

# BPL\_TEST2\_Chemostat - demo

```
In [14]: run -i BPL_TEST2_Chemostat_explore.py
```

Windows - run FMU pre-compiled JModelica 2.14

Model for the process 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

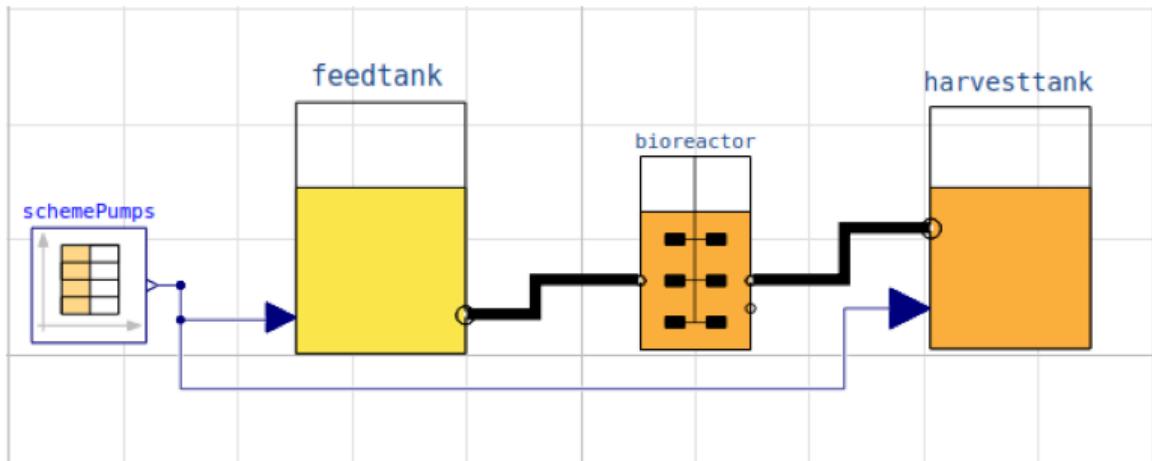
Note that both disp() and describe() takes values from the last simulation and the command process\_diagram() brings up the main configuration

Brief information about a command by help(), eg help(simu)  
Key system information is listed with the command system\_info()  
<Figure size 984.252x787.402 with 0 Axes>

```
In [15]: %matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

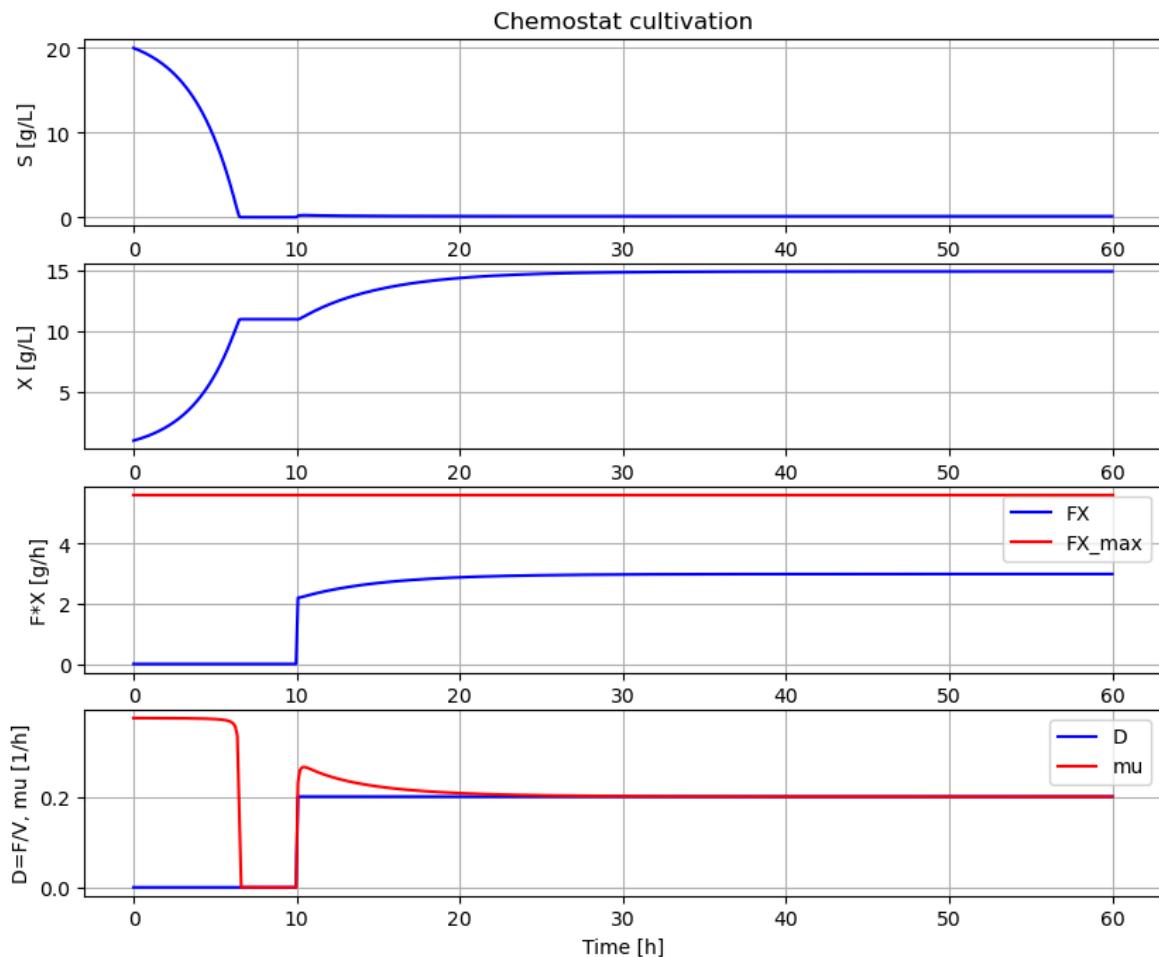
```
In [16]: process_diagram()
```

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



```
In [17]: #fmu_model = 'xBPL_TEST2_Chemostat_Linux_om_me.fmu'
#model = Load_fmu(fmu_model, log_level=0)
```

```
In [18]: newplot()
par(Y=0.50, qSmax=0.75, Ks=0.1)           # Culture parameters
init(V_start=1.0, VX_start=1.0, VS_start=20) # Bioreactor startup
par(S_in=30, t0=0, F0=0, t1=10, F1=0.2)     # Substrate feeding
simu(60)
```



```
In [19]: # The maximal biomass productivity FX_max [g/h] marked red in the diagram above
# can be calculated for CSTR from the FMU and is
cstrProdMax(model)
```

```
Out[19]: np.float64(5.625)
```

```
In [20]: describe('cstrProdMax')
```

Calculate from the model maximal chemostat productivity FX\_max : 5.625 [ g/h ]

```
In [21]: disp('culture')
```

```
Y : 0.5
qSmax : 0.75
Ks : 0.1
```

```
In [22]: describe('mu')
```

Cell specific growth rate variable : 0.2 [ 1/h ]

```
In [23]: describe('parts')
```

```
['bioreactor', 'bioreactor.culture', 'D', 'feedtank', 'harvesttank', 'MSL', 'sche
mePumps']
```

```
In [24]: describe('MSL')
```

MSL: RealInput, RealOutput, CombiTimeTable, Types

```
In [25]: system_info()
```

**System information**

-OS: Windows  
-Python: 3.12.11  
-Scipy: not installed in the notebook  
-PyFMI: 2.19.0  
-FMU by: JModelica.org  
-FMI: 2.0  
-Type: FMUModelCS2  
-Name: BPL.Examples\_TEST2.Chemostat  
-Generated: 2025-07-26T09:39:44  
-MSL: 3.2.2 build 3  
-Description: Bioprocess Library version 2.3.1  
-Interaction: FMU-explore version 1.0.2

In [26]: `!lsb_release -a`

'lsb\_release' is not recognized as an internal or external command,  
operable program or batch file.

In [ ]: