BPL_TEST2_Chemostat - demo

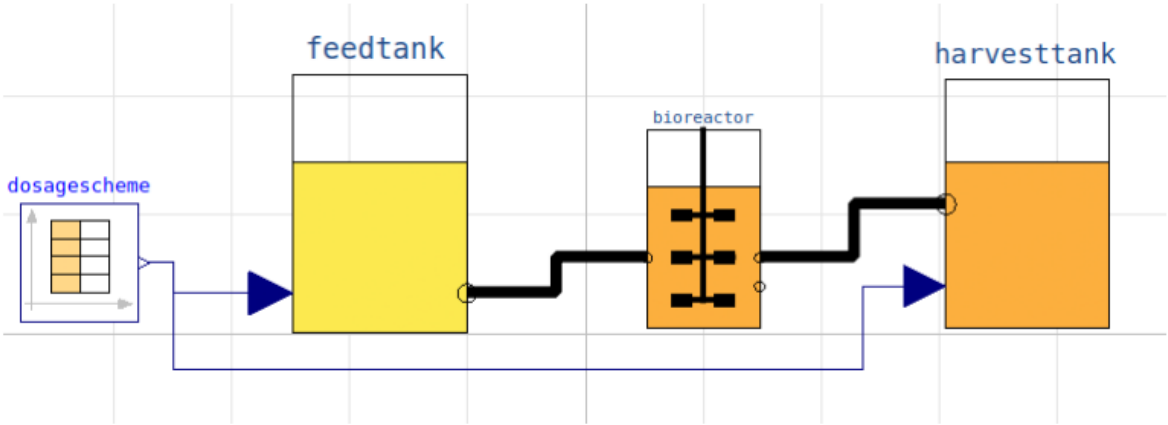
In [1]:
```
run -i BPL_TEST2_Chemostat_explore.py
```

```
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()
```

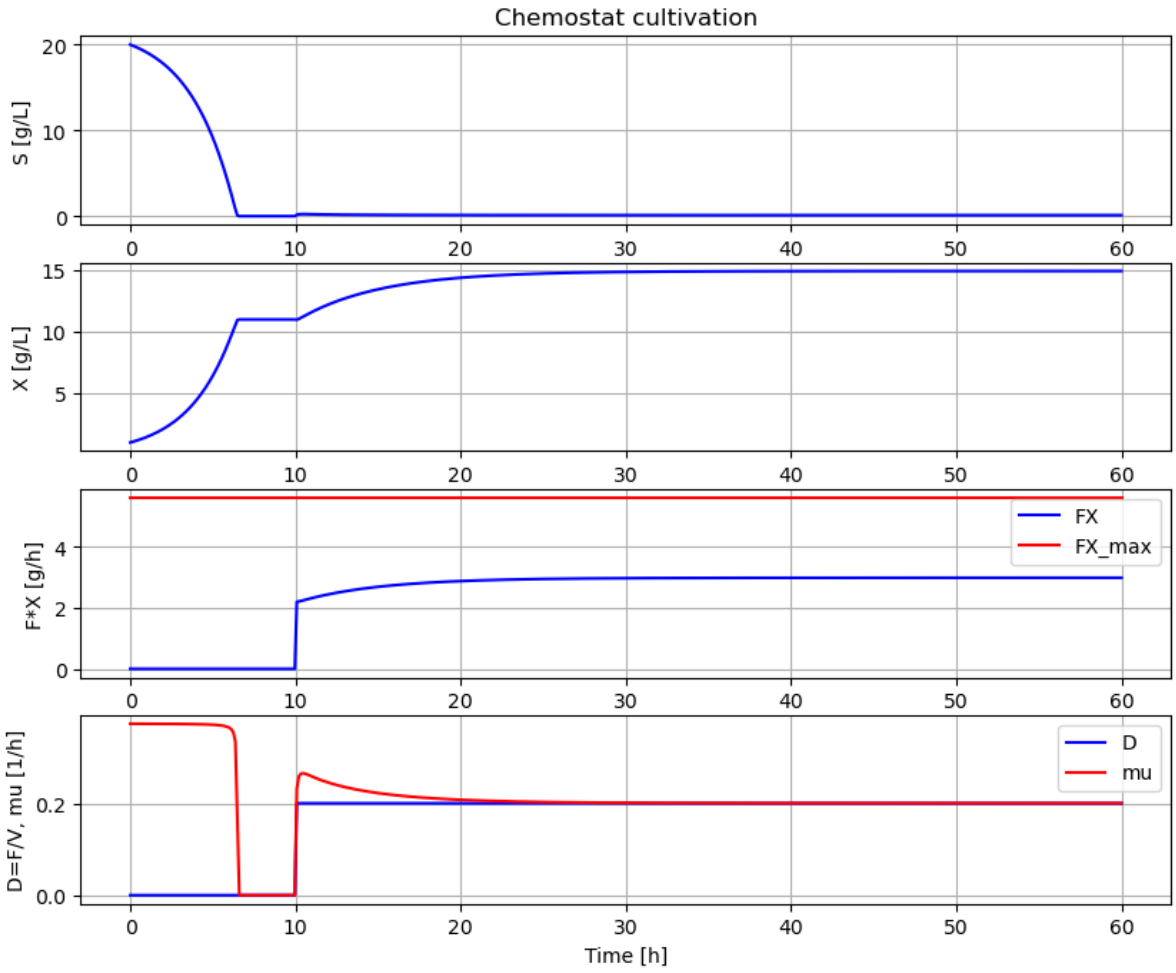
In [2]:
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

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



In [4]:
```
newplot()
par(Y=0.50, qSmax=0.75,  Ks=0.1)          # Culture parameters
init(V_0=1.0, VX_0=1.0, VS_0=20)          # Bioreactor startup
par(S_in=30, t0=0, F0=0, t1=10, F1=0.2)   # Substrate feeding
simu(60)
```



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

In [6]:
```
describe('cstrProdMax')
```

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

In [7]:
```
disp('culture')
```

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

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

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

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

```
['bioreactor', 'bioreactor.culture', 'D', 'dosagescheme', 'feedtank', 'harvesttan
k', 'liquidphase', 'MSL']
```

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

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

In [11]:
```
system_info()
```

```
System information
 -OS: Windows
 -Python: 3.10.6
 -Scipy: not installed in the notebook
 -PyFMI: 2.10.3
 -FMU by: JModelica.org
 -FMI: 2.0
 -Type: FMUModelCS2
 -Name: BPL_TEST2.Chemostat
 -Generated: 2023-03-30T09:13:31
 -MSL: 3.2.2 build 3
 -Description: Bioprocess Library version 2.1.1
 -Interaction: FMU-explore version 0.9.8
```

In [12]:
```
model.get('bioreactor.n_outlets')
```

Out[12]:
```
array([1])
```

In [13]:
```
model.get('bioreactor.n_inlets')
```

Out[13]:
```
array([1])
```

In [ ]:
```

```