

BPL_TEST2_Chemostat - demo

In [14]: `run -i BPL_TEST2_Chemostat_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)`

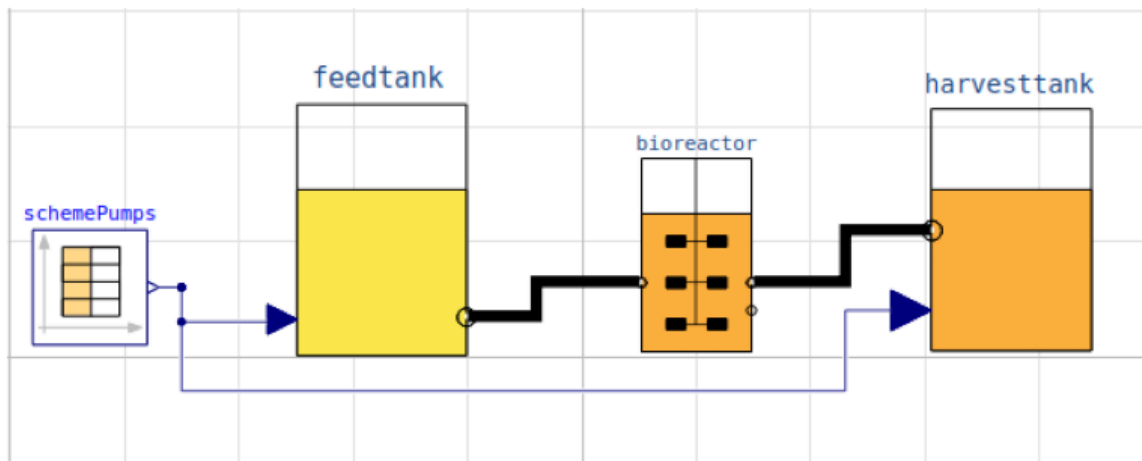
Key system information is listed with the command `system_info()`

<Figure size 984.252x787.402 with 0 Axes>

In [15]: `%matplotlib inline`
`plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]`

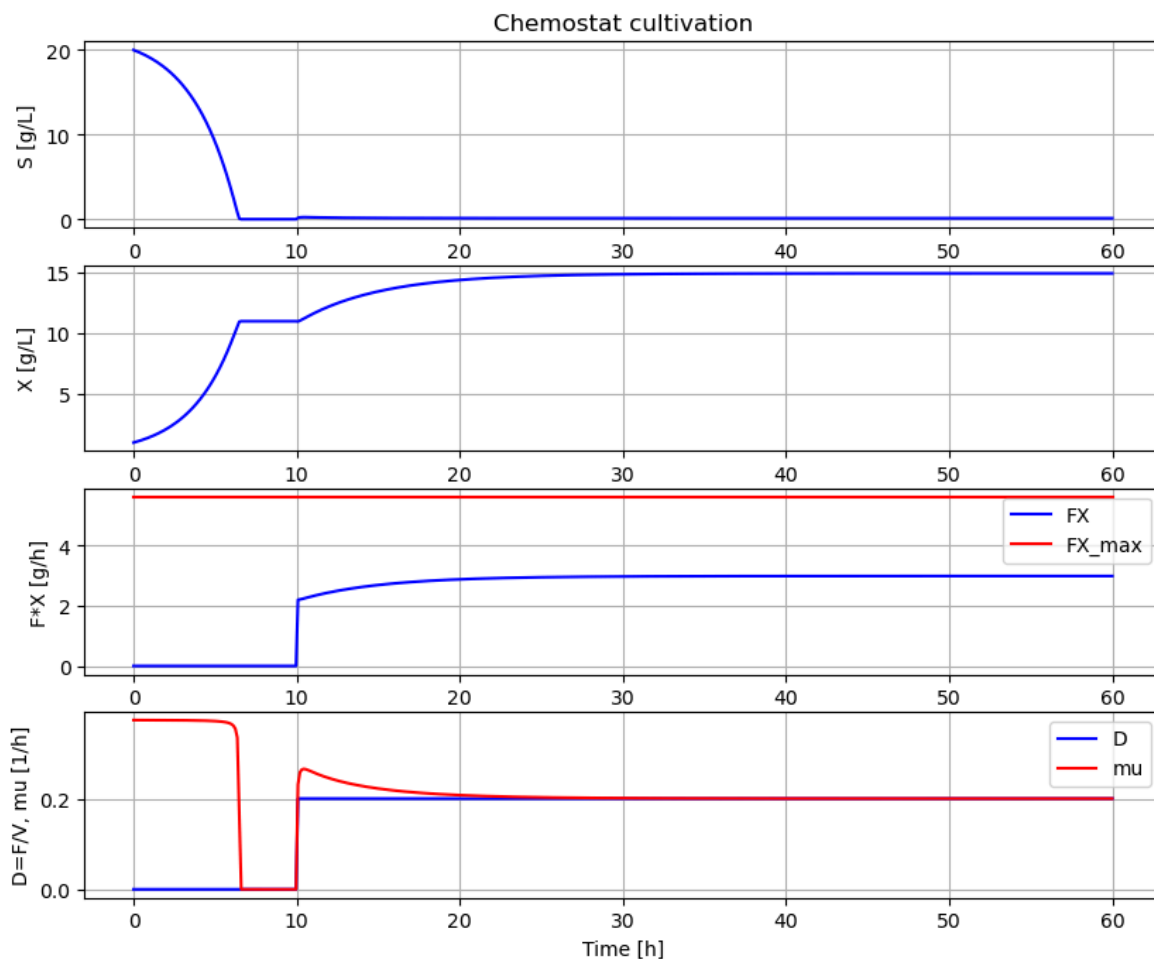
In [16]: `process_diagram()`

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



In [17]: `#fmu_model = 'xBPL_TEST2_Chemostat_linux_om_me.fmu'`
`#model = load_fmu(fmu_model, log_level=0)`

In [18]: `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 [19]: # 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[19]: np.float64(5.625)
```

```
In [20]: describe('cstrProdMax')
```

Calculate from the model maximal chemostat productivity FX_{\max} : 5.625 [g/h]

```
In [21]: disp('culture')
```

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

```
In [22]: describe('mu')
```

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

```
In [23]: describe('parts')
```

```
['bioreactor', 'bioreactor.culture', 'D', 'feedtank', 'harvesttank', 'MSL', 'schemePumps']
```

```
In [24]: describe('MSL')
```

MSL: RealInput, RealOutput, CombiTimeTable, Types

```
In [25]: system_info()
```

System information

- OS: Windows
- Python: 3.12.11
- Scipy: not installed in the notebook
- PyFMI: 2.19.0
- FMU by: JModelica.org
- FMI: 2.0
- Type: FMUModelCS2
- Name: BPL.Examples_TEST2.Chemostat
- Generated: 2025-07-26T09:39:44
- MSL: 3.2.2 build 3
- Description: Bioprocess Library version 2.3.1
- Interaction: FMU-explore version 1.0.2

In [26]: `!lsb_release -a`

'lsb_release' is not recognized as an internal or external command,
operable program or batch file.

In []: