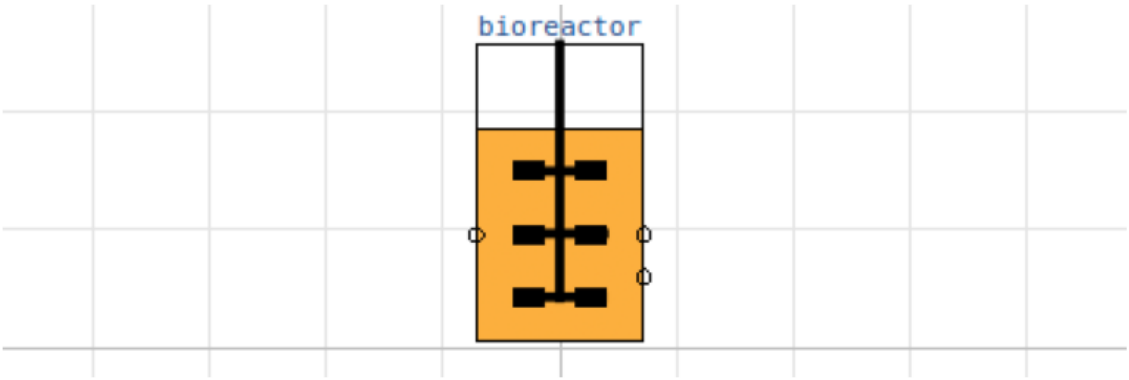
# BPL_TEST2_Batch - demo

In [1]:
```
run -i BPL_TEST2_Batch_fmpy_explore.py
```

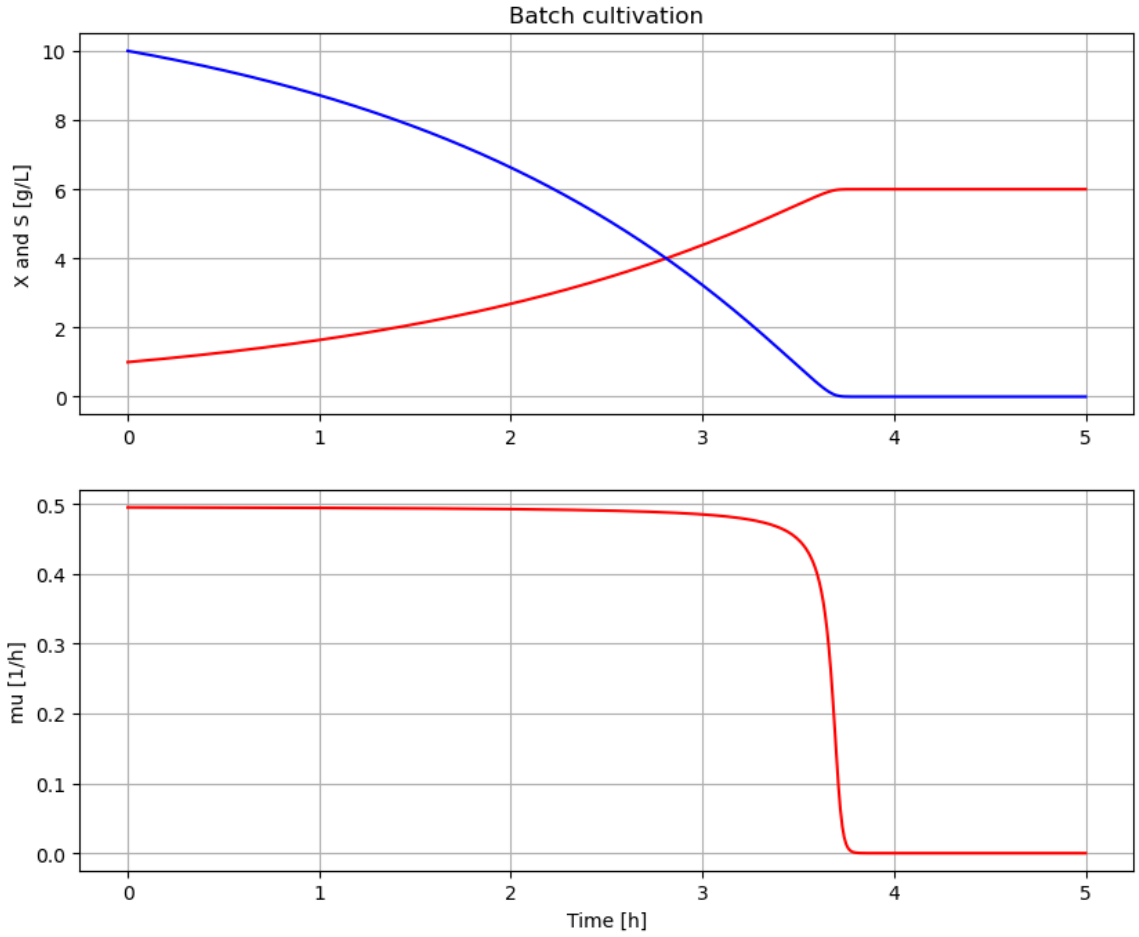
```
Windows - run FMU pre-compiled JModelica 2.14

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/uni
ts

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]
```

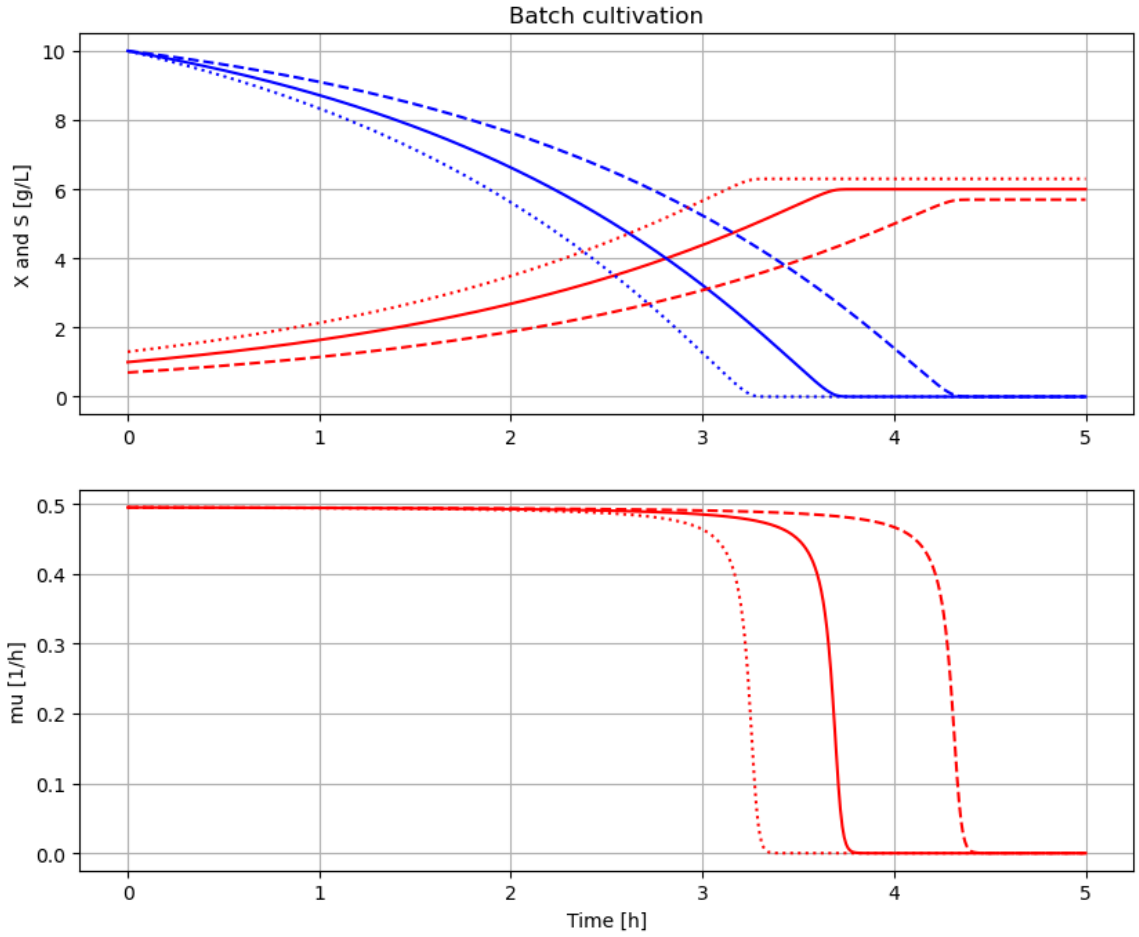
In [3]:
```
process_diagram()
```



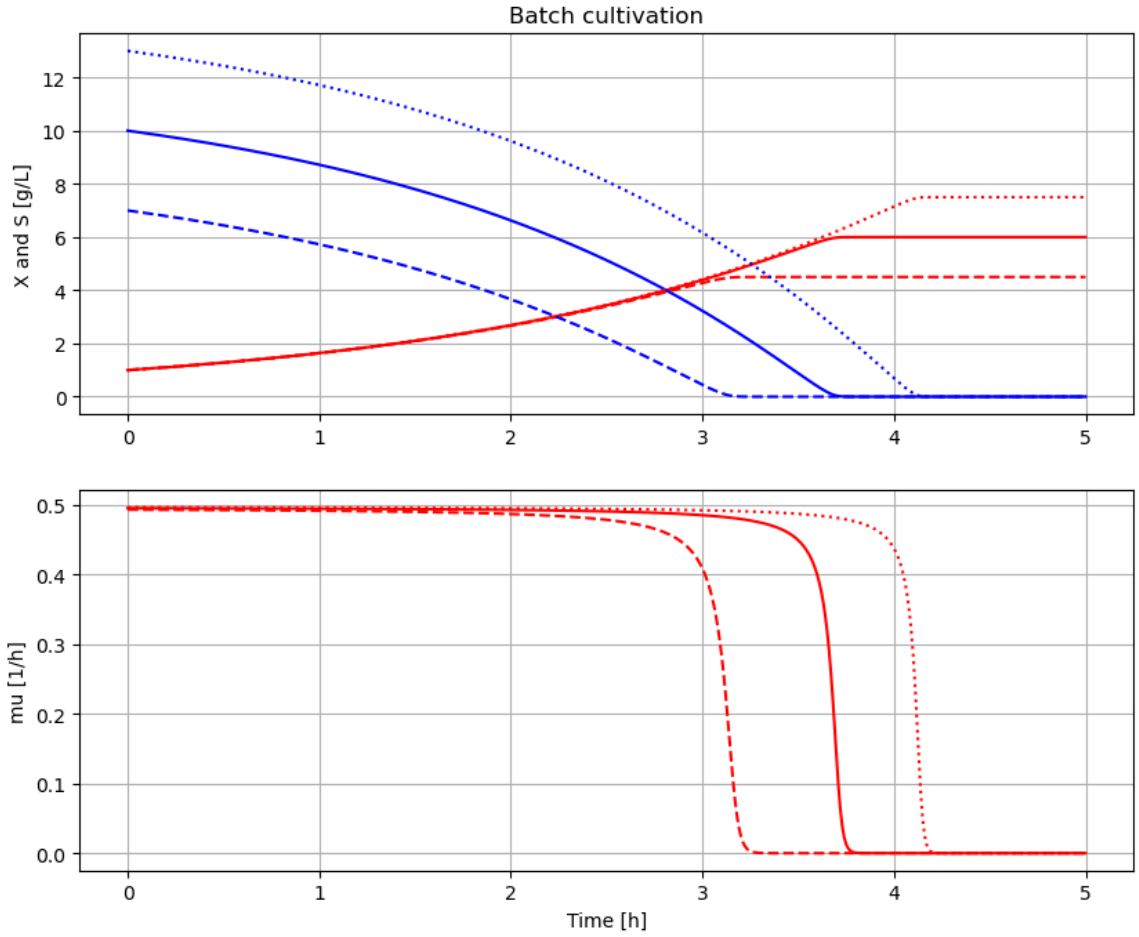

In [4]:
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu()
```



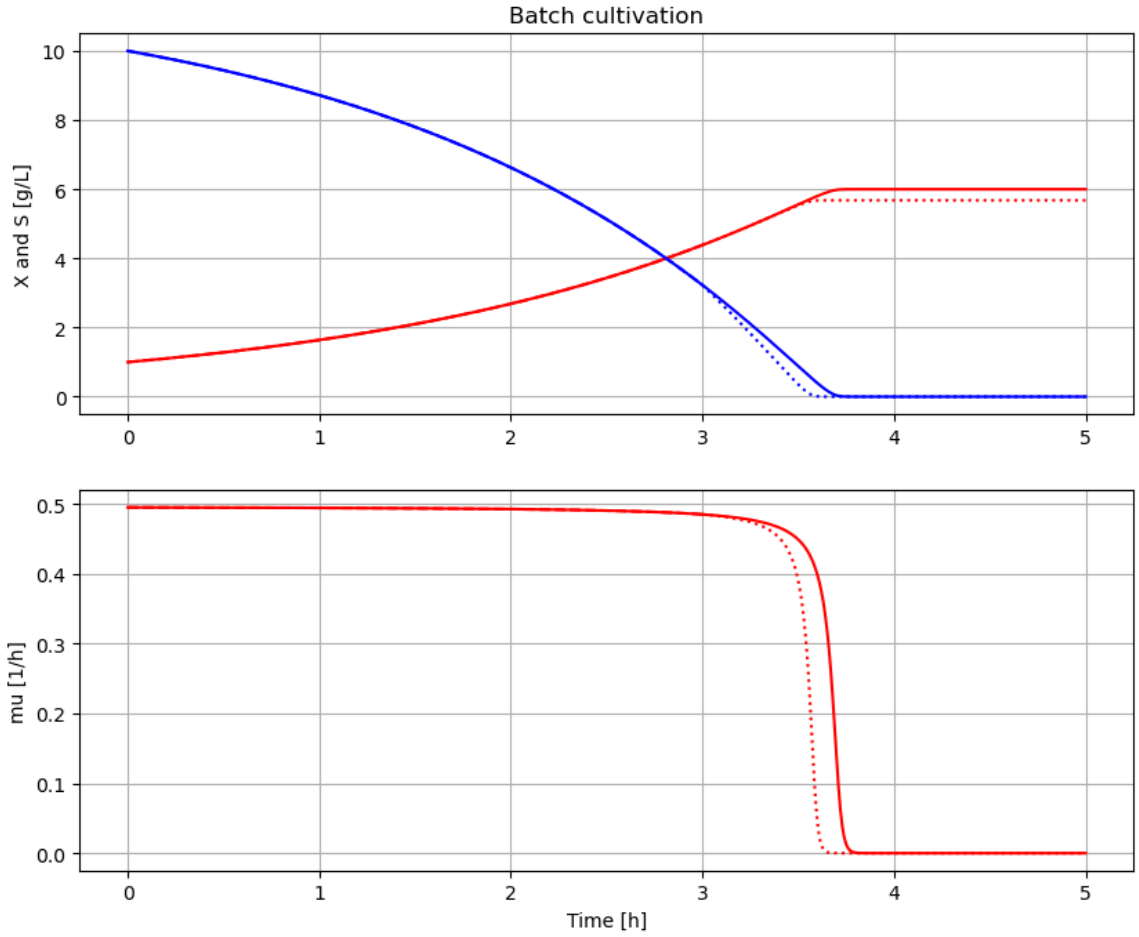

In [5]:
```
# Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_0=value); simu(5)

# Restore default value of VX_0
init(VX_0=1.0)
```




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

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




In [7]:
```
# 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)
```




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', 'liquidphase', 'MSL']
```

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

```
MSL: none
```

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

```
System information
 -OS: Windows
 -Python: 3.9.16
 -Scipy: not installed in the notebook
 -FMPy: 0.3.15
 -FMU by: JModelica.org
 -FMI: 2.0
 -Type: CS
 -Name: BPL_TEST2.Batch
 -Generated: 2023-09-02T07:30:42
 -MSL: 3.2.2 build 3
 -Description: Bioprocess Library version 2.1.2 prel
 -Interaction: FMU-explore for FMPy version 0.9.8
```

In [ ]: