

# BPL\_TEST2\_Chemostat - demo

In [1]: `run -i BPL_TEST2_Chemostat_fmpy_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

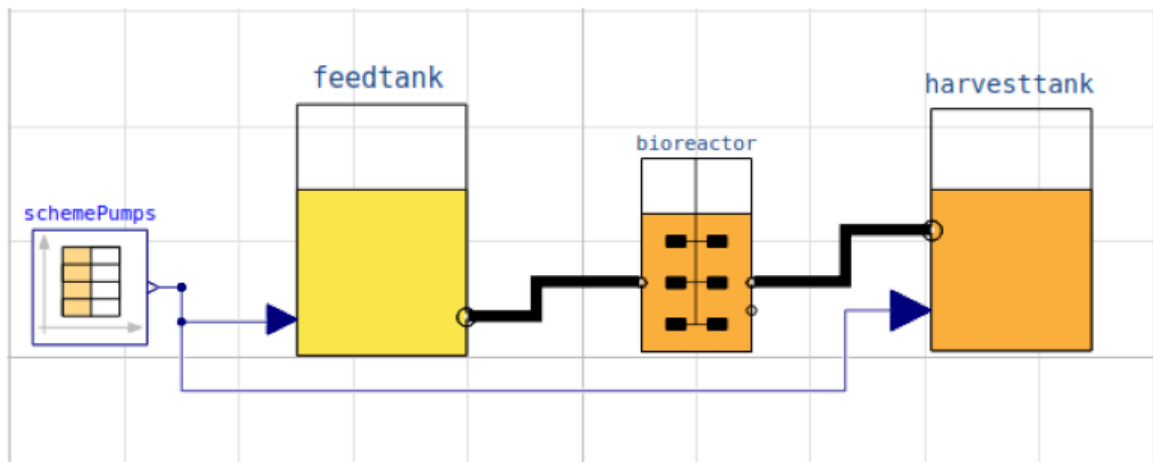
Brief information about a command by `help()`, eg `help(simu)`

Key system information is listed with the command `system_info()`

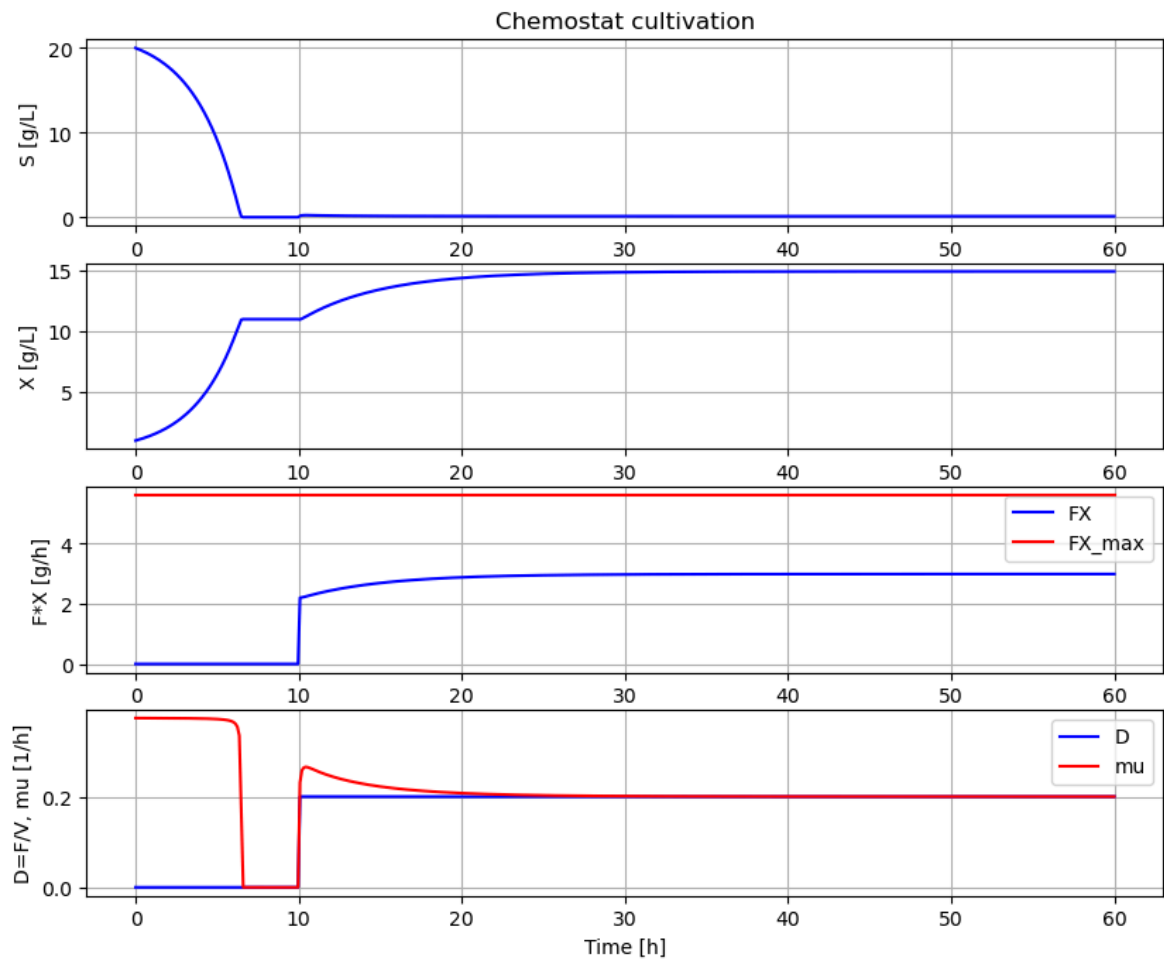
In [2]: `%matplotlib inline`  
`plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]`

In [3]: `process_diagram()`

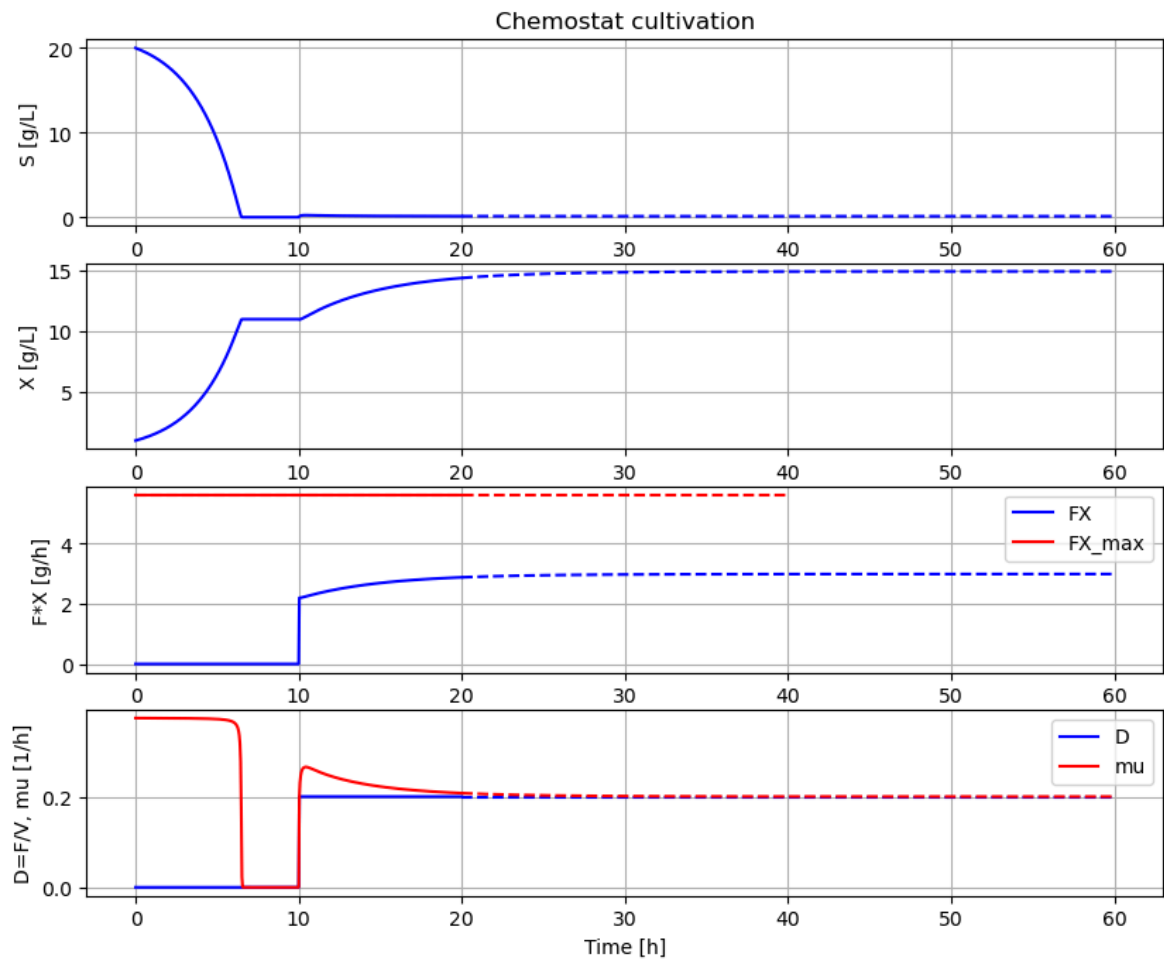
No `processDiagram.png` file in the FMU, but try the file on disk.



In [4]: `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 [5]: # Check simu('cont')
newplot()
simu(20)
simu(40, 'cont')
```



```
In [6]: disp('culture')
```

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

```
In [7]: describe('mu')
```

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

```
In [8]: describe('parts')
```

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

```
In [9]: describe('MSL')
```

```
MSL: RealInput, RealOutput, CombiTimeTable, Types
```

```
In [10]: system_info()
```

## System information

-OS: Windows  
-Python: 3.12.11  
-Scipy: not installed in the notebook  
-FMPy: 0.3.25  
-FMU by: JModelica.org  
-FMI: 2.0  
-Type: CS  
-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 for FMPy version 1.0.2

In [11]: `!lsb_release -a`

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

In [12]: `stateValue`

Out[12]: {'bioreactor.V': np.float64(1.0),  
'bioreactor.m[1]': np.float64(14.942674040405413),  
'bioreactor.m[2]': np.float64(0.11428871522479758),  
'feedtank.V': np.float64(89.99999999999838),  
'harvesttank.V': np.float64(10.000000000000096),  
'harvesttank.m[1]': np.float64(145.38113591443783),  
'harvesttank.m[2]': np.float64(1.2380913683058212)}

In [13]: `parValue`

Out[13]: {'V\_start': 1.0,  
'VX\_start': 1.0,  
'VS\_start': 20,  
'Y': 0.5,  
'qSmax': 0.75,  
'Ks': 0.1,  
'S\_in': 30,  
'feedtank.V\_start': 100.0,  
't0': 0,  
'F0': 0,  
't1': 10,  
'F1': 0.2,  
't2': 999.0,  
'F2': 0.2,  
't3': 1000.0,  
'F3': 0.2}

In [ ]: