

# Notes: application CHO Perfusion cspr openloop

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

```
In [1]: run -i BPL_CHO_perfusion_cspr_openloop_explore.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

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]: describe('culture'); print(); describe('broth')
```

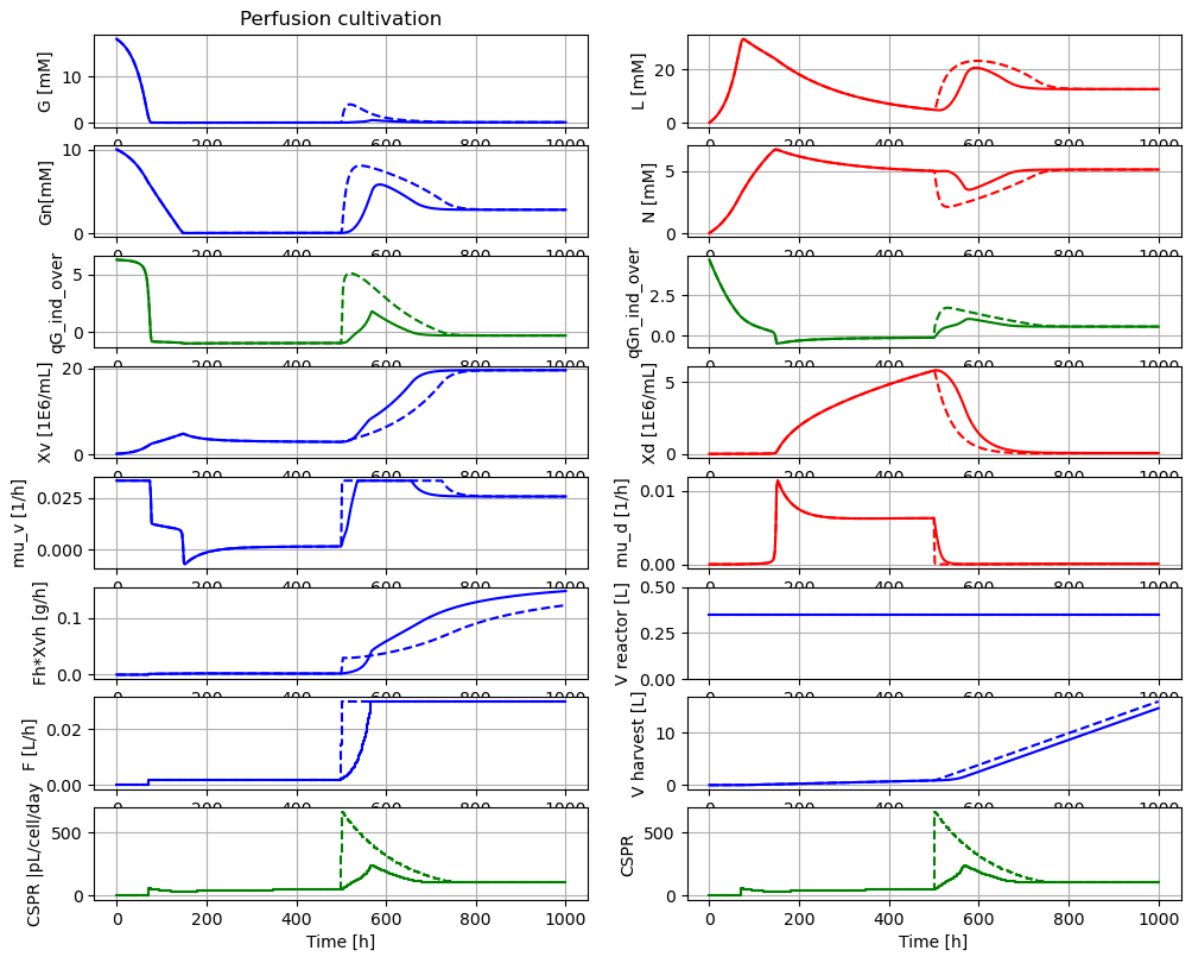
Reactor culture CHO-MAB - cell line HB-58 American Culture Collection ATCC

Reactor broth substances included in the model

Cells viable	index = 1	molecular weight = 24.6 Da
Cells dead	index = 2	molecular weight = 24.6 Da
Glucose	index = 3	molecular weight = 180.0 Da
Glutamine	index = 4	molecular weight = 146.1 Da
Lactate	index = 5	molecular weight = 90.1 Da
Ammonia	index = 6	molecular weight = 17.0 Da
Protein	index = 7	molecular weight = 150000.0 Da

```
In [4]: 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)
```



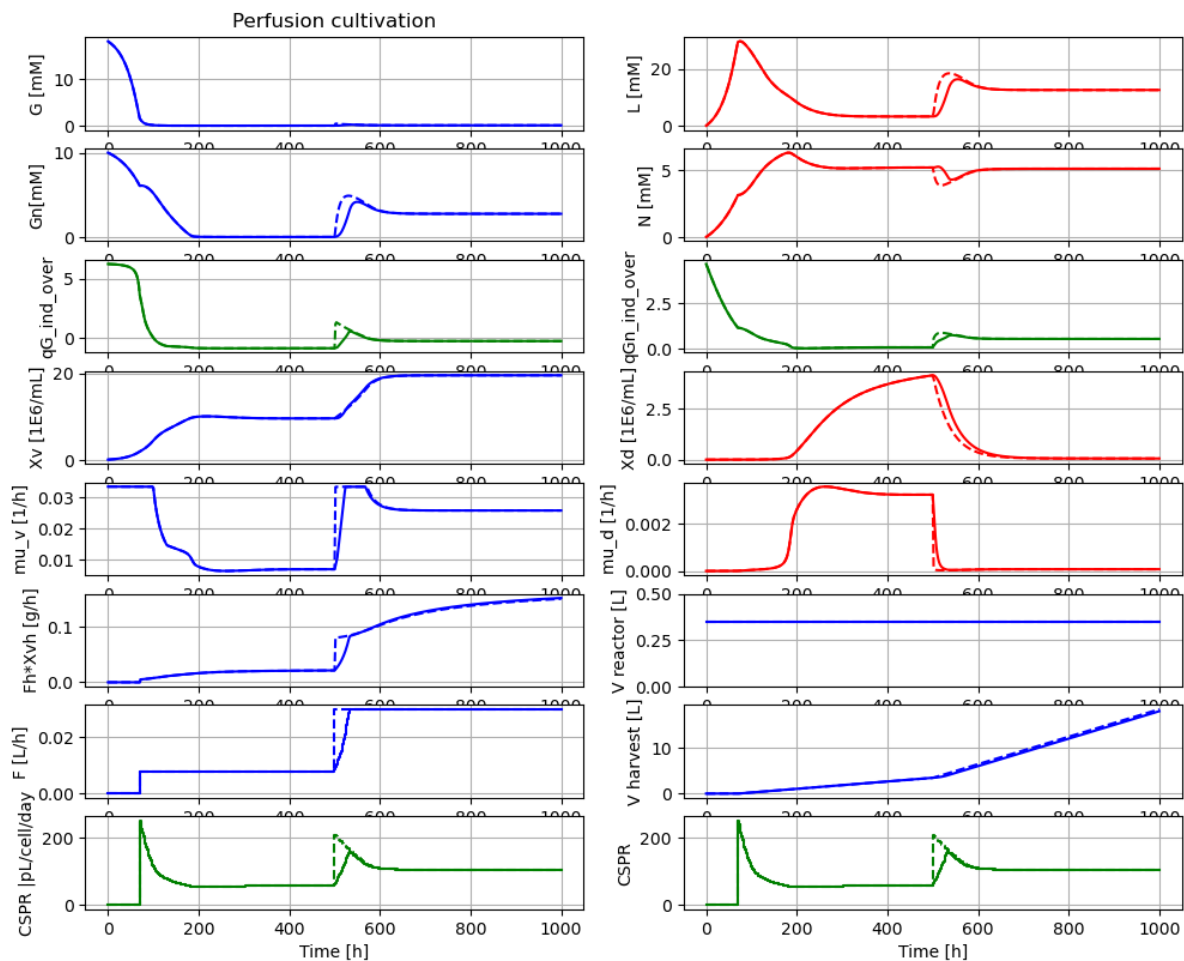
```
In [5]: model.get('CSpr')
```

```
Out[5]: array([105.41560997])
```

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.

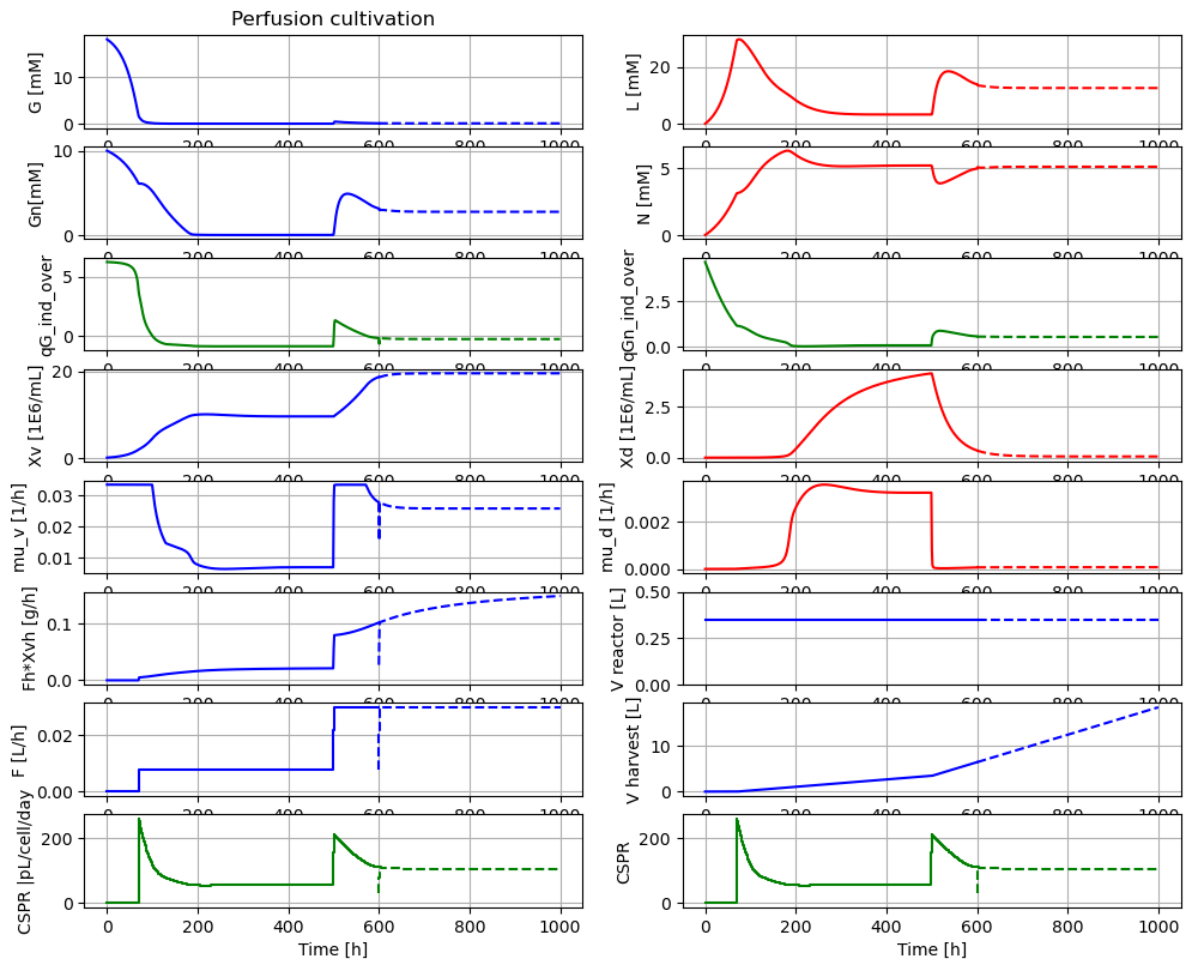
```
In [6]: newplot('Perfusion cultivation', plotType='Extended')

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  $X_v$  for the two strategies to almost disappear.

```
In [7]: newplot('Perfusion cultivation', plotType='Extended')
        simu(600)
        simu(400, 'cont')
```



In [8]: `describe('feedtank.W')`

Reactor broth weight : 81.928 [ kg ]

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

Feed volume : 81.577 [ L ]

In [10]: `81.928/81.577`

Out[10]: 1.004302683354377

In [11]: `describe('bioreactor.broth_decay.k_decay')`

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

In [12]: `describe('k_lysis')`

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

In [13]: `disp('culture')`

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

In [14]: `describe('mu')`

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

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

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

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

```
MSL: RealInput, RealOutput
```

```
In [17]: system_info()
```

```
System information
```

```
-OS: Windows  
-Python: 3.10.6  
-Scipy: not installed in the notebook  
-PyFMI: 2.9.8  
-FMU by: JModelica.org  
-FMI: 2.0  
-Type: FMUModelCS2  
-Name: BPL_CHO.Perfusion_cspr_openloop  
-Generated: 2022-10-10T10:03:56  
-MSL: 3.2.2 build 3  
-Description: Bioprocess Library version 2.1.0  
-Interaction: FMU-explore version 0.9.6
```

```
In [ ]:
```