BPL_TEST2_Chemostat - demo

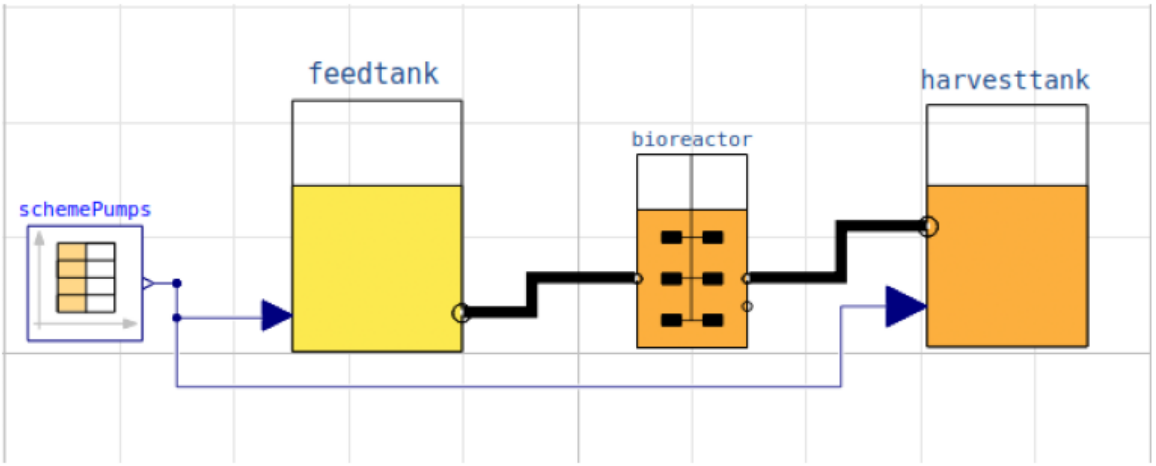
In [1]:
```
run -i BPL_TEST2_Chemostat_explore.py
```

```
Linux - run FMU pre-compiled OpenModelica

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 simul
ation
 - describe()  - describe culture, broth, parameters, variables with value
s/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()
```

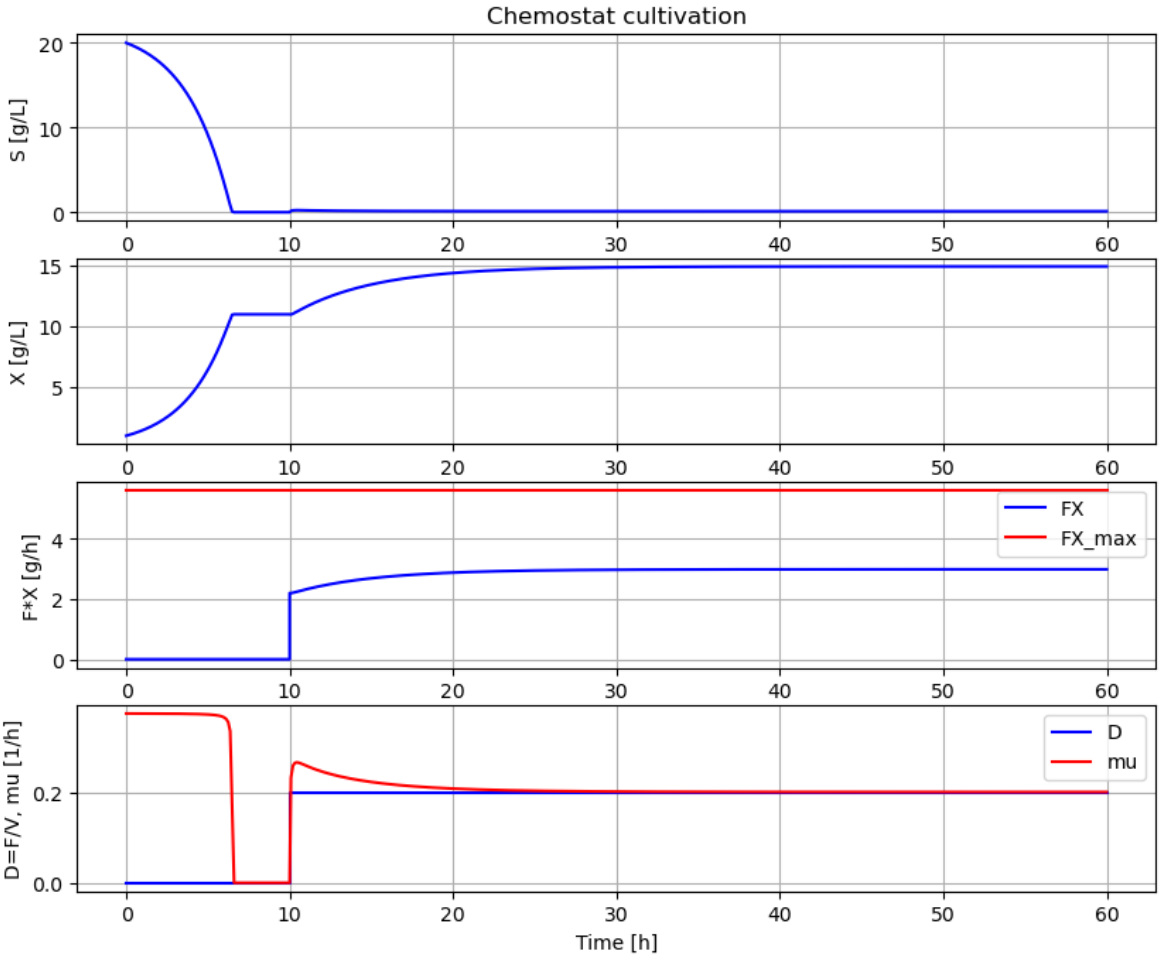
```
No processDiagram.png file in the FMU, but try the file on disk.
```



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)
```

```
Could not find cannot import name 'dopri5' from 'assimulo.lib' (/home/janp
eter/miniconda3/envs/pyfmi/lib/python3.12/site-packages/assimulo/lib/__ini
t__.py)
Could not find cannot import name 'rodas' from 'assimulo.lib' (/home/janpe
ter/miniconda3/envs/pyfmi/lib/python3.12/site-packages/assimulo/lib/__init
__.py)
Could not find cannot import name 'odassl' from 'assimulo.lib' (/home/janp
eter/miniconda3/envs/pyfmi/lib/python3.12/site-packages/assimulo/lib/__ini
t__.py)
Could not find ODEPACK functions.
Could not find RADAR5
Could not find GLIMDA.
```



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

Out[6]: np.float64(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', 'sche
mePumps']
```

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

```
MSL: 4.1.0 - used components: RealInput, RealOutput, CombiTimeTable, Types
```

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

```
System information
 -OS: Linux
 -Python: 3.12.9
 -Scipy: not installed in the notebook
 -PyFMI: 2.18.0
 -FMU by: OpenModelica Compiler OpenModelica 1.26.0~dev-200-gcb3254b
 -FMI: 2.0
 -Type: FMUModelME2
 -Name: BPL.Examples_TEST2.Chemostat
 -Generated: 2025-07-28T07:59:17Z
 -MSL: 4.1.0
 -Description: Bioprocess Library version 2.3.1
 -Interaction: FMU-explore version 1.0.0
```

In [13]:
```
!lsb_release -a
```

```
No LSB modules are available.
Distributor ID: Ubuntu
Description:    Ubuntu 24.04.3 LTS
Release:        24.04
Codename:       noble
```

In [ ]:
```

```