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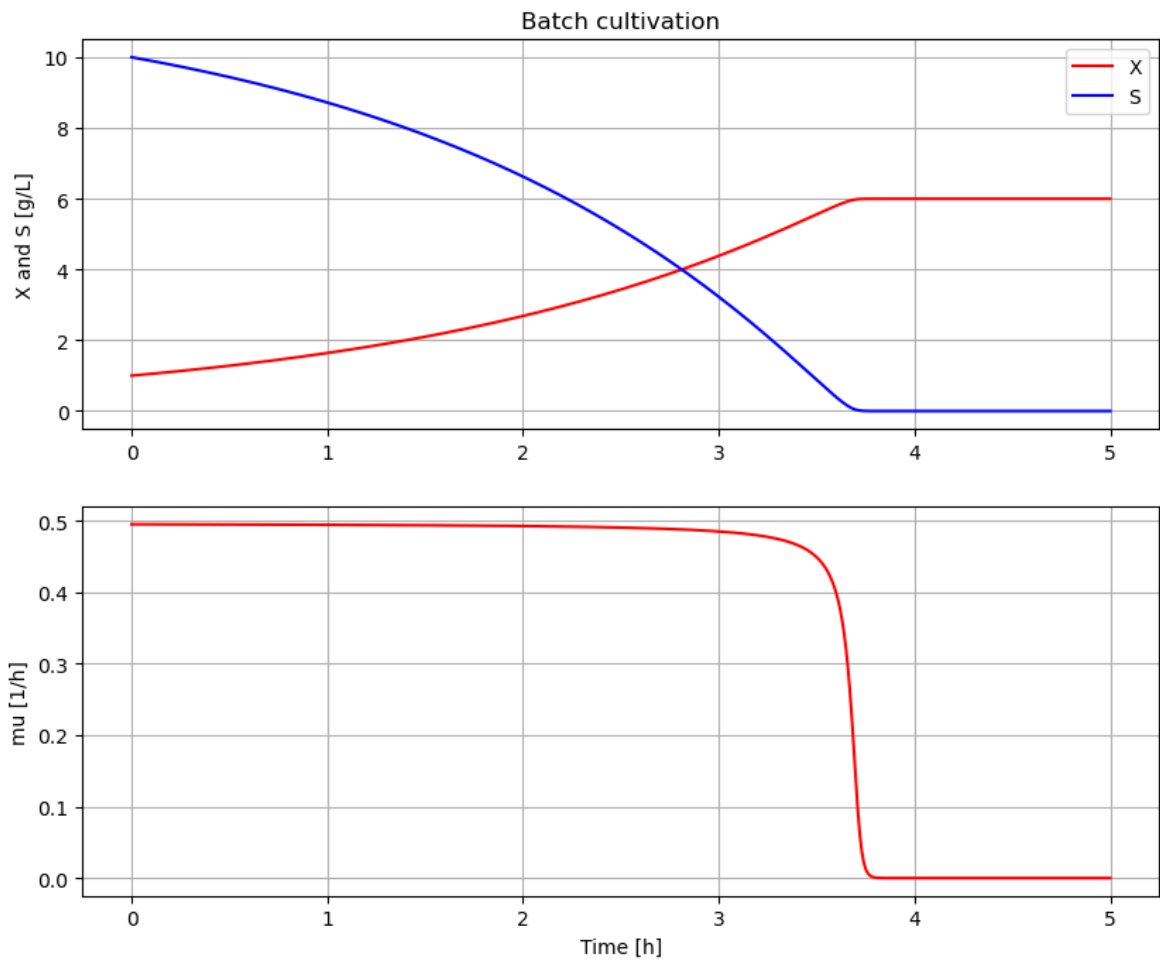
```
In [3]: process_diagram()
```
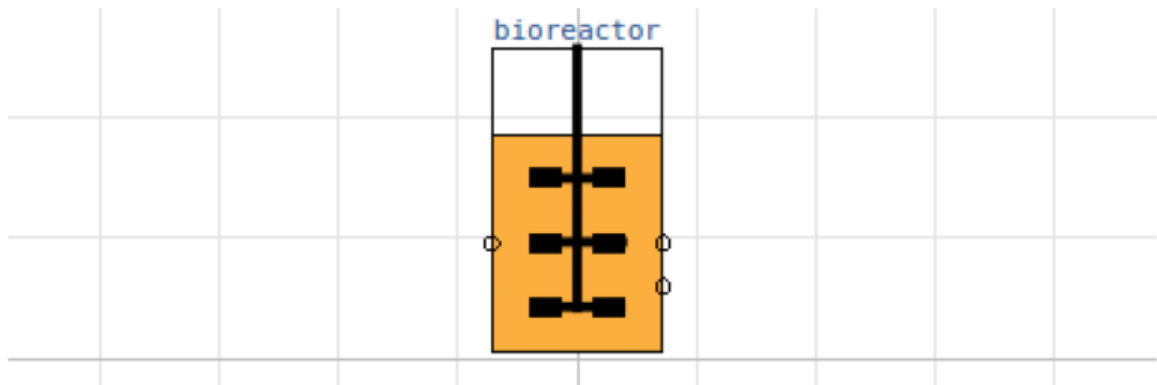


```
In [4]: disp('bioreactor', mode='long')
```

bioreactor.V_0 : V_0 : 1.0
bioreactor.m_0[1] : VX_0 : 0.0
bioreactor.m_0[2] : VS_0 : 0.0
bioreactor.culture.Y : Y : 0.5
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1

```
In [5]: # Simulation with default values of the process
        newplot(plotType='TimeSeries')
        simu()
```

Batch cultivation


```
In [6]:  # 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)
```

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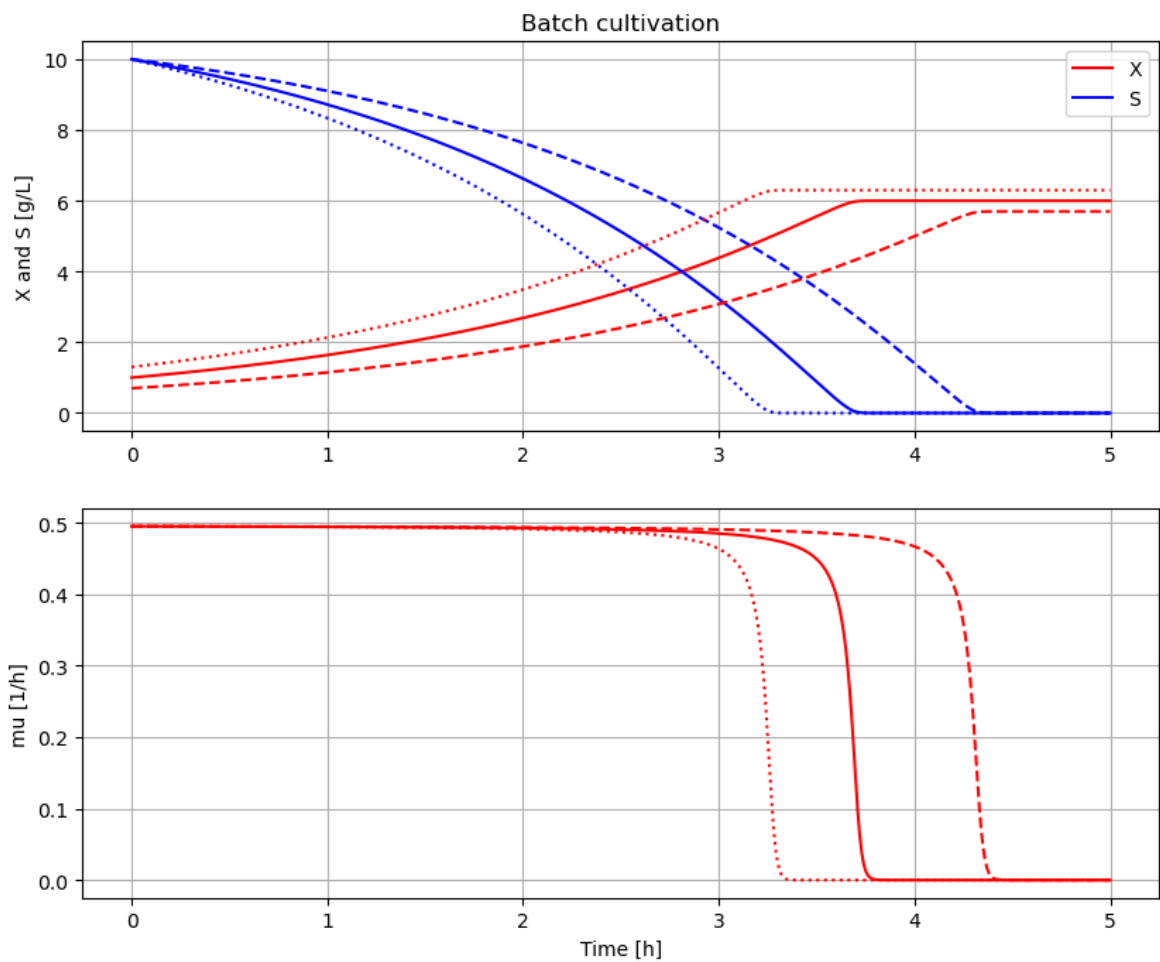
```
In [7]:  # Simulation were initial value of substrate VS_0 is varied
         newplot(plotType='TimeSeries')
         for value in [10, 7, 13]: init(VS_0=value); simu(5)

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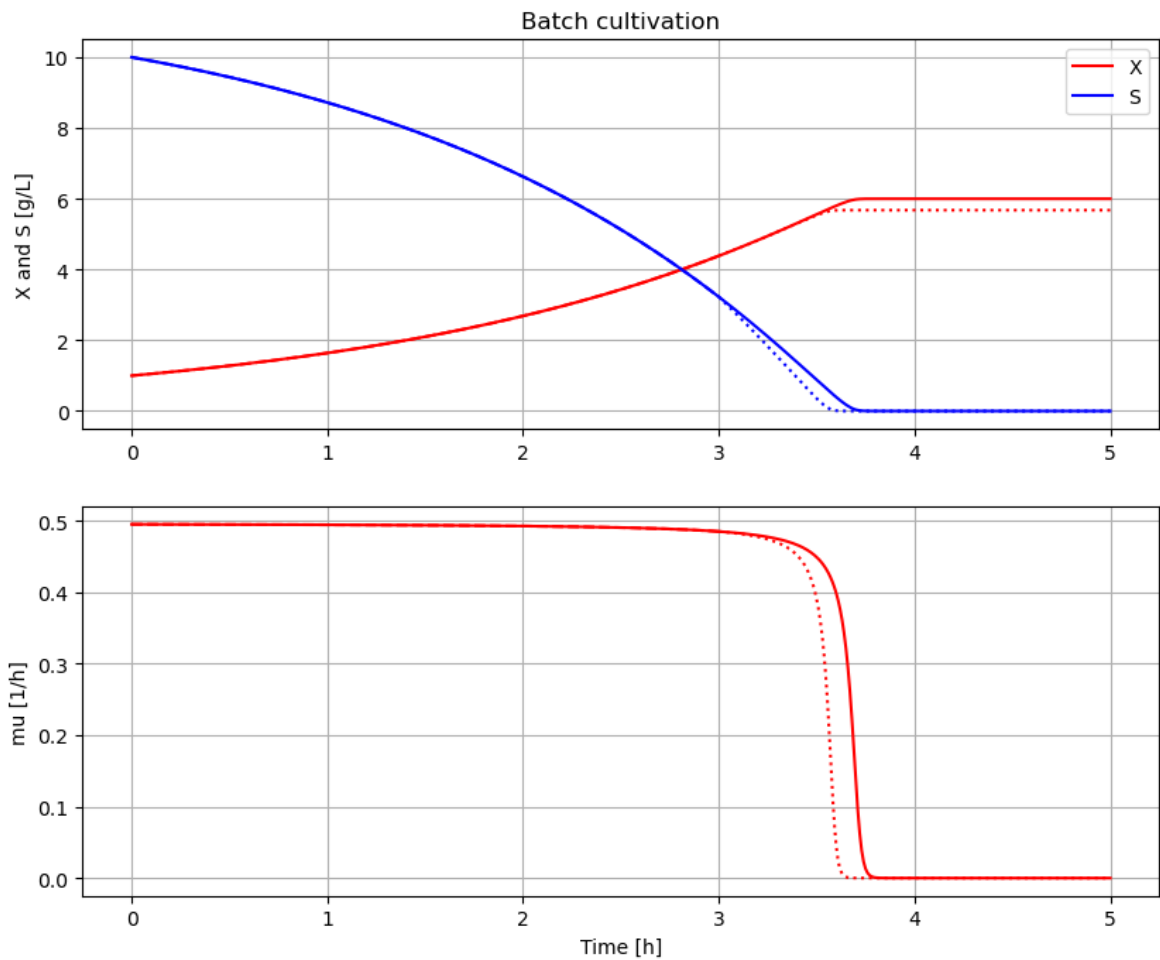
Batch cultivation
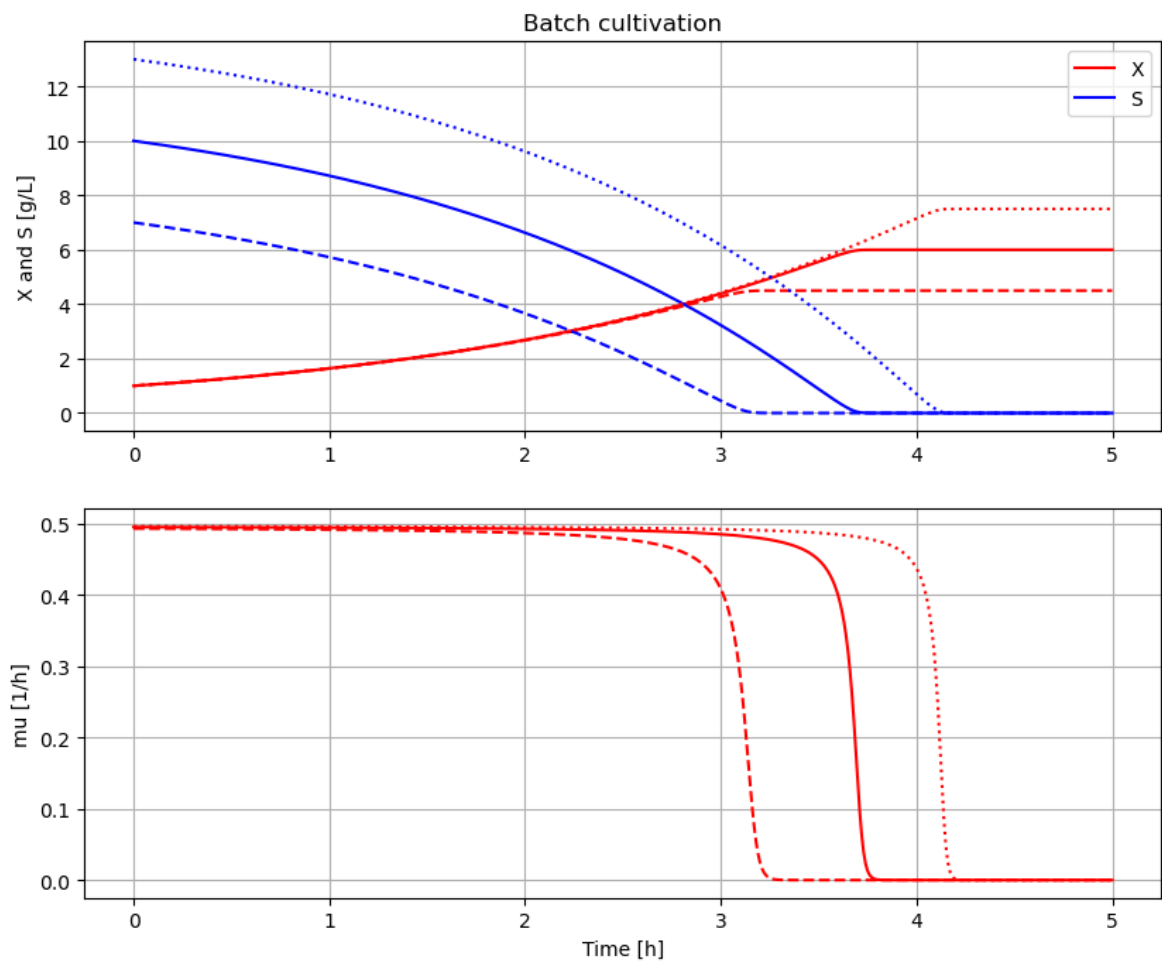

```
In [8]:   # Simulation where metabolism is changed after 3 hours
          newplot(plotType='TimeSeries')
          simu(5)

          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 [9]: `disp('culture')`

```
Y : 0.4
qSmax : 1.25
Ks : 0.1
```

In [10]: `describe('mu')`

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

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

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

In [12]: `describe('MSL')`

MSL: none

In [13]: `system_info()`

```
System information
 -OS: Windows
 -Python: 3.10.13
 -Scipy: not installed in the notebook
 -PyFMI: 2.11.0
 -FMU by: JModelica.org
 -FMI: 2.0
 -Type: FMUModelCS2
 -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 version 0.9.8
```

In [ ]: