BPL_TEST2_Chemostat - demo

```
In [1]:   run -i BPL_TEST2_Chemostat_explore.py
```

```
Windows - run FMU pre-compiled JModelica 2.14

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 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()
```
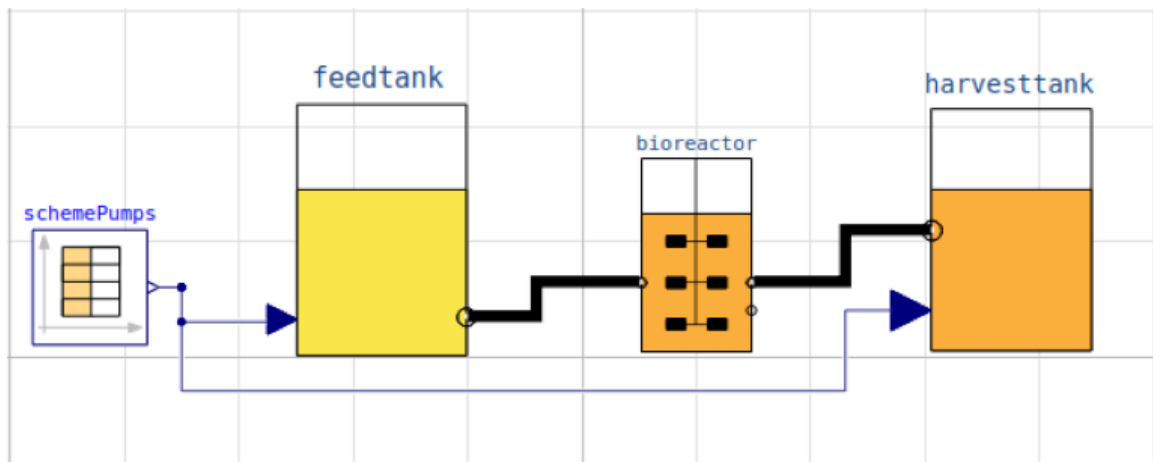
```
In [2]:   %matplotlib inline
          plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```
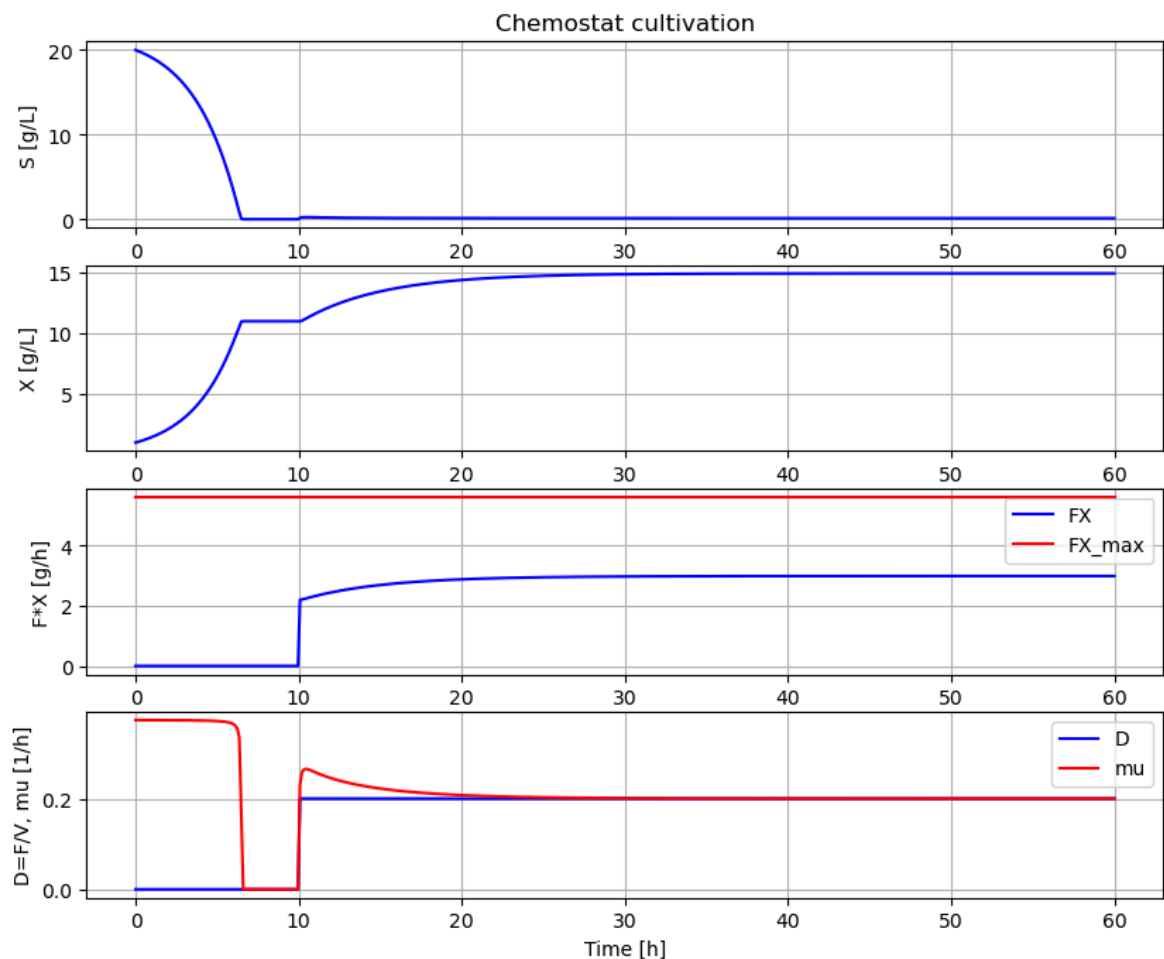
```
In [3]:   process_diagram()
```

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


```
In [4]:   #fmu_model ='xBPL_TEST2_Chemostat_linux_om_me.fmu'
          #model = load_fmu(fmu_model, log_level=0)
```

```
In [5]:   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 [6]:   # 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[6]: 5.625

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

Calculate from the model maximal chemostat productivity FX_max : 5.625 [g/h]

```
In [8]:   disp('culture')
```

Y : 0.5
qSmax : 0.75
Ks : 0.1

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

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

```
In [10]:  describe('parts')
```

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

```
In [11]:  describe('MSL')
```

MSL: RealInput, RealOutput, CombiTimeTable, Types

```
In [12]:  system_info()
```

```
System information
 -OS: Windows
 -Python: 3.10.14
 -Scipy: not installed in the notebook
 -PyFMI: 2.14.0
 -FMU by: JModelica.org
 -FMI: 2.0
 -Type: FMUModelCS2
 -Name: BPL.Examples_TEST2.Chemostat
 -Generated: 2024-10-24T08:57:28
 -MSL: 3.2.2 build 3
 -Description: Bioprocess Library version 2.2.2 - GUI
 -Interaction: FMU-explore version 1.0.0
```

In [ ]: