

Animate

Out[18]:

CRN synthesis for generating cosine(time)+1

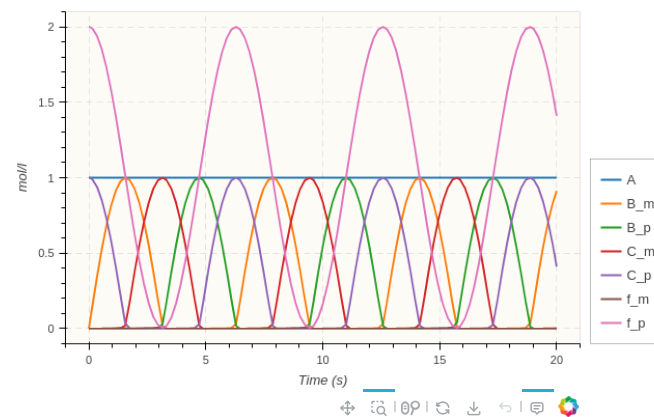
In [19]: `compile_from_expression(cos+1, f).`

Out[19]:

In [20]: `list_model.`

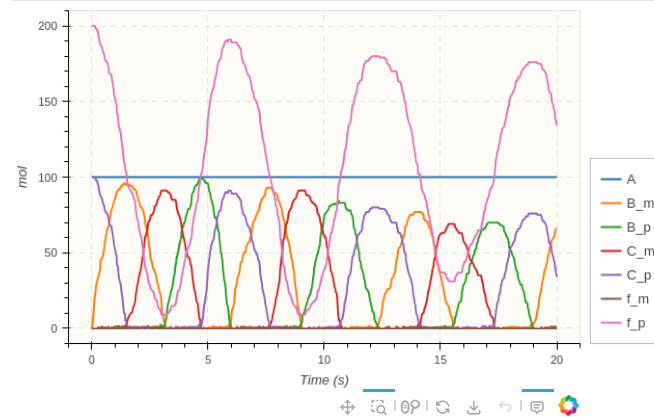
```
Out[20]: MA(fast) for f_m+f_p=>_.
MA(fast) for C_m+C_p=>_.
MA(fast) for B_m+B_p=>_.
MA(1.0) for B_p=>B_p+C_p+f_p.
MA(1.0) for B_m=>B_m+C_m+f_m.
MA(1.0) for C_m=>B_p+C_m.
MA(1.0) for C_p=>B_m+C_p.
initial_state(f_p=2).
initial_state(C_p=1).
initial_state(A=1).
parameter(
  fast = 1000
).
```

In [21]: `numerical_simulation. plot.`



Out[21]:

In [22]: `numerical_simulation(method:ssa). plot.`



Out[22]:

CRN synthesis for computing cosine(x)

In [23]: `clear_model.`

Out[23]:

In [24]: `compile_from_expression(cos, x, f).`

Out[24]:

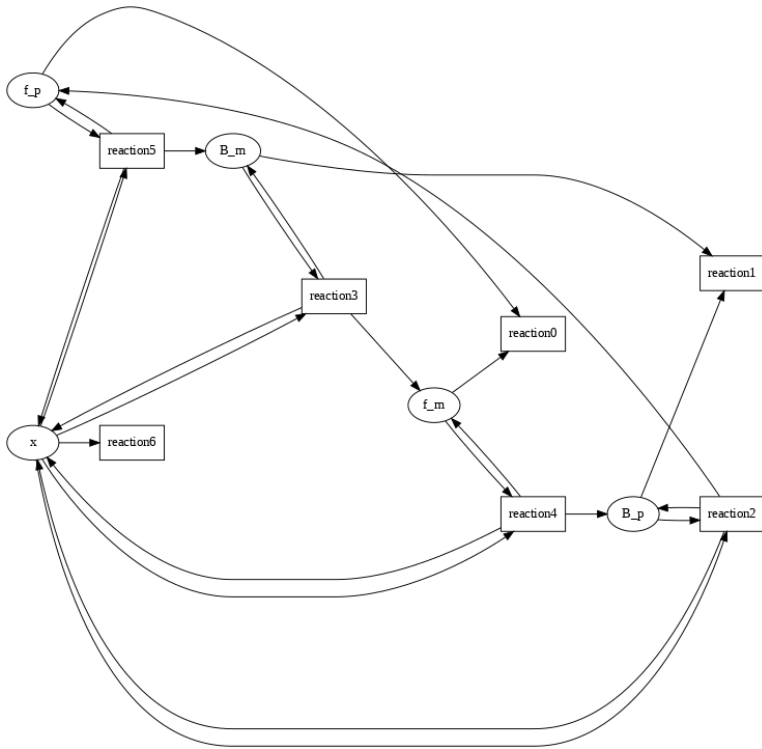
In [25]: `parameter(input=4).`

Out[25]:

```
In [26]: list_model.
```

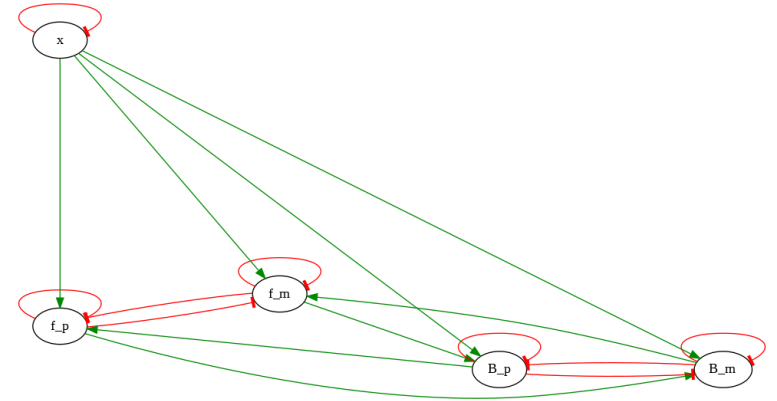
```
Out[26]: MA(fast) for f_m+f_p=>_.  
MA(fast) for B_m+B_p=>_.  
MA(1.0) for B_p+x=>B_p+f_p+x.  
MA(1.0) for B_m+x=>B_m+f_m+x.  
MA(1.0) for f_m+x=>B_p+f_m+x.  
MA(1.0) for f_p+x=>B_m+f_p+x.  
MA(1.0) for x=>_.  
initial_state(f_p=1).  
initial_state(x=input).  
parameter(  
  fast = 1000,  
  input = 4  
).
```

```
In [27]: draw_reactions.
```



Out[27]:

```
In [28]: draw_influences.
```



Out[28]:

```
In [29]: list_ode.
```

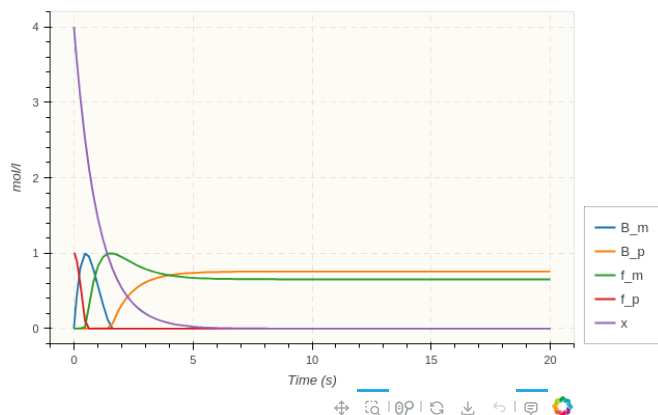
$$\begin{aligned}x_0 &= 4 \\ B_{m_0} &= 0 \\ B_{p_0} &= 0 \\ f_{m_0} &= 0 \\ f_{p_0} &= 1 \\ fast &= 1000 \\ input &= 4 \\ \frac{dx}{dt} &= -x \\ \frac{dB_m}{dt} &= f_p * x - B_m * B_p * fast \\ \frac{dB_p}{dt} &= f_m * x - B_m * B_p * fast \\ \frac{df_m}{dt} &= B_m * x - f_m * f_p * fast \\ \frac{df_p}{dt} &= B_p * x - f_m * f_p * fast\end{aligned}$$

Out[29]:

```
In [30]: numerical_simulation.
```

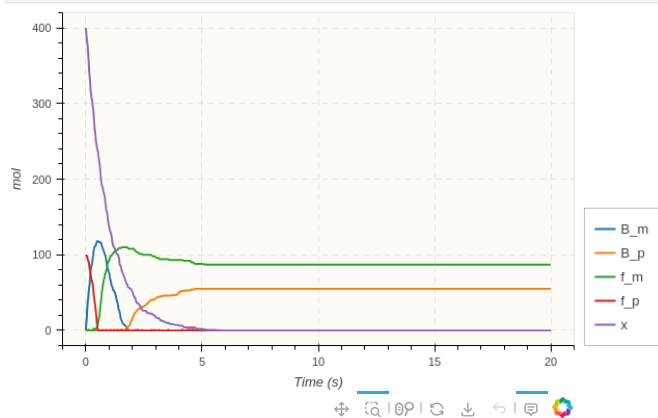
Out[30]:

```
In [31]: plot.
```



Out[31]:

```
In [32]: numerical_simulation(method:ssa).plot.
```



Out[32]:

General CRN Compilation Pipeline for Elementary Mathematical Functions

More generally, Biocham can compile any elementary mathematical function into a finite CRN using the following compilation pipeline:

1. symbolic differentiation of the function as a function of time
2. initial ODE that has the function as solution
3. polynomialization of the ODE

- by introduction of new variables for non monomial terms

- guaranteed to terminate on elementary functions

4. quadratization of the ODE

- by introduction of new variables for non quadratic monomials
- minimizing the number of introduced species is NP-hard
- SAT solver used

5. CRN synthesis from quadratic ODE with dual-rail encoding of negative values

```
In [33]: option(quadratic_reduction:sat_species).
```

Out[33]:

```
In [34]: clear_model.
compile_function(F = cos(X), X).
list_model.
```

Out[34]:

```
A = sin(t)
F = cos(t)

MA(fast) for A_m+A_p=>_.
MA(fast) for F_m+F_p=>_.
MA(1.0) for F_p+X=>A_p+F_p+X.
MA(1.0) for F_m+X=>A_m+F_m+X.
MA(1.0) for X=>t.
MA(1.0) for A_m+X=>A_m+F_p+X.
MA(1.0) for A_p+X=>A_p+F_m+X.
initial_state(A_p=0.0).
initial_state(F_p=1.0).
initial_state(X=input).
parameter(
  input = 1.0,
  fast = 1000
).
```

```
In [35]: clear_model.
compile_function(H1 = X/(1+X), X).
list_model.
```

Out[35]:

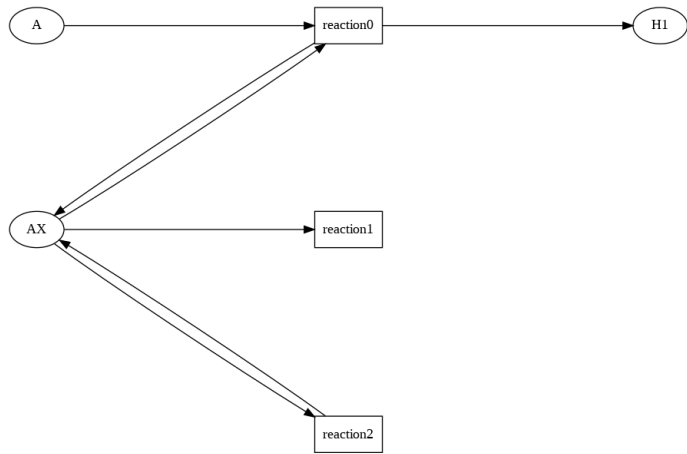
```
A = 1/(1+t)
H1 = t/(1+t)

MA(1.0) for A+AX=>AX+H1.
MA(1.0) for AX=>_.
MA(1.0) for 2*AX=>AX.
initial_state(A=1).
initial_state(AX=input).
parameter(
  fast = 1000,
  input = 1.0
).
```

```
In [36]: search_conservations.
```

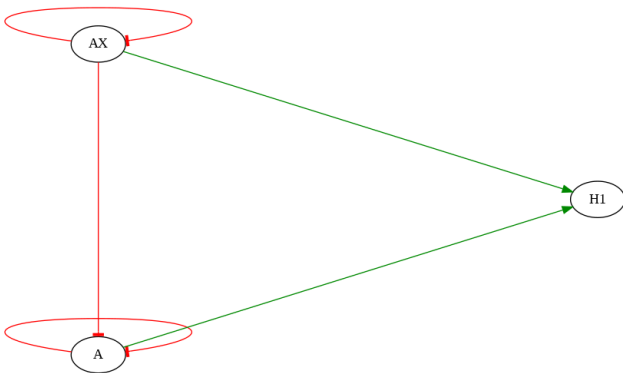
Out[36]: A+H1
1 complex invariant(s)

```
In [37]: draw_reactions.
```



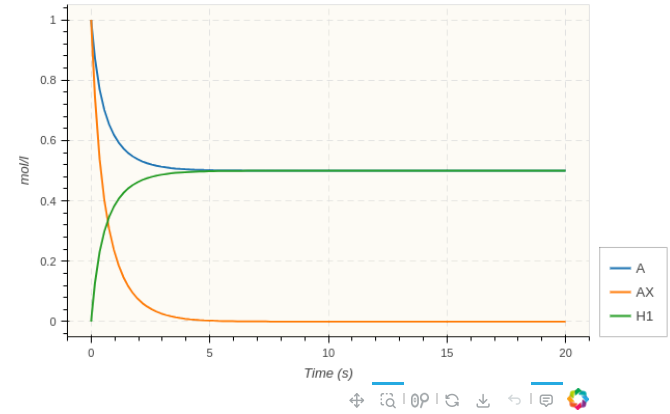
Out[37]:

In [38]: `draw_influences.`



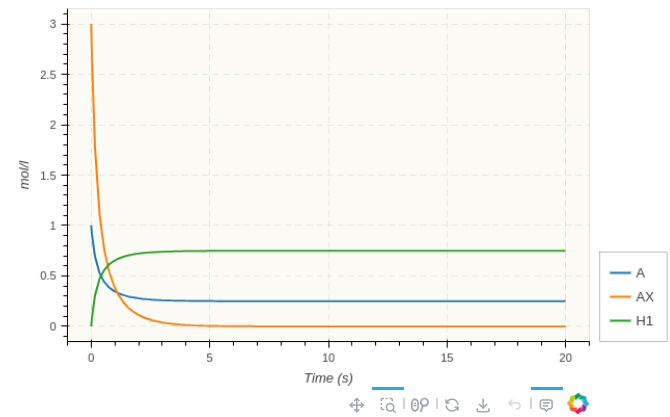
Out[38]:

In [39]: `numerical_simulation. plot.`



Out[39]:

In [40]: `parameter(input=3).`
`numerical_simulation. plot.`



Out[40]:

Hill 5: synthetic CRN analog of MAPK signaling input/output function

In [41]: `clear_model.`
`compile_function(H5 = X^5/(1+X^5), X).`
`list_model.`

```

Out[41]:
A = 1/(1+t^5)
H5 = t^5/(1+t^5)

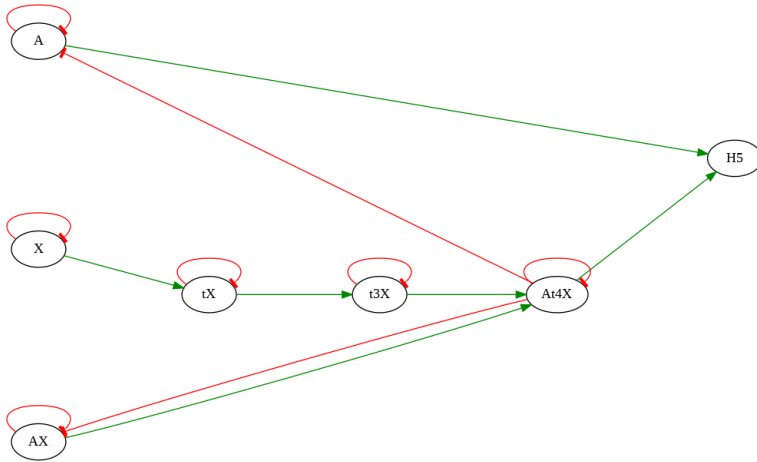
MA(1.0) for X=>_.
MA(5.0) for A+At4X=>At4X+H5.
MA(1.0) for 2*X=>tX+2*X.
MA(1.0) for tX=>_.
MA(3.0) for 2*tX=>t3X+2*tX.
MA(1.0) for t3X=>_.
MA(1.0) for AX=>_.
MA(5.0) for AX+At4X=>At4X.
MA(4.0) for AX+t3X=>AX+At4X+t3X.
MA(1.0) for At4X=>_.
MA(5.0) for 2*At4X=>At4X.
initial_state(X=input).
initial_state(A=1).
initial_state(AX=input).
parameter(
  fast = 1000,
  input = 1.0
).

```

```
In [42]: search_conservations.
```

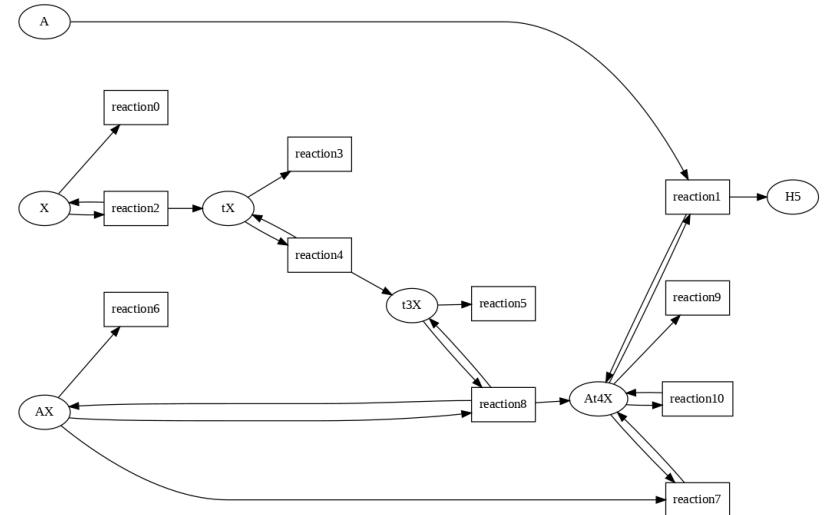
```
Out[42]: A+H5
1 complex invariant(s)
```

```
In [43]: draw_influences.
```



```
Out[43]:
```

```
In [44]: draw_reactions.
```

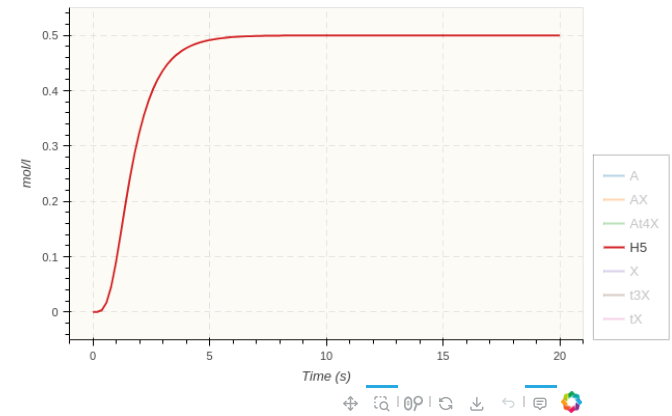


```
Out[44]:
```

```
In [45]: search_conservations.
```

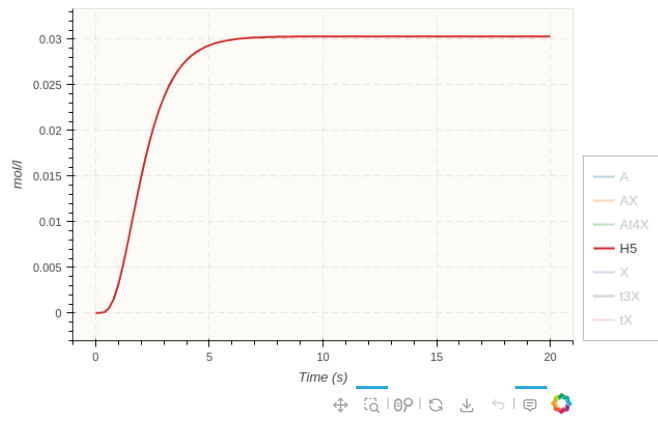
```
Out[45]: A+H5
1 complex invariant(s)
```

```
In [46]: numerical_simulation. plot(show:{H5}).
```



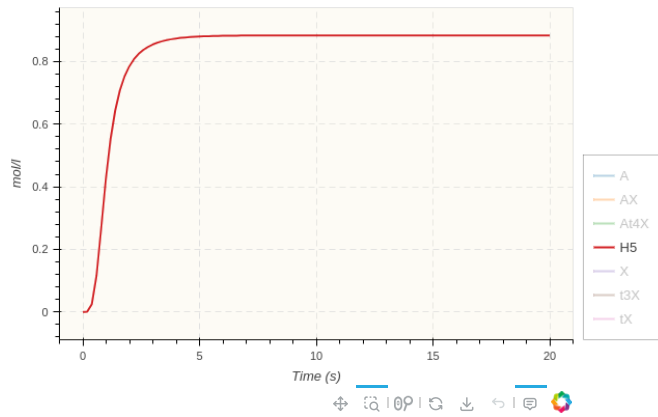
```
Out[46]:
```

```
In [47]: parameter(input=0.5).
numerical_simulation. plot(show:{H5}).
```

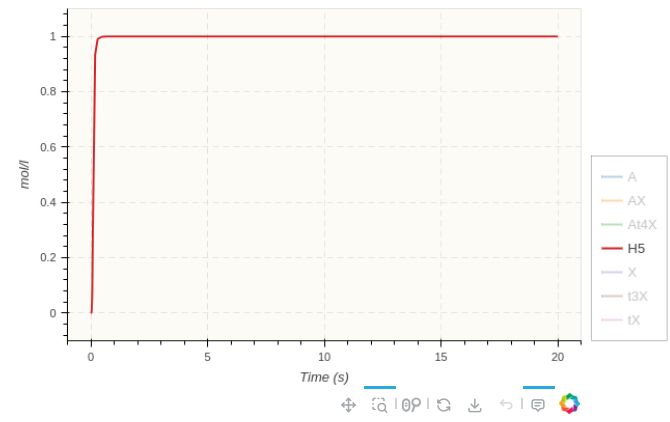
Out[47]:

```
In [48]: parameter(input=1.5).
numerical_simulation.plot(show={H5}).
```



Out[48]:

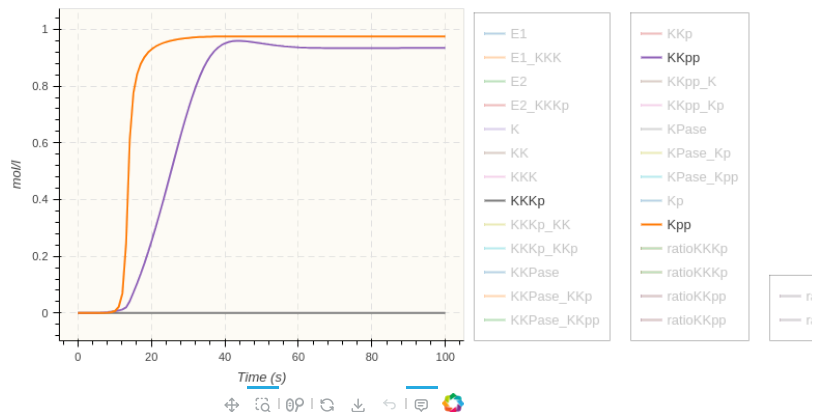
```
In [49]: parameter(input=10).
numerical_simulation.plot(show={H5}).
```



Out[49]:

Trajectories toward output stabilization

In [5]: `numerical_simulation.
plot.`



Out [5]:

Behavioural Specifications in Quantitative Temporal Logic FO-LTL(Rlin)

- First-Order Linear Time Logic with free variables and linear constraints over the reals
- Real-valued states (concentrations of molecular species)
- Bounded model-checking: validity of LTL formulae on a finite trace completed with a loop on the last state

Validity domains of FOLTL(Rlin) constraint variables

- FO-LTL(Rlin) constraint solving: validity domain for variables

In [6]: `validity_domain(F(Kpp = v)). % all values in the trace`

Out [6]: `v=0\|v=3.68e-10\|v=4.9367e-8\|v=8.82573e-7\|v=6.78262e-6\|v=3.31004e-5\|v=0.000122963\|v=0.000385086\|v=0.00108711\|v=0.0029129\|v=0.00777349\|v=0.0218366\|v=0.0690836\|v=0.245708\|v=0.613048\|v=0.7764\|v=0.842407\|v=0.879194\|v=0.902637\|v=0.918798\|v=0.930532\|v=0.939371\|v=0.946214\|v=0.951623\|v=0.95597\|v=0.959507\|v=0.962414\|v=0.964821\|v=0.966823\|v=0.968491\|v=0.969882\|v=0.971038\|v=0.971992\|v=0.972774\|v=0.973407\|v=0.973911\|v=0.974306\|v=0.974608\|v=0.974834\|v=0.974997\|v=0.97511\|v=0.975183\|v=0.975226\|v=0.975245\|v=0.975246\|v=0.975234\|v=0.975213\|v=0.975186\|v=0.975155\|v=0.975123\|v=0.975089\|v=0.975056\|v=0.975025\|v=0.974995\|v=0.974967\|v=0.974942\|v=0.97492\|v=0.9749\|v=0.974882\|v=0.974866\|v=0.974853\|v=0.974842\|v=0.974833\|v=0.974825\|v=0.974819\|v=0.974814\|v=0.974802\|v=0.974803\|v=0.974804\|v=0.974805\|v=0.974806\|v=0.974807\|v=0.974808\|v=0.974809\|v=0.97481\|v=0.974811`

In [7]: `validity_domain(F(G(Kpp = v))). % last value of Kpp on the trace (stable value)`

Out [7]: `v=0.974811`

In [8]: `% times of last value
validity_domain(F(Time = t /\ G(Kpp = v))).`

Out [8]: `t=93.1372\|v=0.974811\|t=94.1372\|v=0.974811\|t=95.1372\|v=0.974811\|t=96.1372\|v=0.974811\|t=97.1372\|v=0.974811\|t=98.1372\|v=0.974811\|t=99.1372\|v=0.974811\|t=100\|v=0.974811`

In [9]: `% time bound for last value
validity_domain(F(Time <= t /\ G(Kpp = v))).`

Out [9]: `t>=93.1372\|v=0.974811`

In [10]: `% switching time
validity_domain(F(Time <= t /\ G(Kpp > 0.5))).`

Out [10]: `t>=14.1372`

Satisfaction degree of FOLTL(Rlin) formulae

- FOLTL(Rlin) constraint given objective values for the free variables
- satisfaction degree in [0,1] as the inverse of the distance between the objective point and the validity domain
- satisfaction degree in $[1, +\infty]$ as the penetration depth of the objective point in the validity domain (i.e. formula robustness)

In [11]: `satisfaction_degree(F(Time < t /\ G(Kpp > 0.5)), [t->14.1372]).`

Out [11]: `1.000000`

In [12]: `satisfaction_degree(F(Time < t /\ G(Kpp > 0.5)), [t->10]).`

Out [12]: `0.194659`

In [13]: `satisfaction_degree(F(Time < t /\ G(Kpp > 0.5)), [t->20]).`

Out [13]: `6.862400`

Robustness of FOLTL(Rlin) formulae with respect to parameter variations (i.e. extrinsic variability)

- Here robustness of the switching time property with respect to variation of the input concentration
- Default coefficient of variation is 0.1 (i.e. variation of parameter values by 10%)

In [14]: `present(E1, e1).
parameter(e1=3e-5).`

Out [14]:

In [15]: `seed(0).
robustness(F(Time < t /\ G(Kpp > 0.5)), [e1], [t->14.2459]).`

Out [15]: `On [e1] robustness degree: 0.812053 sensitivity: 0.187947 (computation time 9.284000 s)`

In [16]: `seed(0).
robustness(F(Time < t /\ G(Kpp > 0.5)), [e1], [t->14.2459], robustness_coeff_var: 0.2).`

Out [16]: `On [e1] robustness degree: 0.755177 sensitivity: 0.244823 (computation time 5.057000 s)`

In [17]: `seed(0).
robustness(F(Time < t /\ G(Kpp > 0.5)), [e1], [t->14.2459], robustness_coeff_var: 0.3).`

Out [17]: `On [e1] robustness degree: 0.694281 sensitivity: 0.305719 (computation time 4.906000 s)`

Robustness w.r.t. variation of kinetic parameters by 10%

```
In [18]: seed(0).
robustness(F(Time < t /\ G(Kpp > 0.5)), [a1, c1, a2, c2], [t-> 14.2459]).
```

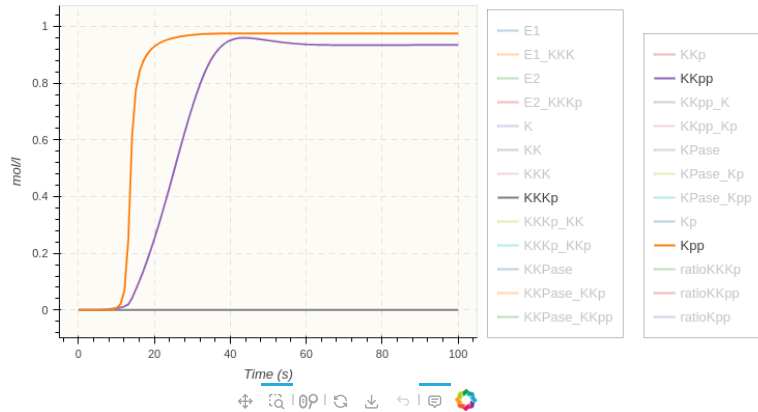
```
Out[18]: On [a1,c1,a2,c2] robustness degree: 0.825163 sensitivity: 0.174837 (computation time 7.913000 s)
```

Parameter search for satisfying an FOLTL(Rlin) constraint with objective values

- Explores the search space of parameters in order to satisfy a FOLTL(Rlin) formula
- Uses a black-box continuous optimization algorithm to maximize the satisfaction degree
- BIOCHAM uses CMAES (covariance matrix adaptive evolution strategy)

E.g. find kinetic parameters a1, c1, a2, c2 for having a switching time before 10

```
In [19]: load(BIOMD9renamedCTLreduced.bc).
option(method: bsimp).
numerical_simulation.plot.
```



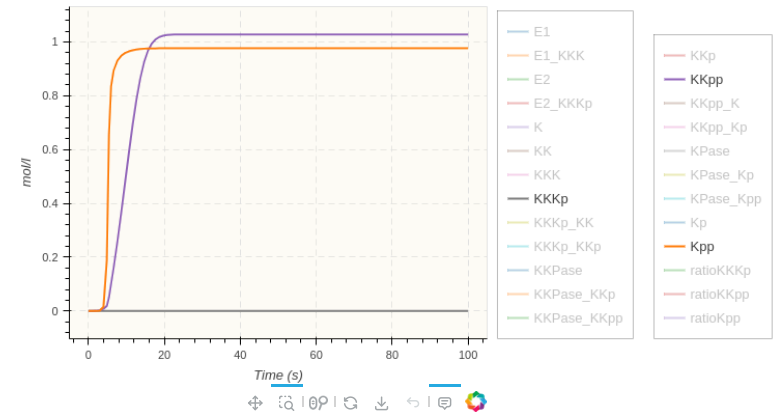
```
Out[19]:
```

```
In [20]: seed(0).
search_parameters(F(Time < t /\ G(Kpp > 0.5)),
[10<=a1<=1e4, 10<=c1<=1e4, 10<=a2<=1e4, 10<=c2<=1e4],
[t-> 10]).
```

```
Out[20]:
```

```
Time: 3.395 s
Stopping reason: Fitness: function value -8.21e-01 <= stopFitness (1.00e-04)
Best satisfaction degree: 5.584296
[0] parameter(a1=7674.210850413168)
[1] parameter(c1=5374.014748948738)
[2] parameter(a2=2795.4498499859073)
[3] parameter(c2=667.86849333378)
```

```
In [21]: numerical_simulation.plot.
```



```
Out[21]:
```

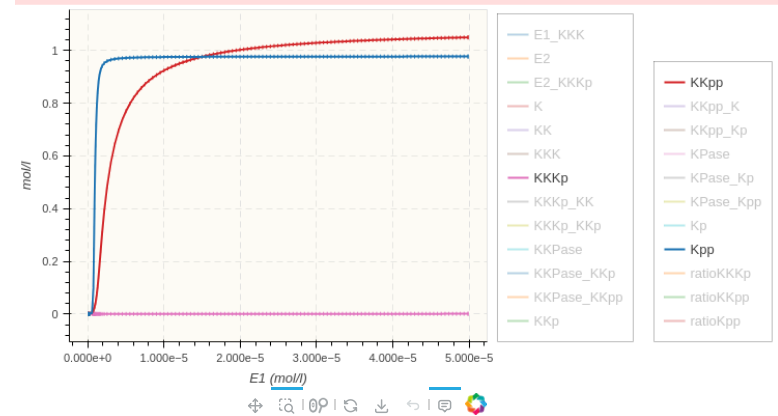
```
In [22]: % switching time
validity_domain(F(Time <= t /\ G(Kpp > 0.5))).
```

```
Out[22]: t>=5.4157
```

Dose-response diagram

- with a long time horizon for reaching the stable state with low values for E1

```
In [23]: option(time:1000).
dose_response(E1, 1e-7, 5e-5).
```



Animate

```
Out[23]:
```