

# Notes: application CHO Perfusion cspr openloop - FMPy

Here we run CHO Perfusion with cspr openloop for change of perfusion rate.

```
In [1]: run -i BPL_CHO_perfusion_cspr_openloop_explore_fmpy.py
```

Windows - run FMU pre-compiled JModelica 2.14

Model for bioreactor has been setup. Key commands:

- par() - change of parameters and initial values
- init() - change initial values only
- simu() - simulate and plot
- newplot() - make a new plot
- show() - show plot from previous simulation
- disp() - display parameters and initial values from the last simulation
- describe() - describe culture, broth, parameters, variables with values/units

Note that both disp() and describe() takes values from the last simulation and the command process\_diagram() brings up the main configuration

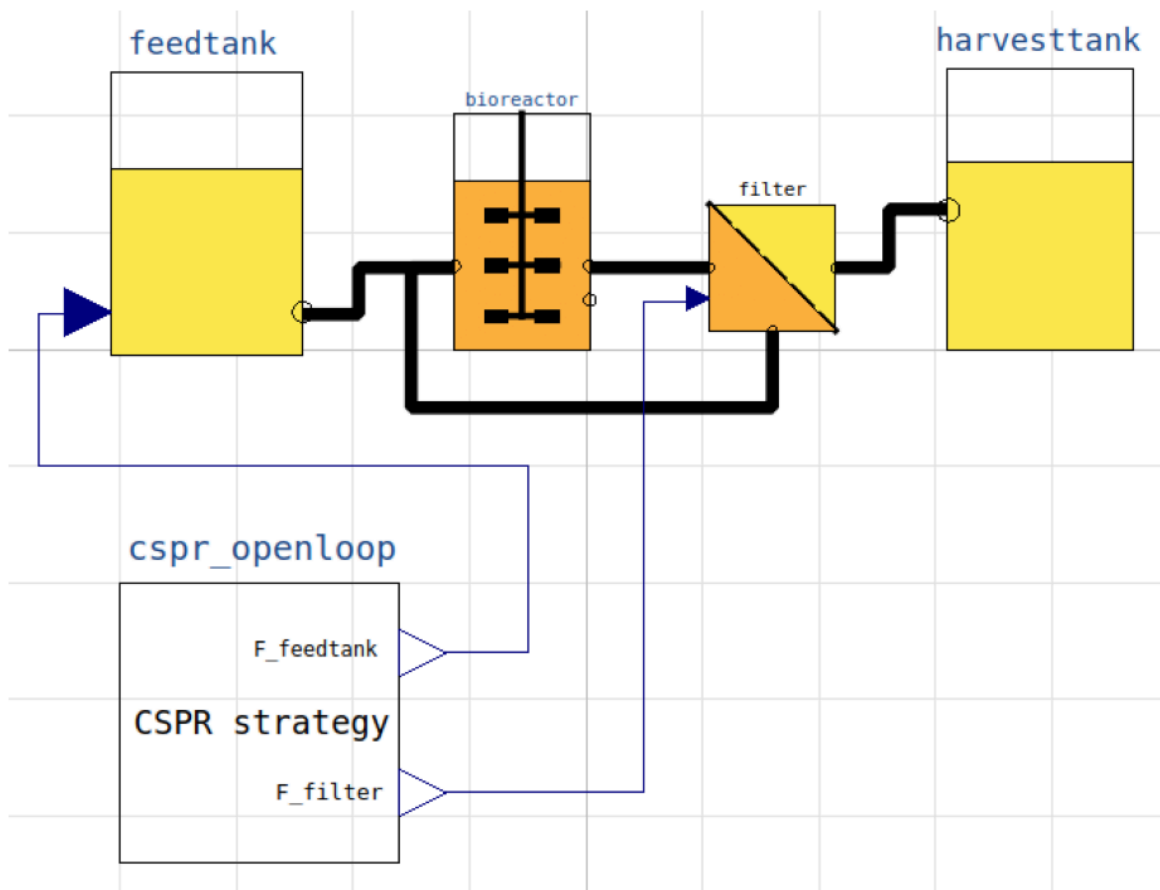
Brief information about a command by help(), eg help(simu)

Key system information is listed with the command system\_info()

```
In [2]: plt.rcParams['figure.figsize'] = [30/2.54, 24/2.54]
```

```
In [3]: process_diagram()
```

No processDiagram.png file in the FMU, but try the file on disk.

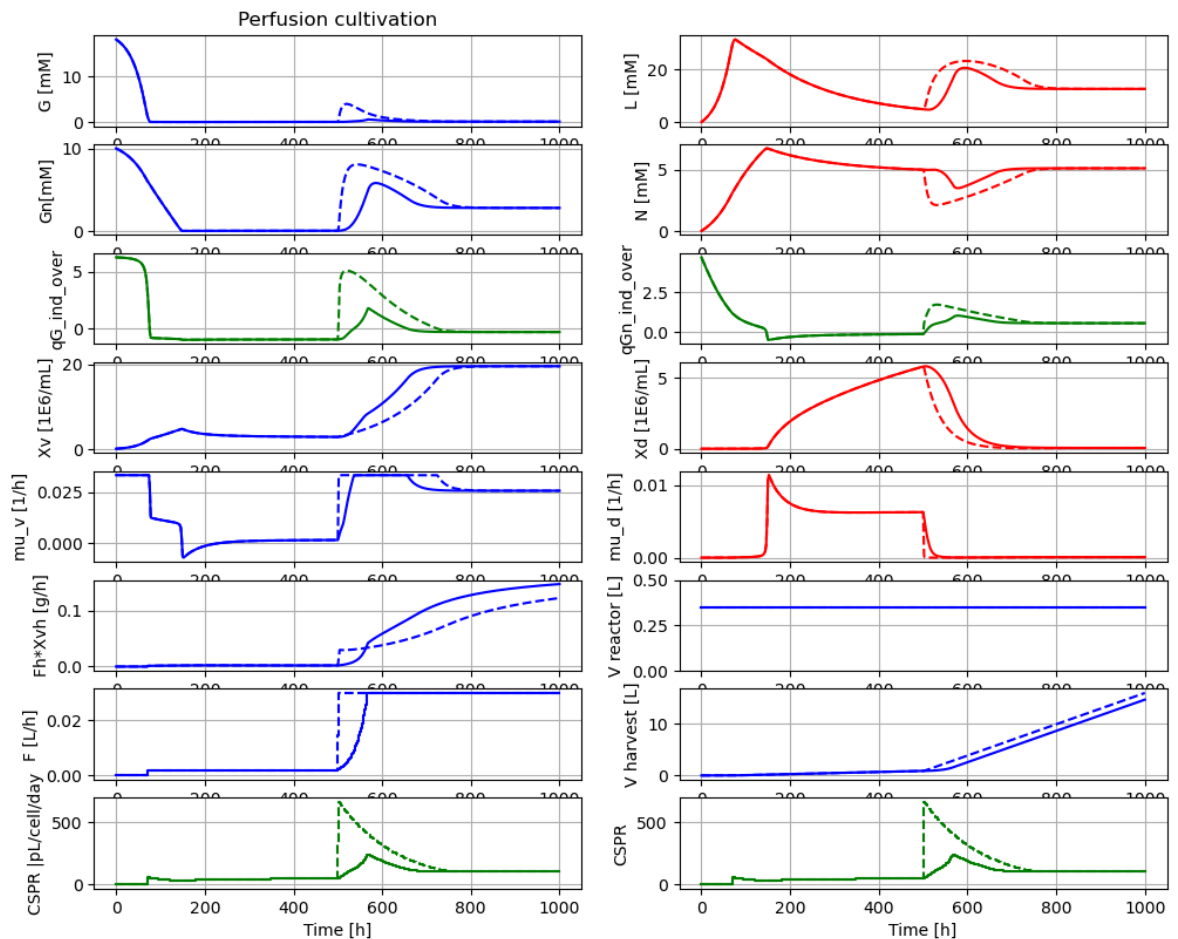


```
In [4]: describe('culture'); print(); #describe('broth')
```

Reactor culture CHO-MAb - cell line HB-58 American Culture Collection ATCC

```
In [5]: newplot('Perfusion cultivation', plotType='Extended')
```

```
par(samplePeriod=1); par(F1=0.0020)           # General parameters
par(mu_ref=0.04); simu()                       # First simulation (solid)
par(mu_ref=1); simu()                         # Second simulation (dashed)
```



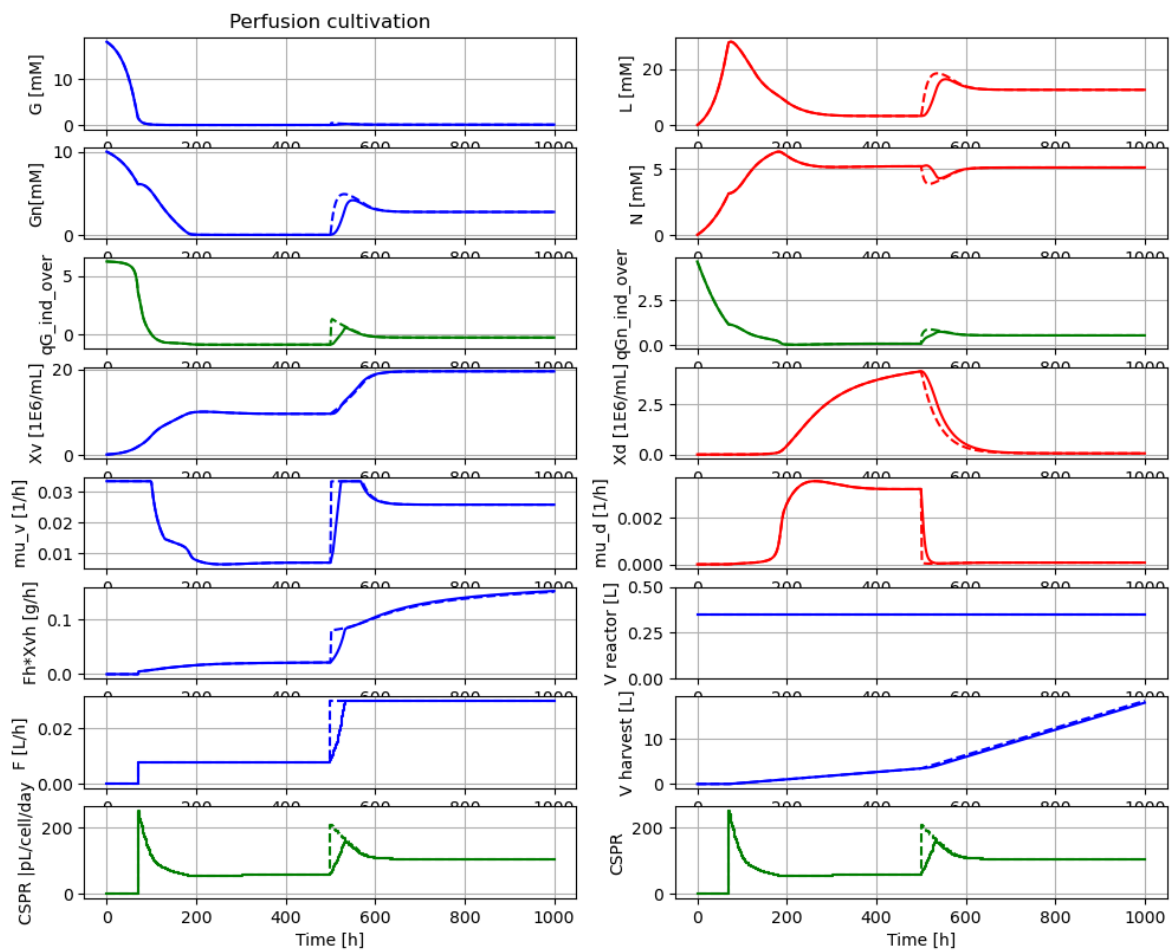
```
In [6]: model_get('CSPR')
```

```
Out[6]: 105.41560996941271
```

We see here the shorter settling time for cell conc  $X_v$  when the slower exponential increase of perfusion rate is used, compared to an abrupt change.

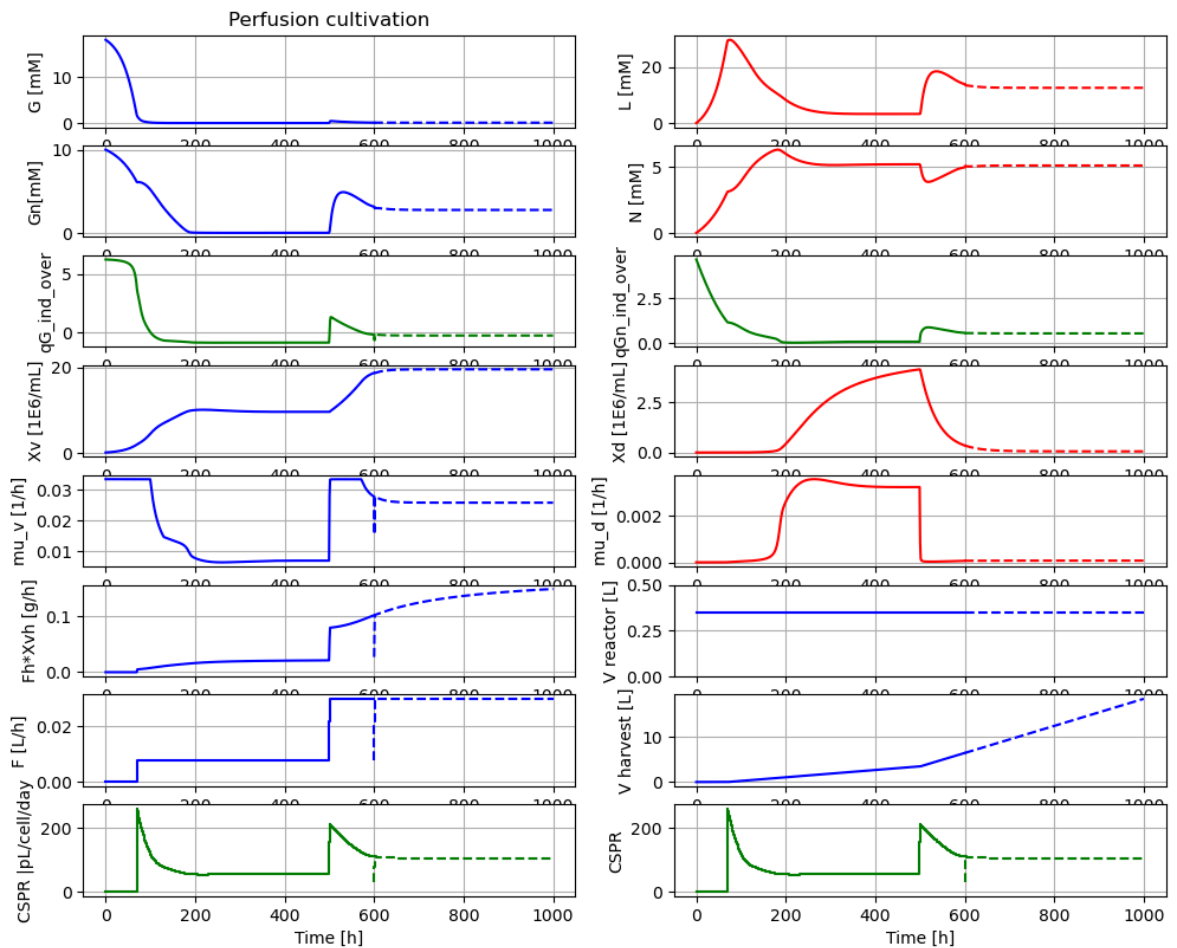
```
In [7]: newplot('Perfusion cultivation', plotType='Extended')

par(samplePeriod=1); par(F1=0.0080)           # General parameters
par(mu_ref=0.04); simu()                       # First simulation (solid)
par(mu_ref=1); simu()                         # Second simulation (dashed)
```



We see that a somewhat smaller change in perfusion rate make the difference in settling time of Xv for the two strategies to almost disappear.

```
In [8]: newplot('Perfusion cultivation', plotType='Extended')
simu(600)
simu(400, 'cont')
```



```
In [9]: describe('feedtank.W')
```

Reactor broth weight : 81.928 [ kg ]

```
In [10]: describe('feedtank.V')
```

Feed volume : 81.577 [ L ]

```
In [11]: 78.915/78.577
```

```
Out[11]: 1.0043015131654303
```

```
In [12]: describe('bioreactor.broth_decay.k_decay')
```

Rate of decay of viable cells : 0.0 [ 1E9 cells/(L\*h) ]

```
In [13]: describe('k_lysis')
```

Specific rate of lysis of dead cells : 0.0 [ 1/h ]

```
In [14]: disp('culture')
```

qG\_max1 : 0.297  
qG\_max2 : 0.038  
qGn\_max1 : 0.124  
qGn\_max2 : 0.022  
mu\_d\_max : 0.13

```
In [15]: describe('mu')
```

Specific cell growth rate variable : 0.026 [ 1/h ]

In [16]: `describe('parts')`

```
['bioreactor', 'bioreactor.broth_decay', 'bioreactor.culture', 'CSPR', 'cspr_openloop', 'D', 'feedtank', 'filter', 'harvesttank', 'liquidphase', 'MSL']
```

In [17]: `describe('MSL')`

MSL: RealInput, RealOutput

In [18]: `system_info()`

System information

- OS: Windows
- Python: 3.12.3
- Scipy: not installed in the notebook
- FMPy: 0.3.20
- FMU by: JModelica.org
- FMI: 2.0
- Type: CS
- Name: BPL\_CHO.Perfusion\_cspr\_openloop
- Generated: 2024-05-15T09:00:03
- MSL: 3.2.2 build 3
- Description: Bioprocess Library version 2.2.0
- Interaction: FMU-explore for FMPy version 1.0.0

In [ ]: