

# 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

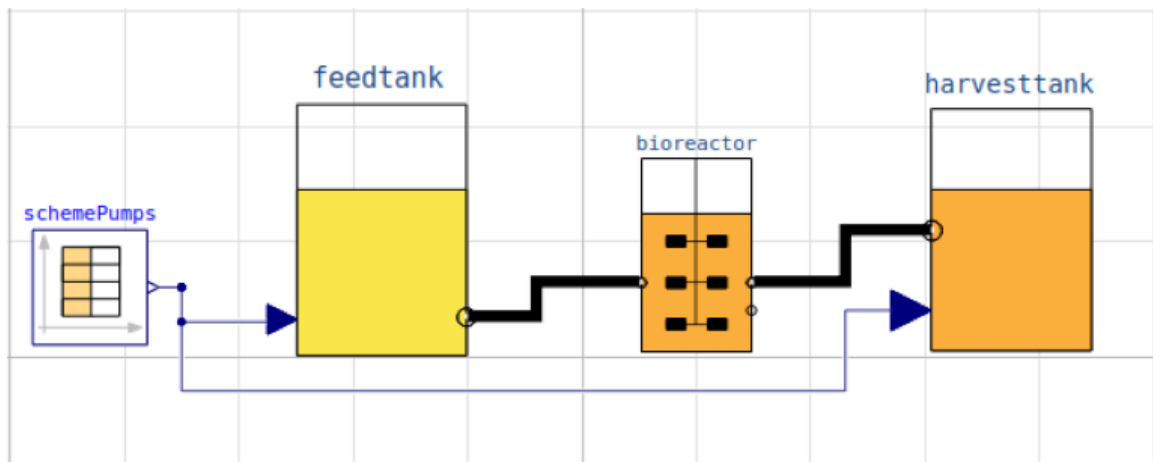
Brief information about a command by `help()`, eg `help(simu)`

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

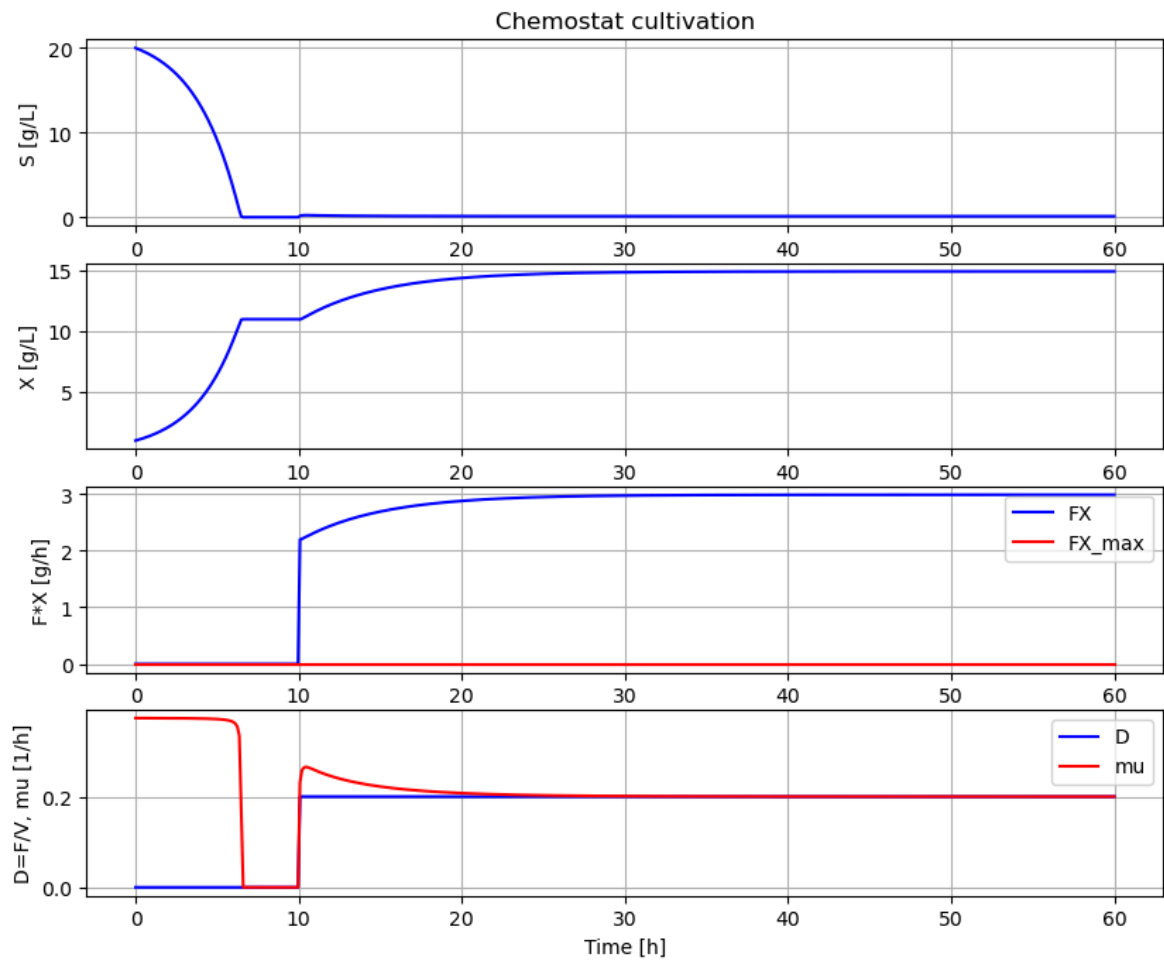
In [2]: `%matplotlib inline`  
`plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]`

In [3]: `process_diagram()`

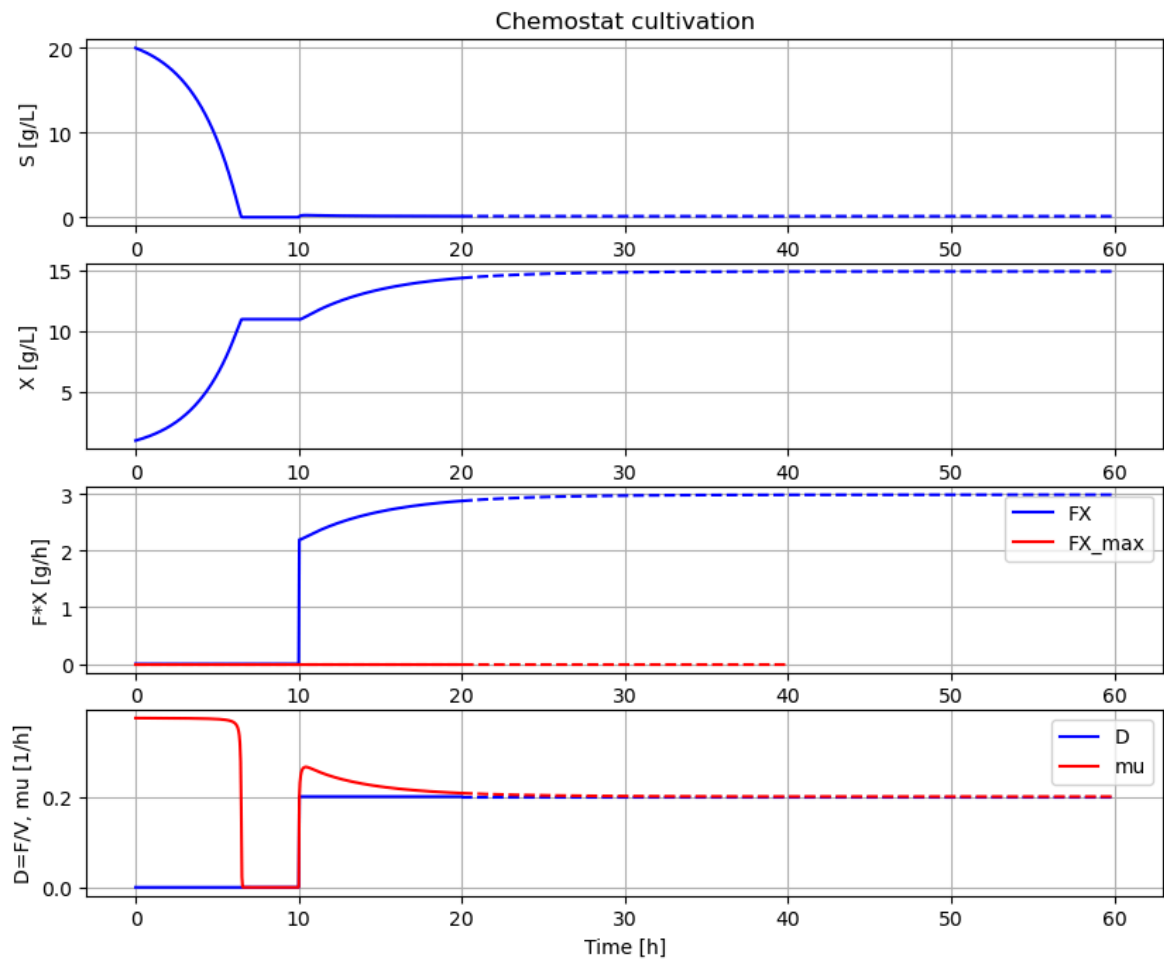
No `processDiagram.png` file in the FMU, but try the file on disk.



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 : 1.0
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: 3.12.8
- Scipy: not installed in the notebook
- FMPy: 0.3.22
- FMU by: JModelica.org
- FMI: 2.0
- Type: CS
- Name: BPL.Examples\_TEST2.Chemostat
- Generated: 2024-11-06T16:32:56
- MSL: 3.2.2 build 3
- Description: Bioprocess Library version 2.3.0
- Interaction: FMU-explore for FMPy version 1.0.1

In [ ]: