BPL_TEST2_Batch - demo

In [1]:
```
run -i BPL_TEST2_Batch_fmpy_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

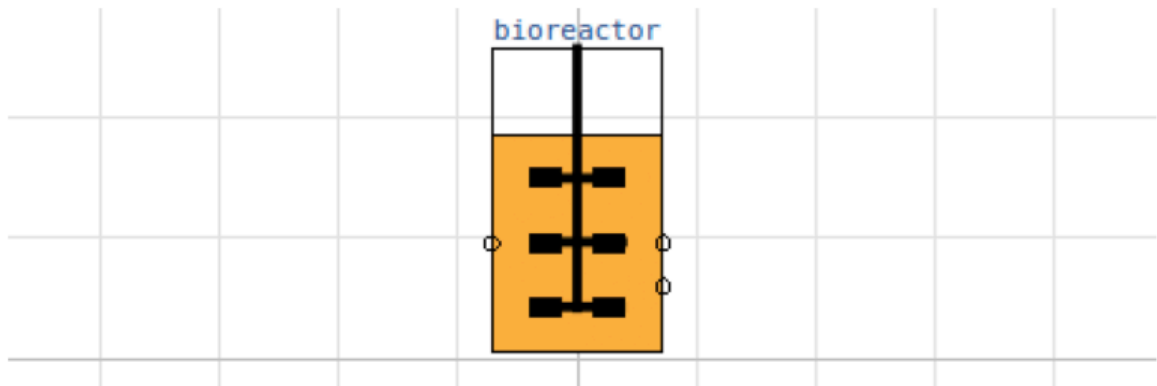Brief information about a command by help(), eg help(simu)
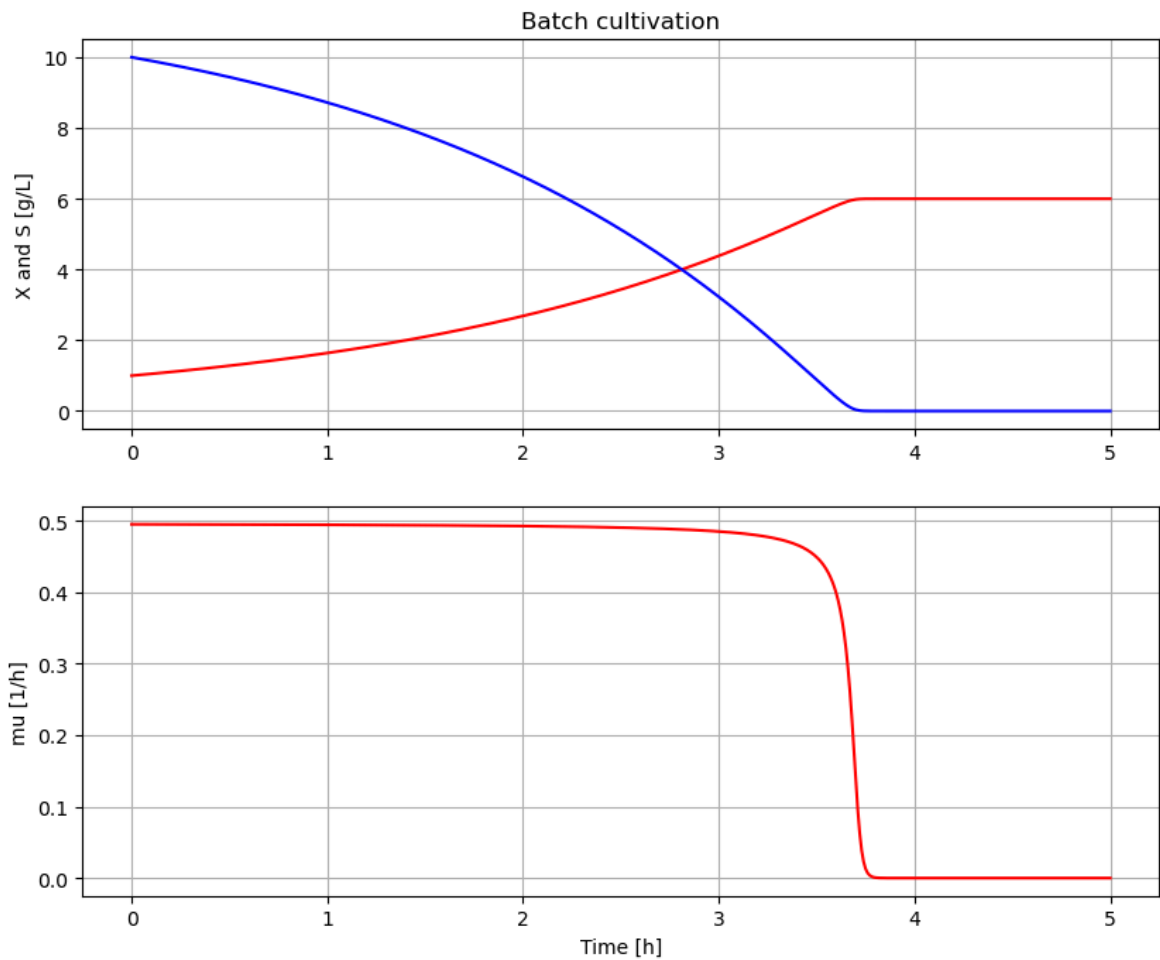Key system information is listed with the command system_info()

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

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

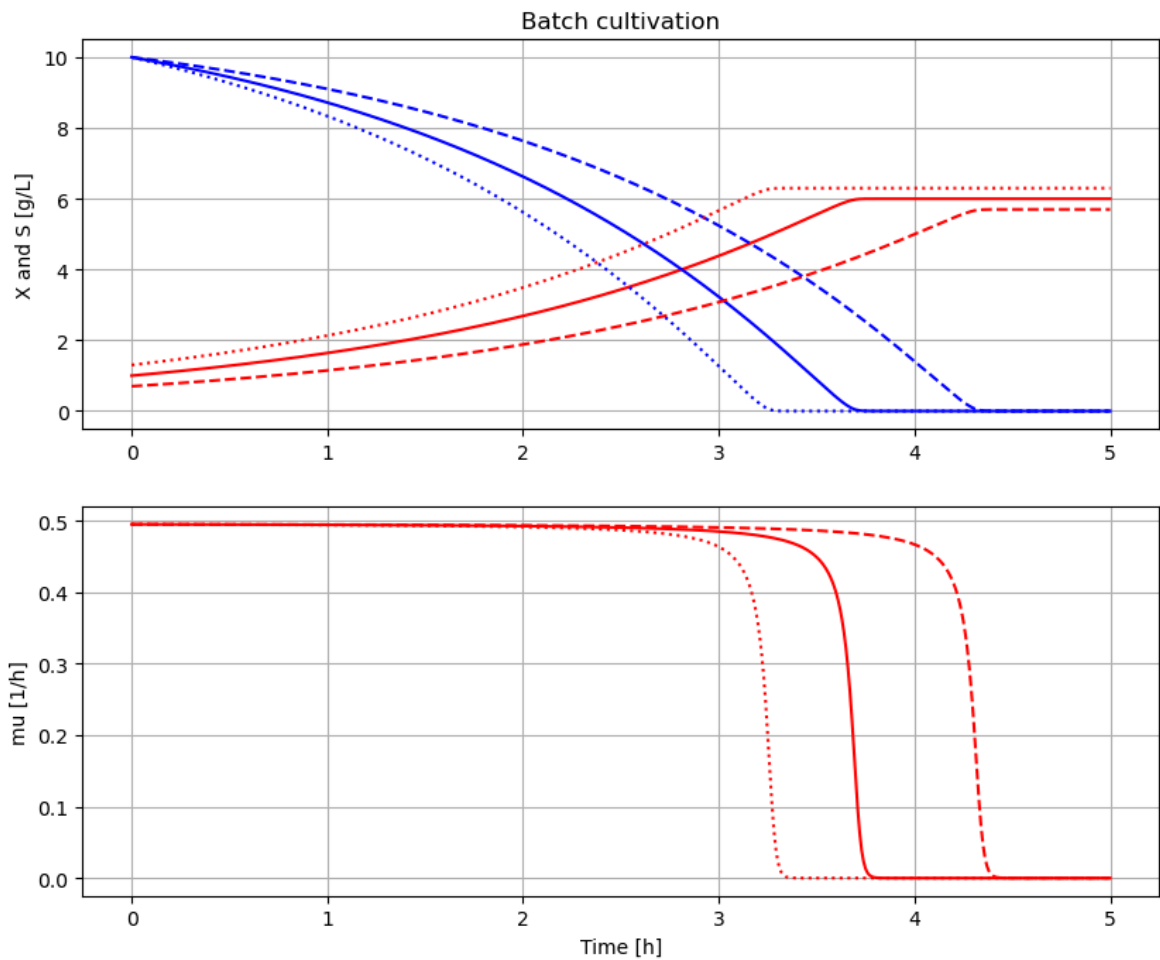No processDiagram.png file in the FMU, but try the file on disk.

In [4]:
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu()
```
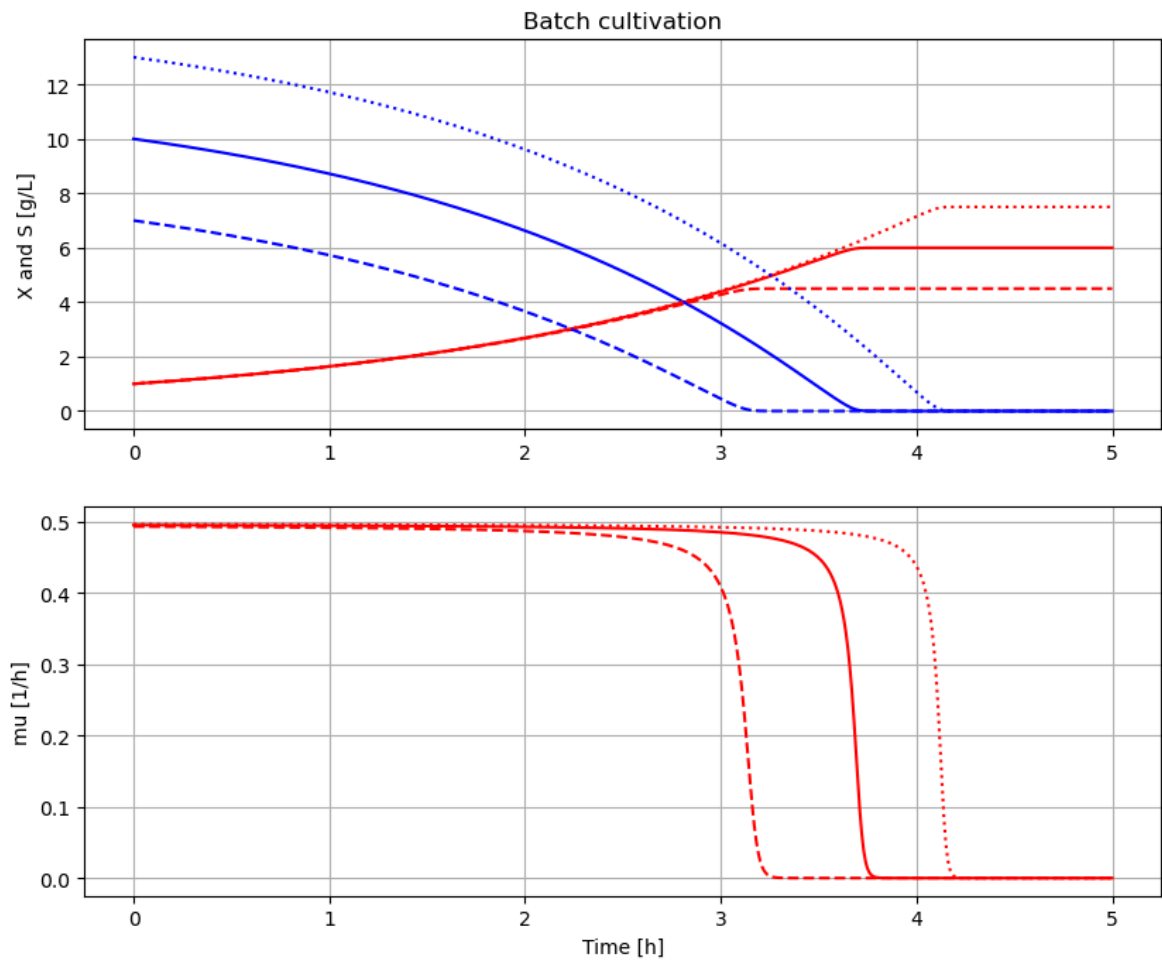
Batch cultivation

In [5]:
```python
# Simulation were initial value of biomass VX_start is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

# Restore default value of VX_start
init(VX_start=1.0)
```

Batch cultivation


```
In [6]:  # Simulation were initial value of substrate VS_0 is varied
         newplot(plotType='TimeSeries')
         for value in [10, 7, 13]: init(VS_start=value); simu(5)

         # Restore default value of VS_0
         init(VS_start=10)
```
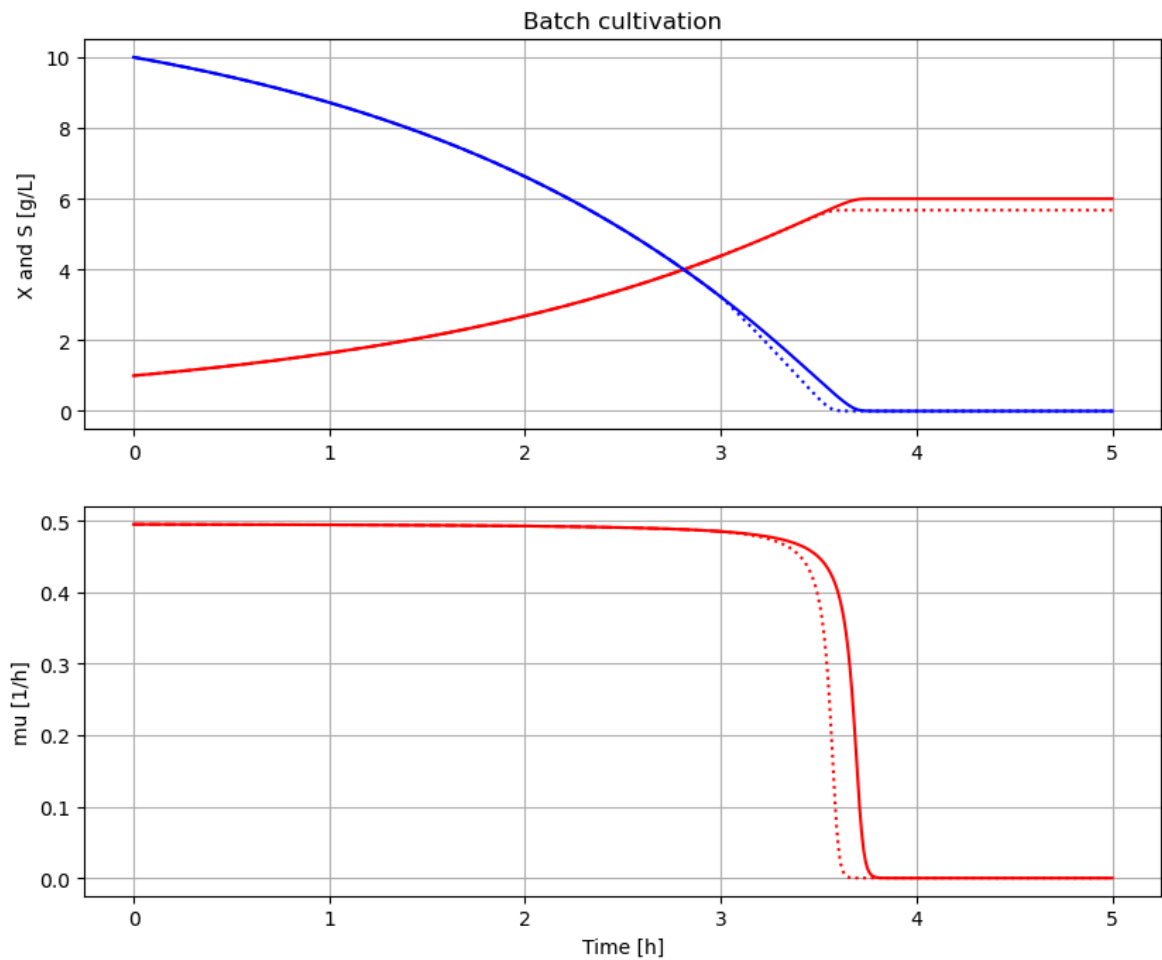
Batch cultivation


```python
# Simulation where metabolism is changed after 3 hours
newplot(plotType='TimeSeries')
simu(5)

simu(3)
par(Y=0.4, qSmax=1.0/(0.4/0.5)); simu(2, 'cont')

# Restore default value of Y and qSmax
par(Y=0.5, qSmax=1.0)
```

Batch cultivation


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

         Y : 0.4
         qSmax : 1.25
         Ks : 0.1

In [9]:  describe('mu')

         Cell specific growth rate variable : 0.0 [ 1/h ]

In [10]: describe('parts')

         ['bioreactor', 'bioreactor.culture', 'MSL']

In [11]: describe('MSL')

         MSL: none

In [12]: system_info()
```

```
System information
 -OS: Windows
 -Python: 3.12.11
 -Scipy: not installed in the notebook
 -FMPy: 0.3.25
 -FMU by: JModelica.org
 -FMI: 2.0
 -Type: CS
 -Name: BPL.Examples_TEST2.Batch
 -Generated: 2025-07-26T09:37:39
 -MSL: 3.2.2 build 3
 -Description: Bioprocess Library version 2.3.1
 -Interaction: FMU-explore for FMPy version 1.0.2
```

In [13]: `!lsb_release -a`

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

In [ ]: