Notes: application CHO Perfusion cspr openloop - FMPy

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

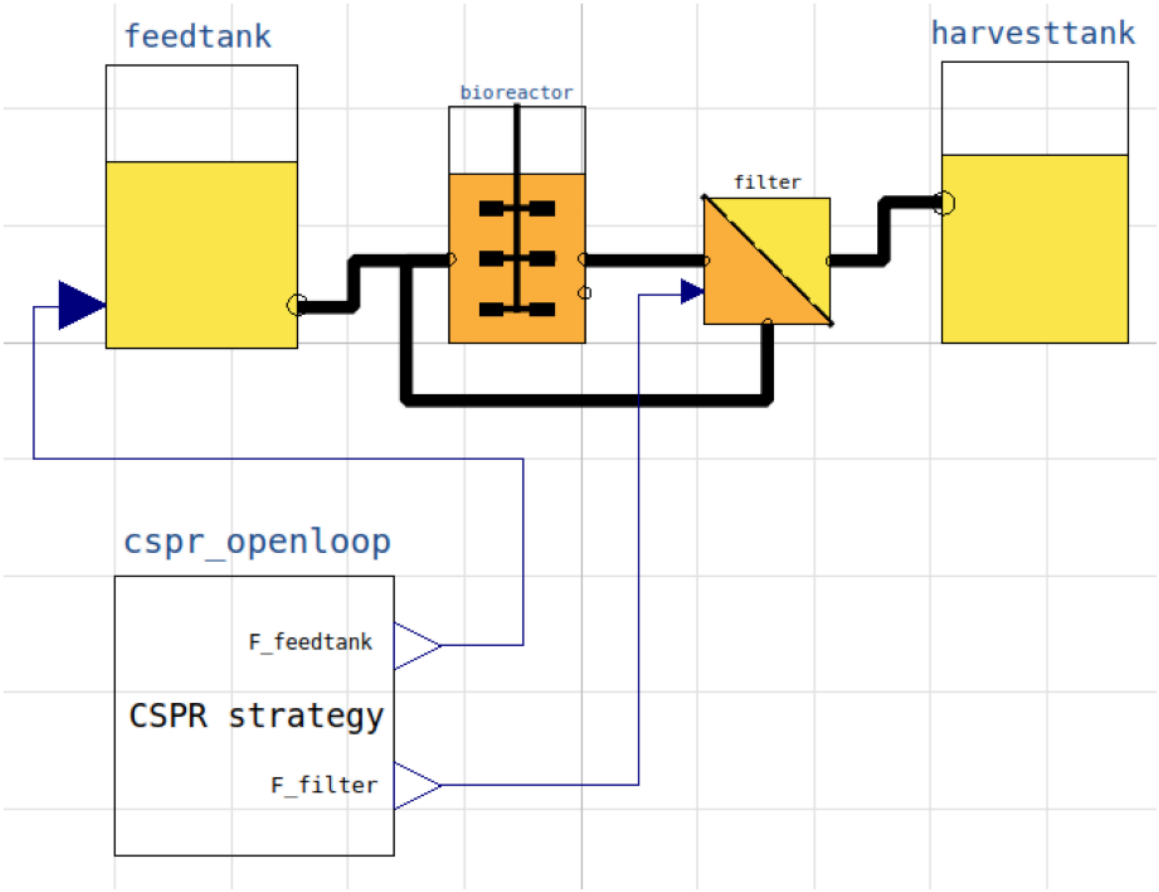
In [1]:
```
run -i BPL_CHO_perfusion_cspr_openloop_explore_fmpy.py
```

```
Linux - run FMU pre-comiled OpenModelica 1.23.0-dev

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 simul
ation
 - describe()  - describe culture, broth, parameters, variables with value
s/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()
```

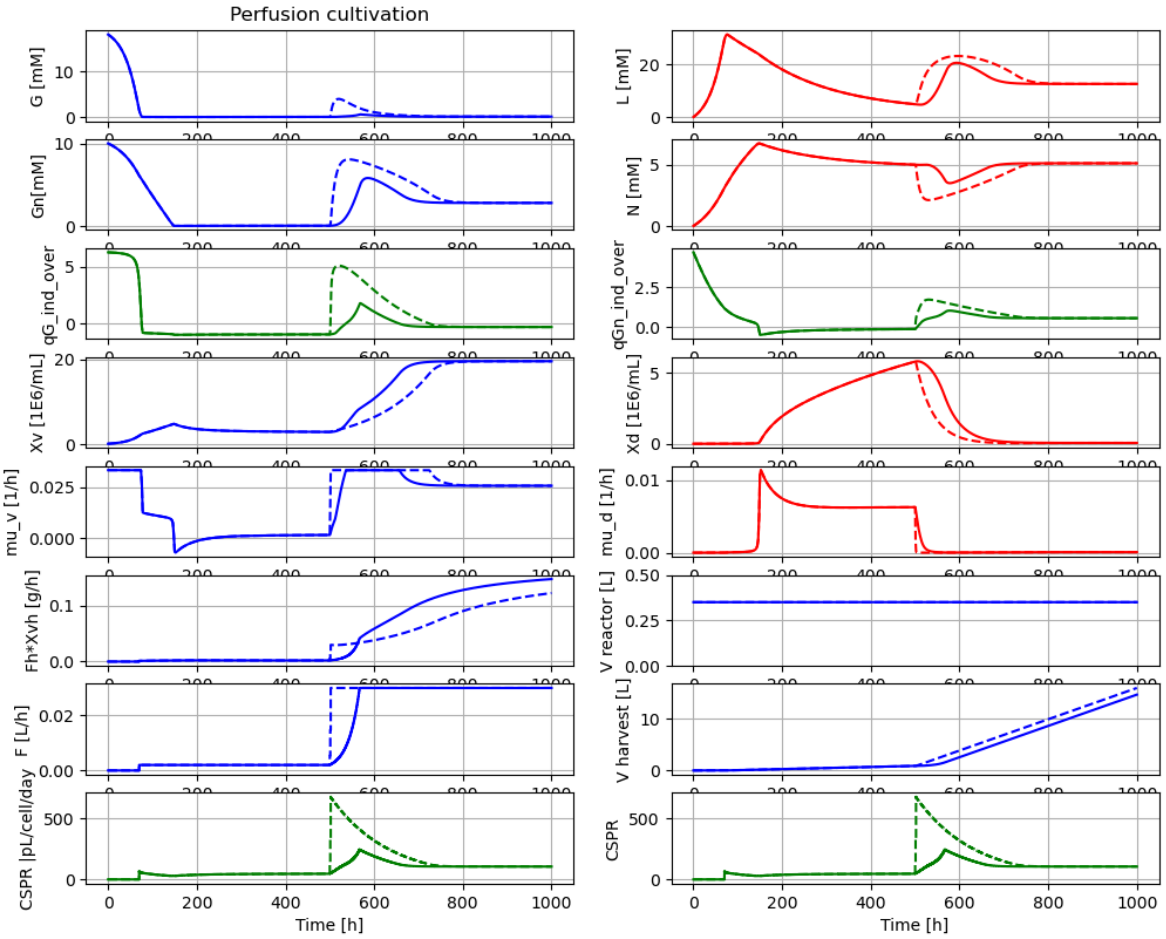
```
No processDiagram.png file in the FMU, but try the file on disk.
```



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 (sc
par(mu_ref=1); simu()                              # Second simulation (a
```

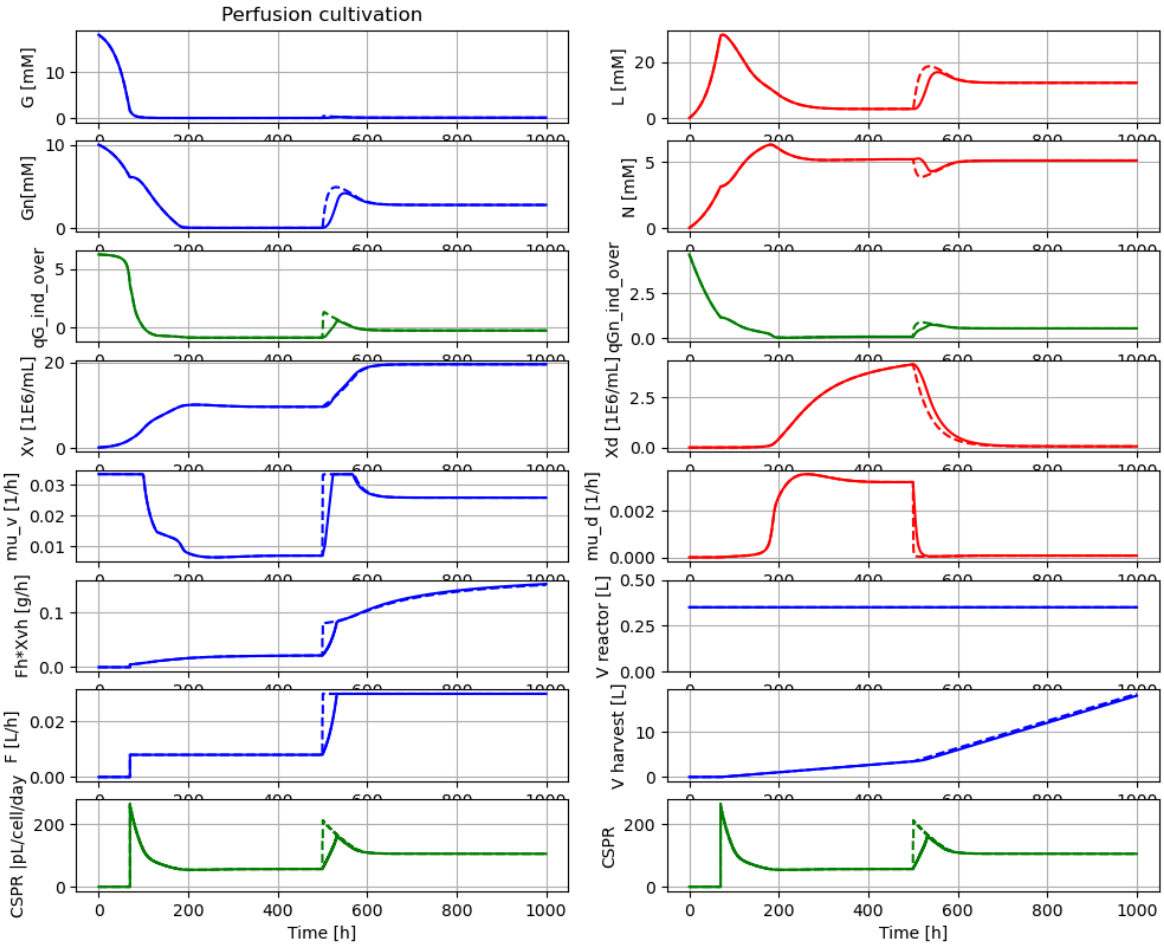


In [6]:
```
model_get('CSPR')
```

Out[6]: 105.41563602162672

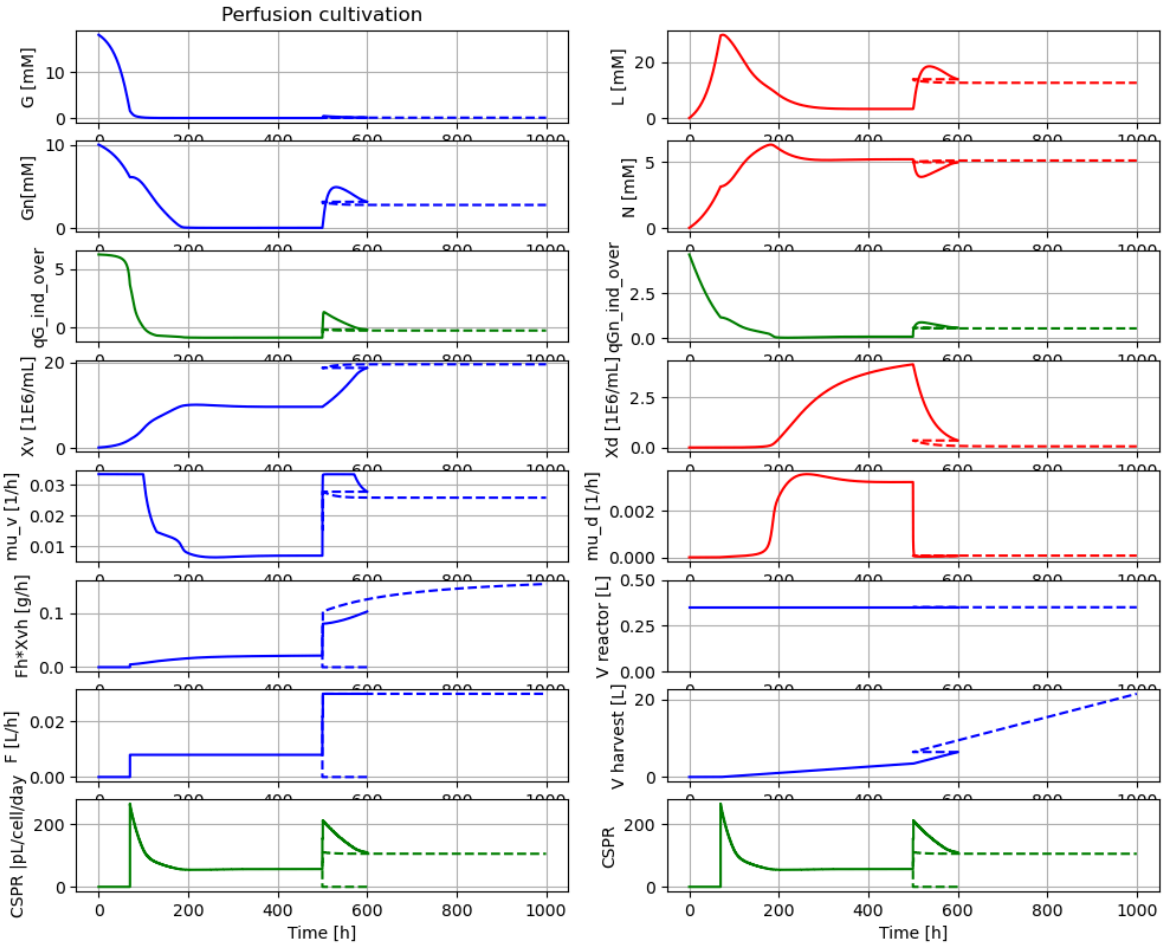
We see here the shorter settling time for cell conc Xv when the slower exponential increase of perfusion rate is used, compared to an abrupt change.

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

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



We see that a somewhat smaller change in perfusion rate make the differnce 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 : 78.915 [ kg ]
```

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

```
Feed volume : 78.577 [ 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', 'cs
pr_openloop', 'D', 'feedtank', 'filter', 'harvesttank']
```

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

```
MSL: 3.2.3 - used components: RealInput, RealOutput, CombiTimeTable, Types
```

In [18]:
```
system_info()
```

```
System information
 -OS: Linux
 -Python: 3.10.12
 -Scipy: not installed in the notebook
 -FMPy: 0.3.19
 -FMU by: OpenModelica Compiler OpenModelica 1.23.0~dev.beta.1-1-g379f714
 -FMI: 2.0
 -Type: ME
 -Name: BPL_CHO.Perfusion_cspr_openloop
 -Generated: 2024-05-20T19:01:47Z
 -MSL: 3.2.3
 -Description: Bioprocess Library version 2.2.0
 -Interaction: FMU-explore for FMPy version 1.0.0
```

In [ ]:
```
```