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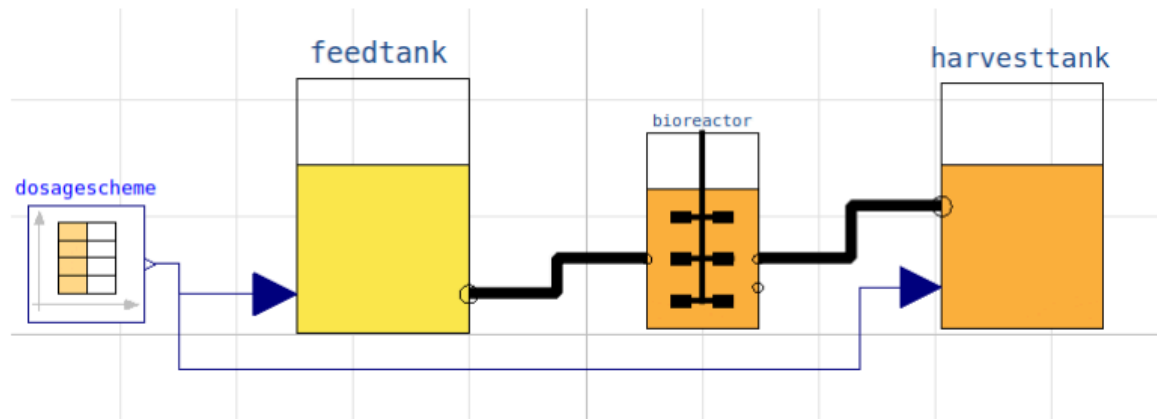
`In [2]:`
```python
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

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


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

`In [5]:`
```python
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
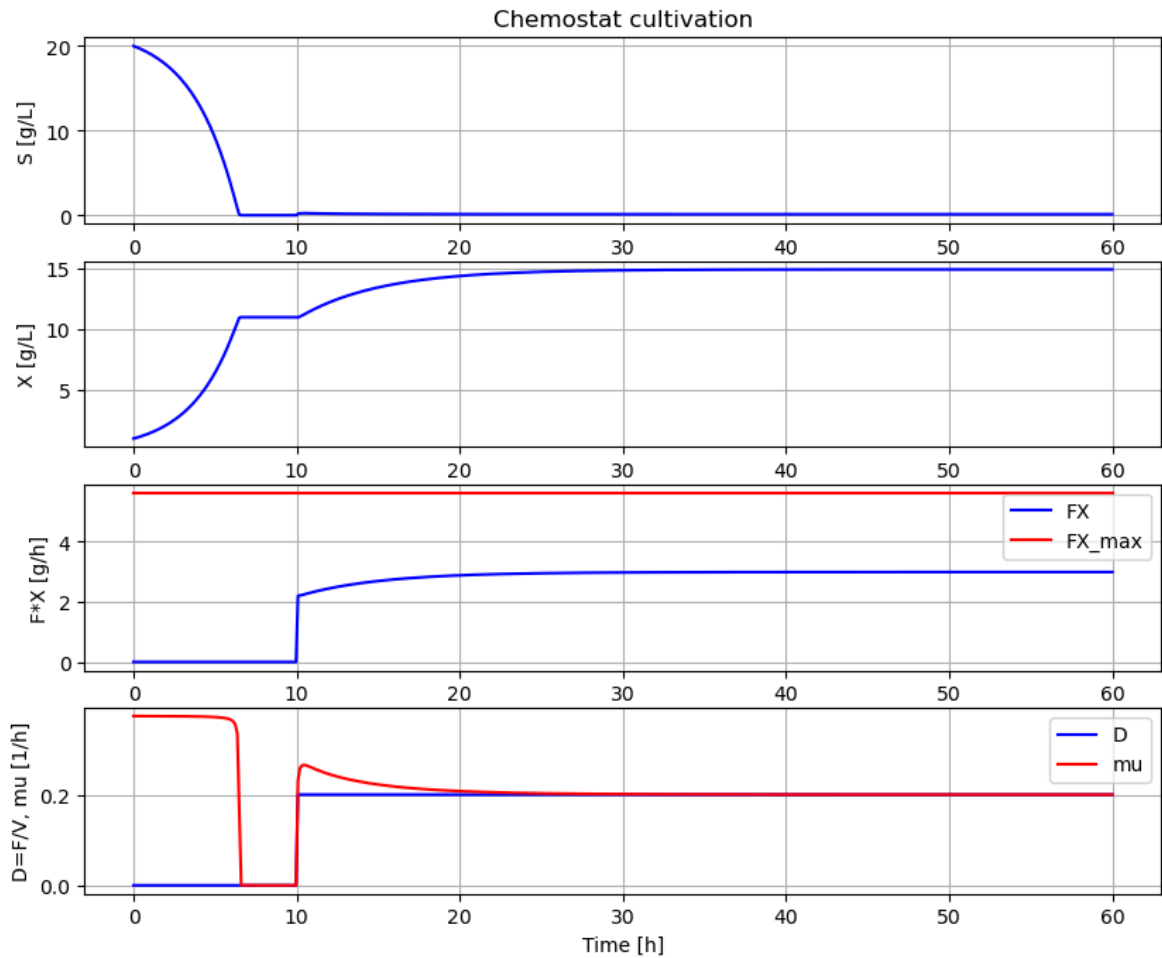
In [6]:
```python
# The maximal biomass productivity FX_max [g/h] marked red in the diagram above
# can be calculated for CSTR from the FMU and is
cstrProdMax(model)
```

Out[6]: 5.625

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

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

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

Y : 0.5
qSmax : 0.75
Ks : 0.1

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

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

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

['bioreactor', 'bioreactor.culture', 'D', 'dosagescheme', 'feedtank', 'harvesttank', 'liquidphase', 'MSL']

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

MSL: RealInput, RealOutput, CombiTimeTable, Types

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

```
System information
 -OS: Windows
 -Python: 3.10.14
 -Scipy: not installed in the notebook
 -PyFMI: 2.13.0
 -FMU by: JModelica.org
 -FMI: 2.0
 -Type: FMUModelCS2
 -Name: BPL_TEST2.Chemostat
 -Generated: 2024-05-12T20:53:47
 -MSL: 3.2.2 build 3
 -Description: Bioprocess Library version 2.2.0
 -Interaction: FMU-explore version 1.0.0
```

In [ ]: