

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

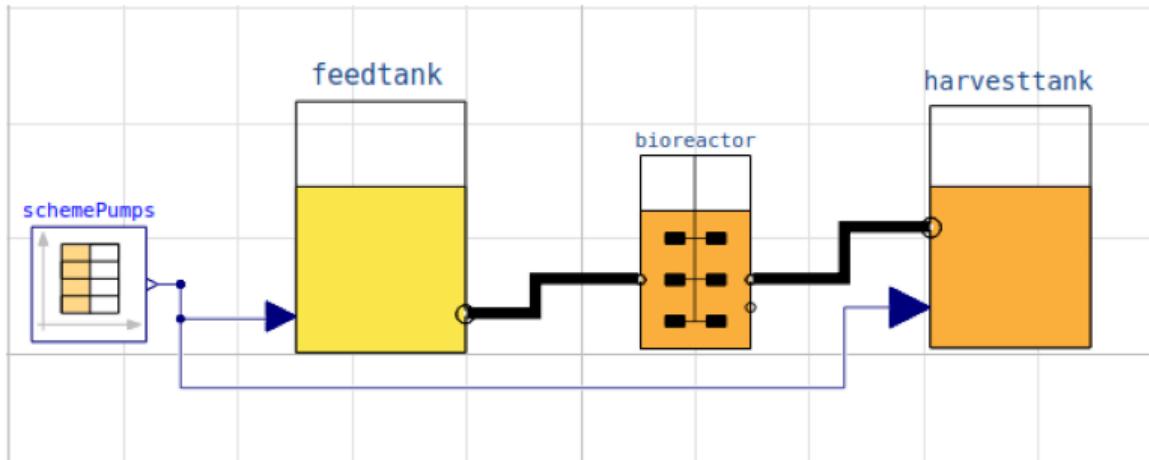
Note that both disp() and describe() takes values from the last simulation and the command process_diagram() brings up the main configuration

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]
```

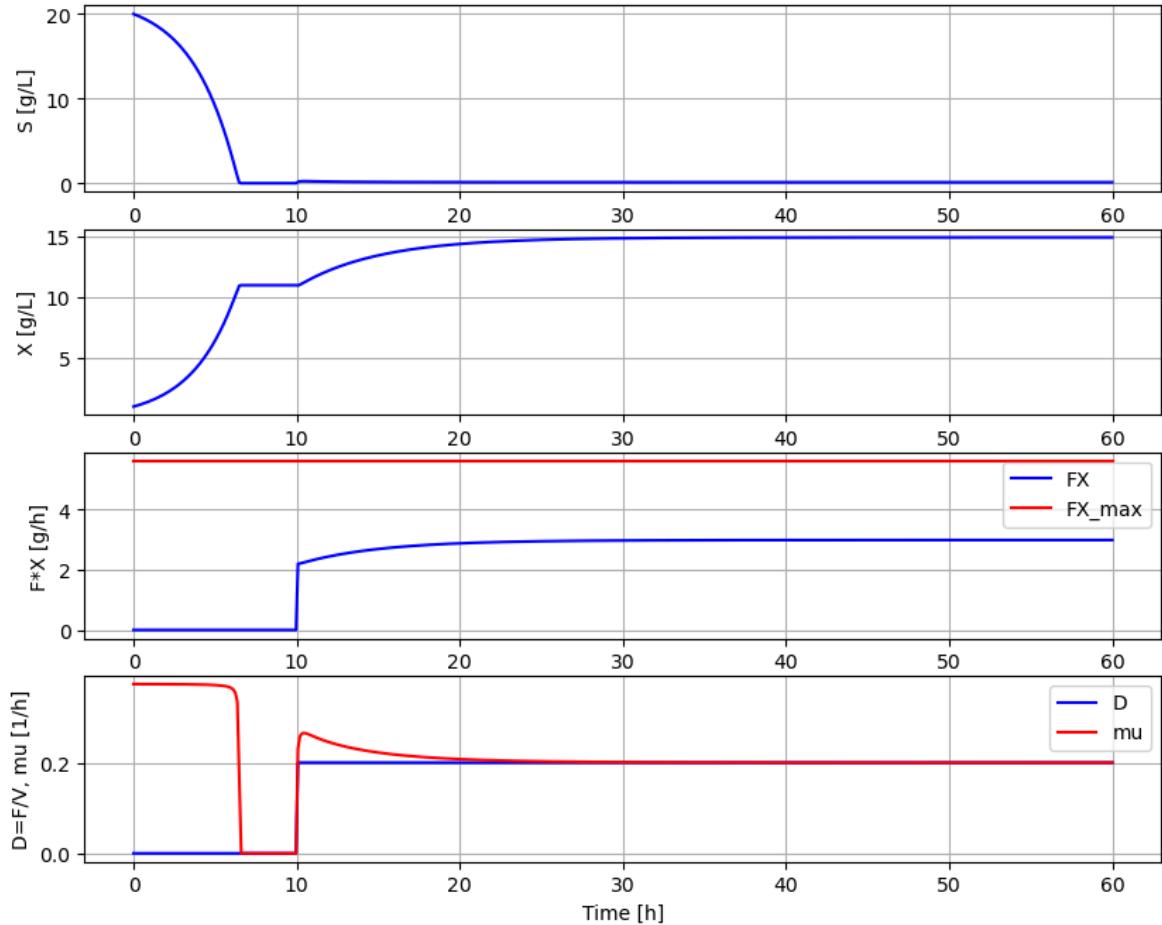
```
In [3]: process_diagram()
```

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



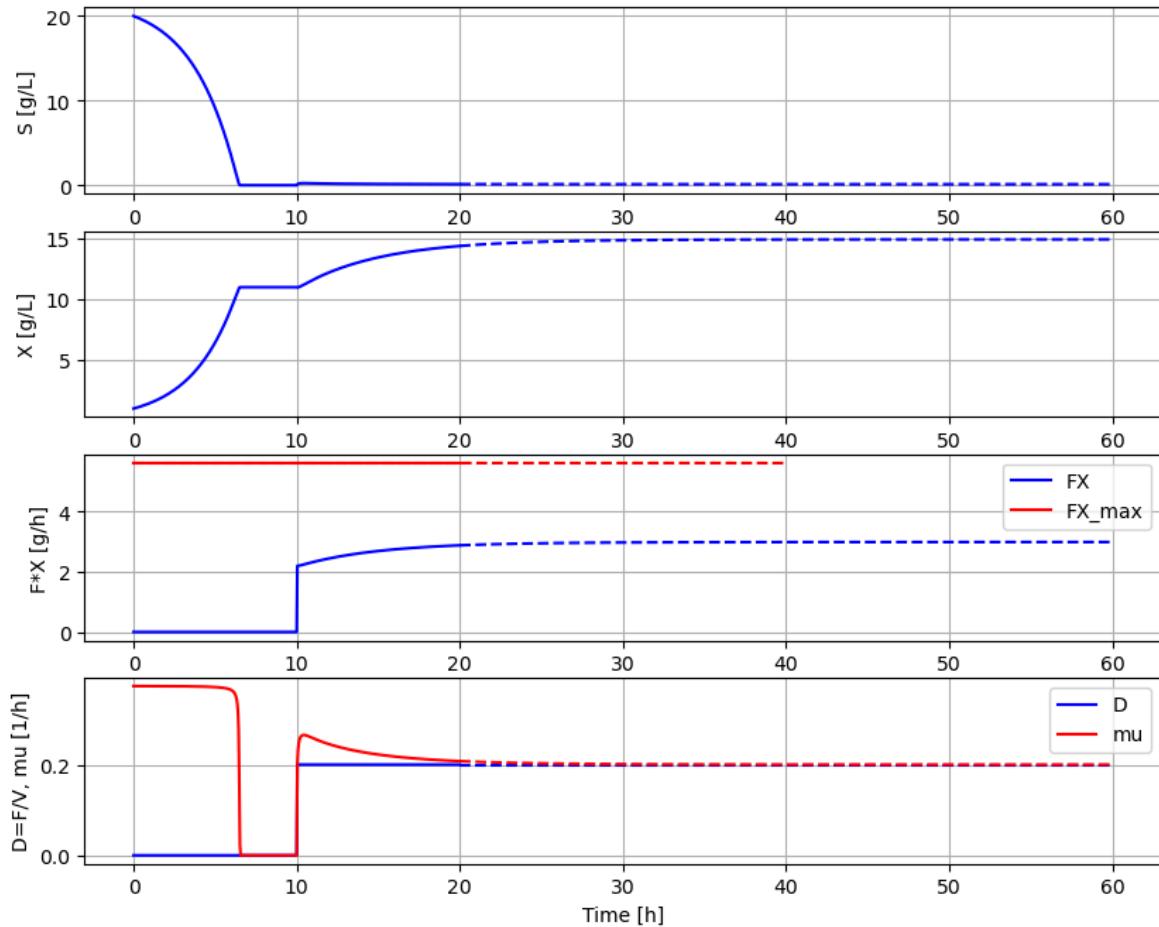
```
In [4]: newplot()
par(Y=0.50, qSmax=0.75, Ks=0.1)           # Culture parameters
init(V_start=1.0, VX_start=1.0, VS_start=20) # Bioreactor startup
par(S_in=30, t0=0, F0=0, t1=10, F1=0.2)     # Substrate feeding
simu(60)
```

Chemostat cultivation



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

Chemostat cultivation



```
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', 'sche  
mePumps']
```

```
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(10.00000000000096),
'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 []: