mean_square_error:
    weighted_root_mean_square_error:
                                       0.0002075526312040566
```

[15]: fig = plot_overview(PCP_result.data["dataset1"], linlog=False)



As can be seen in the above plot (compared to the original one), cleaning the dataset only influenced the residual and SVD's of the residual and data, but not the SAS and DAS.

[16]: print_md(PCP_result.optimized_parameters)

• input:

\overline{Label}	Value	StdErr	Min	Max	Vary	Non-Negative	Expr
1	1	0	-inf	inf	False	False	None
0	0	0	-inf	\inf	False	False	None

• irf:

Label	Value	StdErr	Min	Max	Vary	Non-Negative	Expr
center	0.00917684	1.31584	-inf	\inf	True	False	None
width	0.0663091	0.94223	-inf	\inf	True	False	None

• kinetic:

Label	Value	StdErr	Min	Max	Vary	Non-Negative	Expr
1	11	0	-inf	inf	False	False	None
2	4.1	0	-inf	\inf	False	False	None
3	0.6	0	-inf	\inf	False	False	None
4	0.2	0	-inf	\inf	False	False	None
5	0.4	0	-inf	\inf	False	False	None
6	0.02	0	-inf	\inf	False	False	None
7	0.0005	0	-inf	\inf	False	False	None
8	0.8	0	-inf	\inf	False	False	None
9	0.04	0	-inf	\inf	False	False	None

2.6 chl prime

2.6.1 Load model and parameters

Compared to the full data with the erroneous values for time==78.7 the scaling of the flow to chl prime needed to be changed from

scaling:

- [0.75, {vary: false}] - [0.25, {vary: false}]

to

scaling:

- [0.80, {vary: false}]
- [0.20, {vary: false}]

in order to counter the bleaching.

Your model is valid.

```
[18]: print_md(PCP_chl_prime_model)
```

3 Model

Type: kinetic-spectrum

3.1 Initial Concentration

- input1:
 - Label: input1
 - Compartments: ['s1', 's2', 's3', 's4', 's5', 's6']
 - Parameters: [input.1, input.0, input.0, input.0, input.0, input.0]
 - Exclude From Normalize: []

3.2 K Matrix

- km1:
 - Label: km1
 - Matrix:
 - * ('s1', 's1'): kinetic.9
 - * ('s2', 's1'): kinetic.1
 - * ('s5', 's1'): kinetic.11
 - * ('s6', 's1'): kinetic.15
 - * ('s2', 's2'): kinetic.9
 - * ('s3', 's2'): kinetic.3
 - * ('s4', 's2'): kinetic.4
 - * ('s5', 's2'): kinetic.12
 - * ('s6', 's2'): kinetic.16
 - * ('s3', 's3'): kinetic.9
 - * ('s5', 's3'): kinetic.13
 - * ('s6', 's3'): kinetic.17
 - * ('s4', 's4'): kinetic.9
 - * (34, 34). KIIIEUC.3
 - * ('s5', 's4'): kinetic.14
 - * ('s6', 's4'): kinetic.18
 - * ('s5', 's5'): kinetic.7
 - * ('s6', 's6'): kinetic.10

3.3 Irf

• irf1 (gaussian):

- Label: irf1

Type: gaussian
Center: irf.center
Width: irf.width
Normalize: True
Backsweep: False

3.4 Dataset

• dataset1:

- Label: dataset1

- Megacomplex: ['mc1']

- Initial Concentration: input1

− *Irf*: irf1

3.5 Megacomplex

• mc1:

- Label: mc1

- K Matrix: ['km1']

3.6 Spectral Relations

• - Compartment: s5

- Target: s6

- Parameter: rel.r1- Interval: [[0, 1000]]

3.6.1 Create sceme and optimize it

```
[19]: PCP_chl_prime_scheme = Scheme(
          PCP_chl_prime_model, PCP_chl_prime_parameters, {"dataset1": dataset_cleaned}
)
PCP_chl_prime_result = optimize(PCP_chl_prime_scheme)
```

Iteration	Total nfev	Cost	Cost reduction	Step norm
Optimality O	1	9.3012e-04		
3.56e-02	1	9.3012e-04		
1	2	5.7945e-04	3.51e-04	1.51e-02
3.84e-03				
2	3	5.6709e-04	1.24e-05	5.71e-03
9.06e-04				
3	4	5.6583e-04	1.26e-06	1.96e-03
2.96e-04				
4	5	5.6571e-04	1.19e-07	6.01e-04

	0 05 05						
	9.05e-05	2	5 0570 04	4 44 00	1 01 01		
	5	6	5.6570e-04	1.11e-08	1.84e-04		
	2.77e-05	_					
	6	7	5.6570e-04	1.04e-09	5.61e-05		
	8.43e-06						
	7	8	5.6570e-04	9.63e-11	1.71e-05		
	2.57e-06						
	8	9	5.6570e-04	8.94e-12	5.21e-06		
	7.83e-07						
	9	10	5.6570e-04	8.30e-13	1.59e-06		
	2.38e-07						
	`ftol` terminat						
	Function evalua	tions 10, init:	ial cost 9.3012e	e-04, final cost	t 5.6570e-04, first-		
	order optimality	y 2.38e-07.					
[00].	DCD abl maxima a		±===±1 II T				
[20]:	PCP_chl_prime_n	result.data["da	itaseti"]				
[20] •	<pre><xarray.dataset< pre=""></xarray.dataset<></pre>	->					
[20].	Dimensions:			(cln labol: 6	5, component: 6,		
		S loft gingula	er value index.	-	gular_value_index:		
	-	_	27, species: 6,				
	to_species: 6)	/alue_liidex. 12	ir, species. 0,	spectial. 127,	cime. 197,		
	Coordinates:						
	* time			(+ima) floa+6	S/I _0 80E 76 7		
				(time) float64 -0.825 76.7 (spectral) float64 473.2 745.3			
	* spectral			(clp_label) <u2 '45.5<="" 's1'="" 's2'="" td=""></u2>			
	* clp_label						
	* species			(species) <u2 's1'="" 's2'="" 's6'<="" td=""></u2>			
	rate			(component) float64 -15.14			
	lifetime			(component) float64 -0.06605			
	* to_species	_		(to_species) <u2 's1'="" 's6'<br="">(from_species) <u2 's1'="" 's6'<="" td=""></u2></u2>			
	* from_specie			- -			
			es: component, l	~	ilue_index,		
	-		singular_value_i	naex			
	Data variables:	(12/24)		() .	1) (1 + (4 + 0 + 000)		
	data			_	ral) float64 0.0002		
		singular_vector	`S	(time, left_s	singular_value_index)		
	float64						
	data_singul			· -	ue_index) float64		
	~	_singular_vecto	ors	(right_singul	.ar_value_index,		
	spectral) float	564 		,			
	matrix			(spectral, ti	me, clp_label)		
	float64			,	>		
	clp			(spectral, cl	.p_label) float64		
	•••			•••			
	${ t a_matrix}$			-	species) float64 1		
	${ t k_matrix}$			· ·	<pre>from_species) float64</pre>		

```
      k_matrix_reduced
      (to_species, from_species) float64

      ...
      irf_center
      float64 0.011

      irf_width
      float64 0.06682

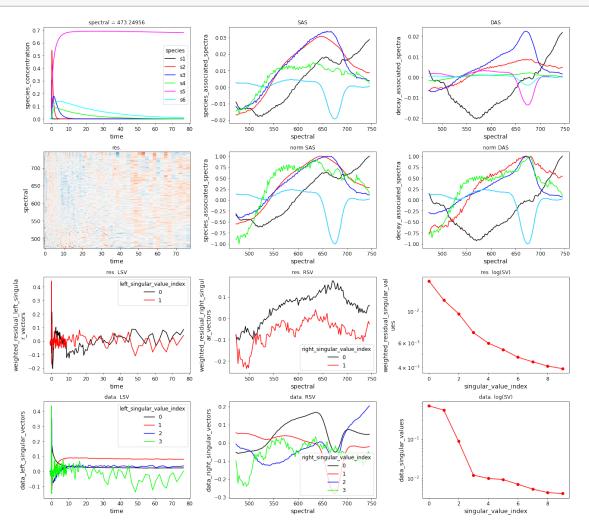
      irf
      (time) float64 1.017e-34 ... 0.0

      Attributes:
      root_mean_square_error:
      0.00021265320925715141

      weighted_root_mean_square_error:
      0.00021265320925715141
```

3.6.2 Result plots

[21]: fig = plot_overview(PCP_chl_prime_result.data["dataset1"], linlog=False)



[22]: print_md(PCP_chl_prime_result.optimized_parameters)

• input:

\overline{Label}	Value	StdErr	Min	Max	Vary	Non-Negative	Expr
1	1	0	-inf	inf	False	False	None
0	0	0	$-\inf$	\inf	False	False	None

• irf:

\overline{Label}	Value	StdErr	Min	Max	Vary	$Non ext{-}Negative$	Expr
center	0.0109996	1.26728	-inf	\inf	True	False	None
width	0.0668175	0.932177	-inf	\inf	True	False	None

• kinetic:

Label	Value	StdErr	Min	Max	Vary	Non-Negative	Expr
1	11	0	-inf	inf	False	False	None
2	4.1	0	-inf	\inf	False	False	None
3	0.6	0	-inf	\inf	False	False	None
4	0.2	0	-inf	\inf	False	False	None
5	0.4	0	-inf	\inf	False	False	None
6	0.02	0	-inf	\inf	False	False	None
7	0.0005	0	-inf	\inf	False	False	None
8	0.6	0	-inf	\inf	False	False	None
9	0.04	0	-inf	\inf	False	False	None
10	0.04	0	-inf	\inf	False	False	None
11	3.28	0	-inf	\inf	False	False	\$kinetic.2 * \$scaling.1
12	0.48	0	-inf	\inf	False	False	\$kinetic.8 * \$scaling.1
13	0.32	0	-inf	\inf	False	False	\$kinetic.5 * \$scaling.1
14	0.016	0	-inf	\inf	False	False	\$kinetic.6 * \$scaling.1
15	0.82	0	-inf	\inf	False	False	\$kinetic.2 * \$scaling.2
16	0.12	0	-inf	\inf	False	False	\$kinetic.8 * \$scaling.2
17	0.08	0	-inf	\inf	False	False	\$kinetic.5 * \$scaling.2
18	0.004	0	-inf	inf	False	False	\$kinetic.6 * \$scaling.2

• rel:

Label	Value	StdErr	Min	Max	Vary	Non-Negative	Expr
r1	1	0	-inf	\inf	False	False	None

• scaling:

Label	Value	StdErr	Min	Max	Vary	Non-Negative	Expr
1	0.8	0	-inf	inf	False	False	None
2	0.2	0	-inf	\inf	False	False	None

[]:[