

# BPL\_TEST2\_Fedbatch - demo

In [15]: `run -i BPL_TEST2_Fedbatch_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)`

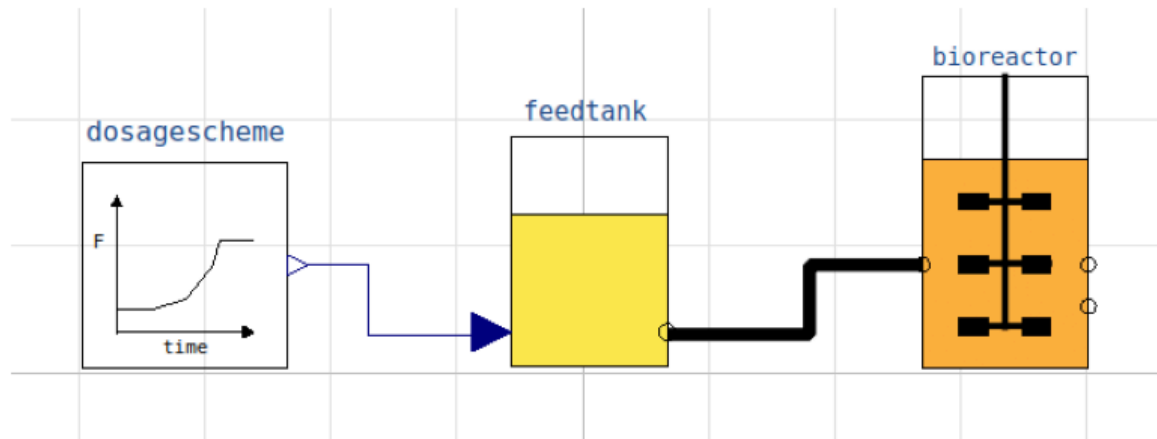
Key system information is listed with the command `system_info()`

<Figure size 984.252x787.402 with 0 Axes>

In [16]: `%matplotlib inline`  
`plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]`

In [17]: `process_diagram()`

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

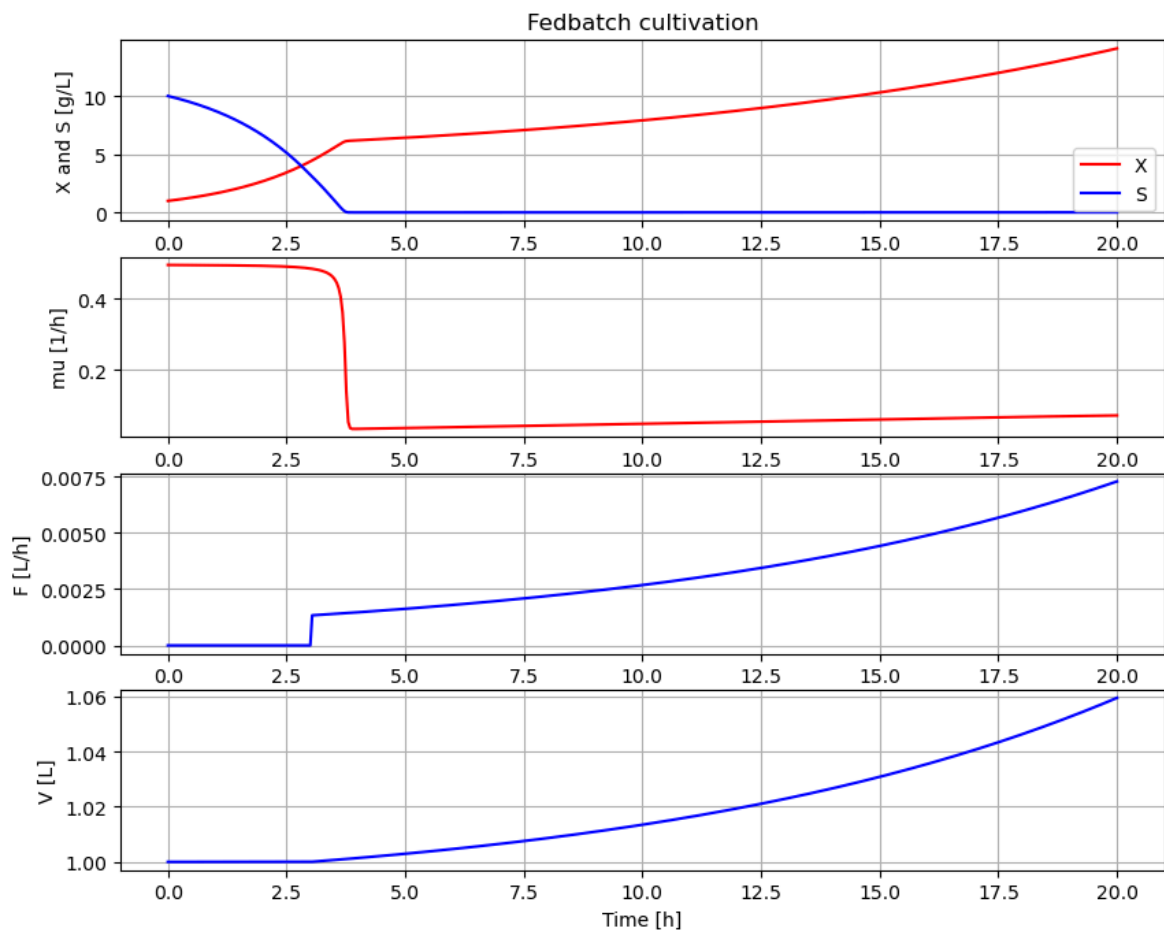


`disp('dosagescheme')`

In [18]: `#disp('feedtank')`

In [19]: `#disp('bioreactor', mode='Long')`

In [20]: `# Simulation with default values of the process`  
`newplot(plotType='TimeSeries')`  
`simu(20)`



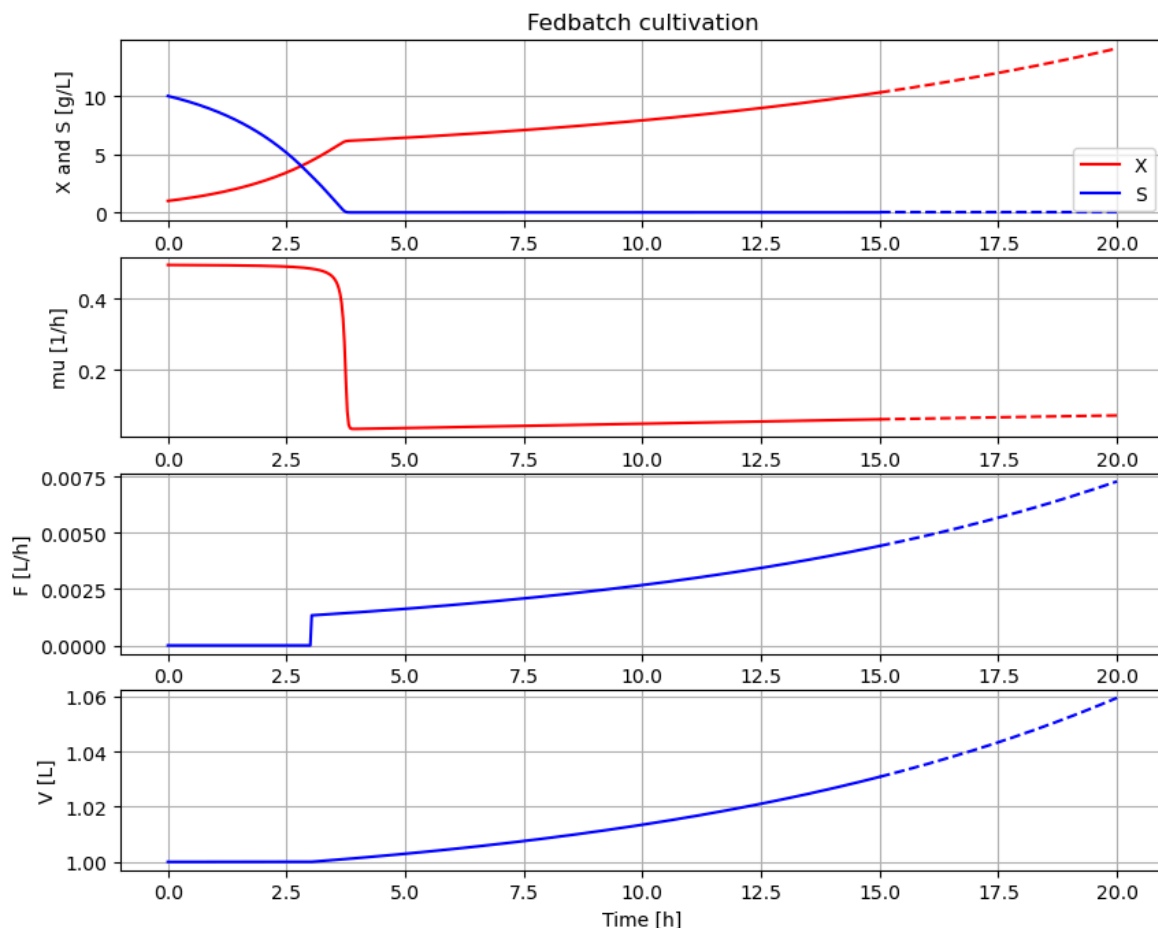
In [21]: `disp(mode='long')`

```

bioreactor.V_start : V_start : 1.0
bioreactor.m_start[1] : VX_start : 1.0
bioreactor.m_start[2] : VS_start : 10.0
bioreactor.culture.Y : Y : 0.5
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1
feedtank.c_in[2] : feedtank.S_in : 300.0
feedtank.V_start : feedtank.V_start : 10.0
dosagescheme.F_start : F_start : 0.0
dosagescheme.mu_feed : mu_feed : 0.1
dosagescheme.t_startExp : t_startExp : 3.0
dosagescheme.F_startExp : F_startExp : 0.001
dosagescheme.F_max : F_max : 0.3

```

In [22]: `# Test function simu(mode='cont')`  
`newplot()`  
`simu(15)`  
`simu(5,'cont')`



```
In [23]: disp('culture')
```

```
Y : 0.5
qSmax : 1.0
Ks : 0.1
```

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

```
Cell specific growth rate variable : 0.073 [ 1/h ]
```

```
In [25]: describe('parts')
```

```
['bioreactor', 'bioreactor.culture', 'dosagescheme', 'feedtank', 'MSL']
```

```
In [26]: describe('MSL')
```

```
MSL: RealInput, RealOutput
```

```
In [27]: system_info()
```

```
System information
-OS: Windows
-Python: 3.12.11
-Scipy: not installed in the notebook
-PyFMI: 2.18.3
-FMU by: JModelica.org
-FMI: 2.0
-Type: FMUModelCS2
-Name: BPL.Examples_TEST2.Fedbatch
-Generated: 2025-07-26T09:38:43
-MSL: 3.2.2 build 3
-Description: Bioprocess Library version 2.3.1
-Interaction: FMU-explore version 1.0.0
```

In [28]: `!lsb_release -a`

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

In [ ]: