# BPL_TEST2_Batch - demo

In [1]:
```
run -i BPL_TEST2_Batch_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/units

Note that both disp() and describe() takes values from the last simulation

Brief information about a command by help(), eg help(simu)
Key system information is listed with the command system_info()
```
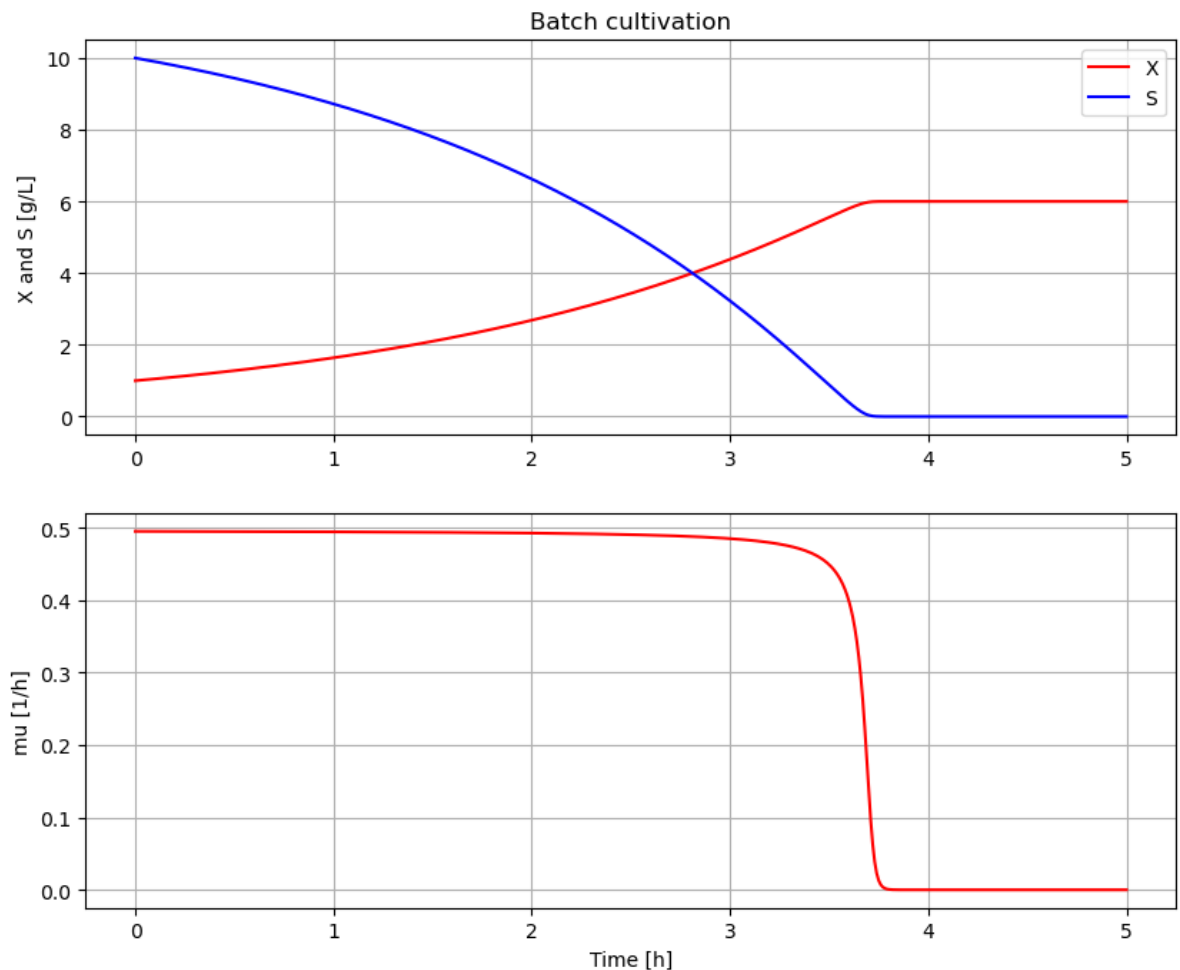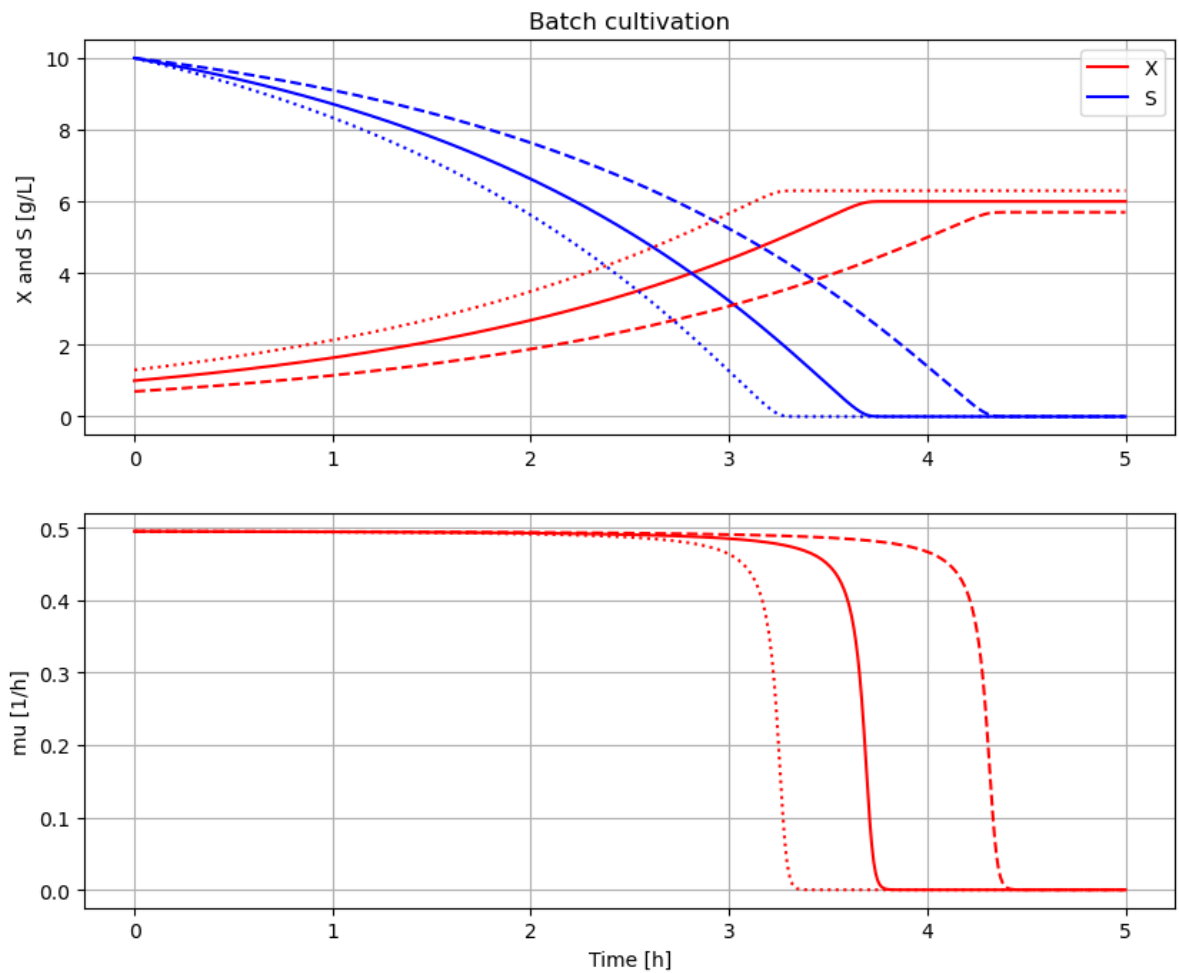
In [2]:
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

In [3]:
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu()
```

In [4]:
```python
# 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 [5]:
```python
# 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)
```
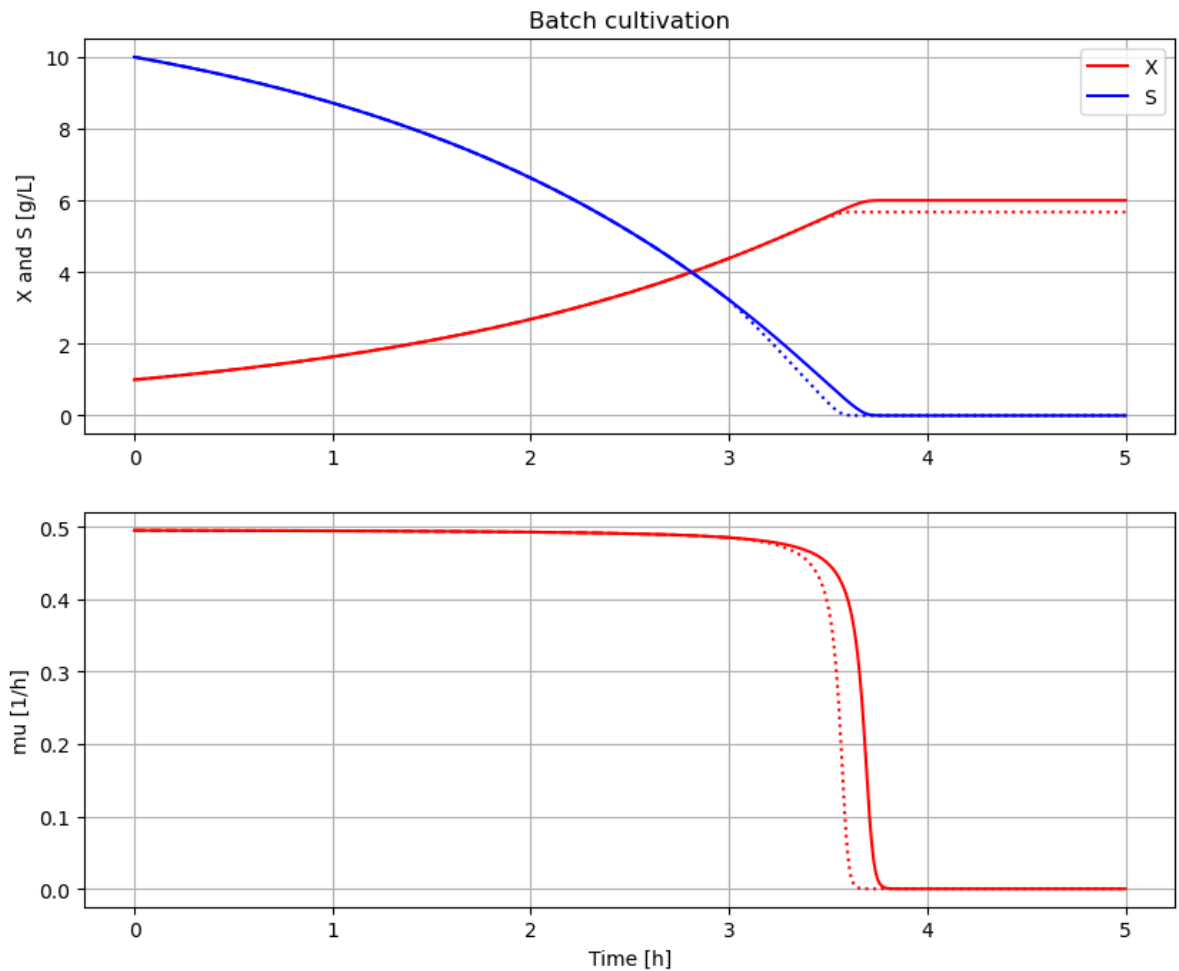
## Batch cultivation
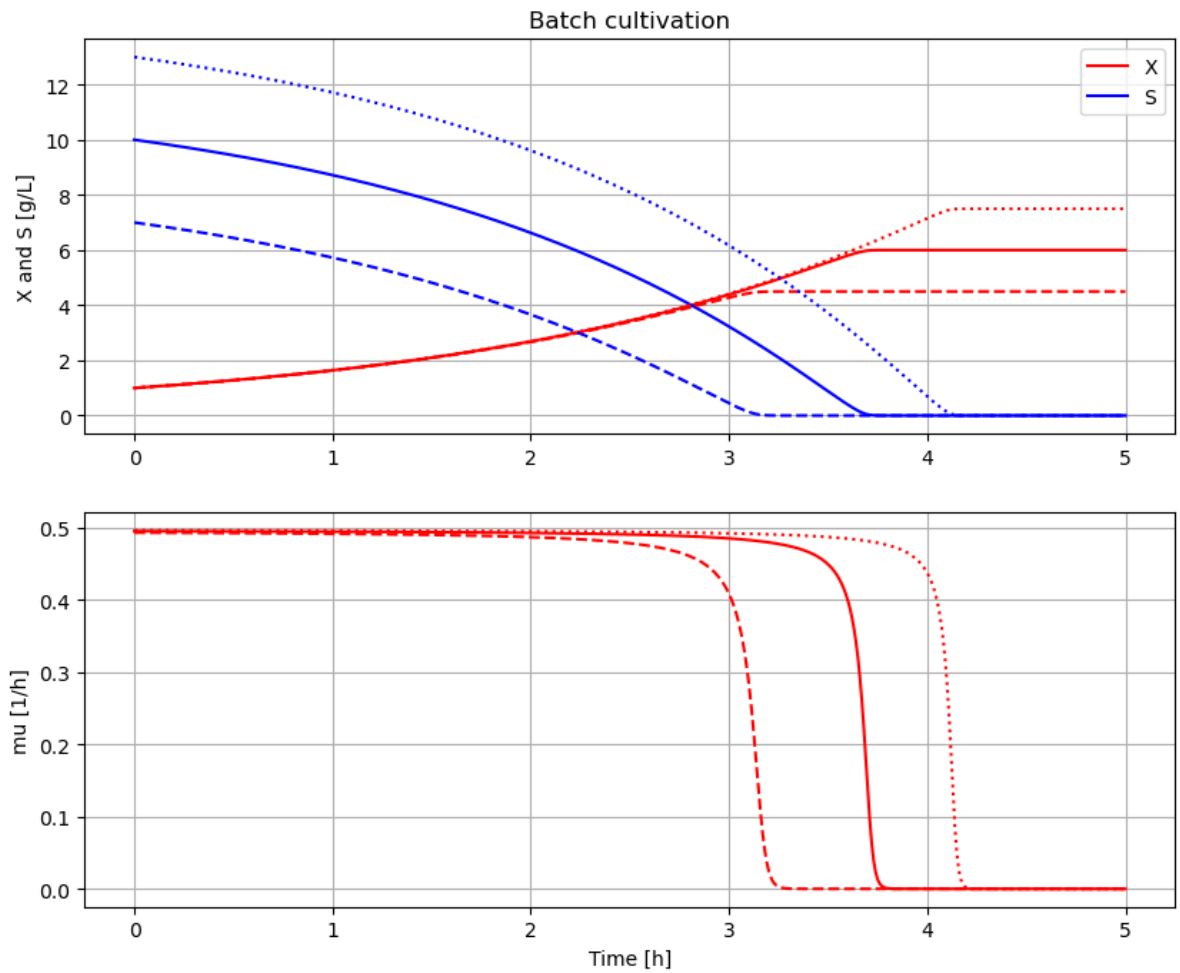


```
In [6]:  # Simulation where metabolism is changed after 3 hours
         newplot(plotType='TimeSeries')
         simu(5)

         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 [7]:  disp('culture')

         Y : 0.4
         qSmax : 1.25
         Ks : 0.1

In [8]:  describe('mu')

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

In [9]:  describe('parts')

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

In [10]: describe('MSL')

         MSL: none

In [11]: system_info()

         System information
          -OS: Windows
          -Python: 3.10.6
          -Scipy: not installed in the notebook
          -PyFMI: 2.10.0
          -FMU by: JModelica.org
          -FMI: 2.0
          -Type: FMUModelCS2
          -Name: BPL_TEST2.Batch
          -Generated: 2022-10-06T08:12:54
          -MSL: 3.2.2 build 3
          -Description: Bioprocess Library version 2.1.0
          -Interaction: FMU-explore version 0.9.6
```

In [ ]: