BPL_TEST2_Batch - demo

```
In [1]: run -i BPL_TEST2_Batch_explore.py
```

Linux - run FMU pre-compiled OpenModelica

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 simul
ation
 - describe()   - describe culture, broth, parameters, variables with value
s/units

Note that both disp() and describe() takes values from the last simulation
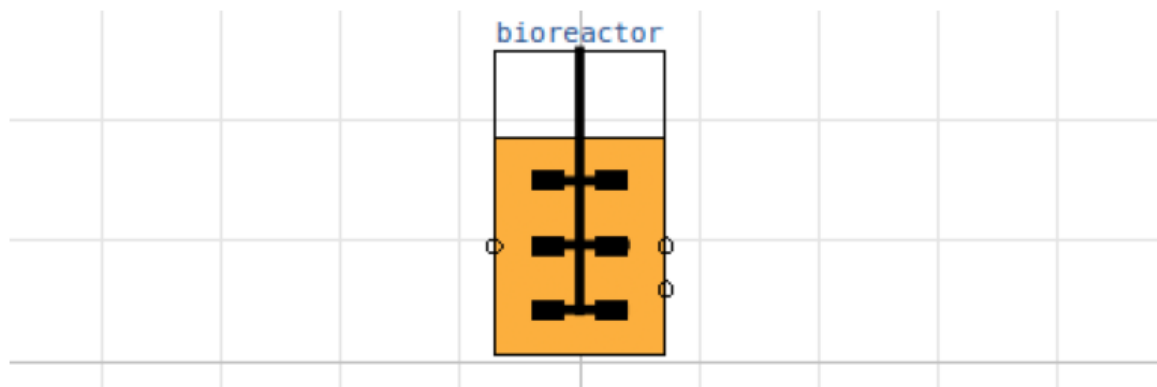and the command process_diagram() brings up the main configuration

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.

disp('bioreactor', mode='long')

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

```
Could not find cannot import name 'dopri5' from 'assimulo.lib' (/home/janp
eter/miniconda3/envs/pyfmi/lib/python3.12/site-packages/assimulo/lib/__ini
t__.py)
Could not find cannot import name 'rodas' from 'assimulo.lib' (/home/janpe
ter/miniconda3/envs/pyfmi/lib/python3.12/site-packages/assimulo/lib/__init
__.py)
Could not find cannot import name 'odassl' from 'assimulo.lib' (/home/janp
eter/miniconda3/envs/pyfmi/lib/python3.12/site-packages/assimulo/lib/__ini
t__.py)
Could not find ODEPACK functions.
Could not find RADAR5
Could not find GLIMDA.
```
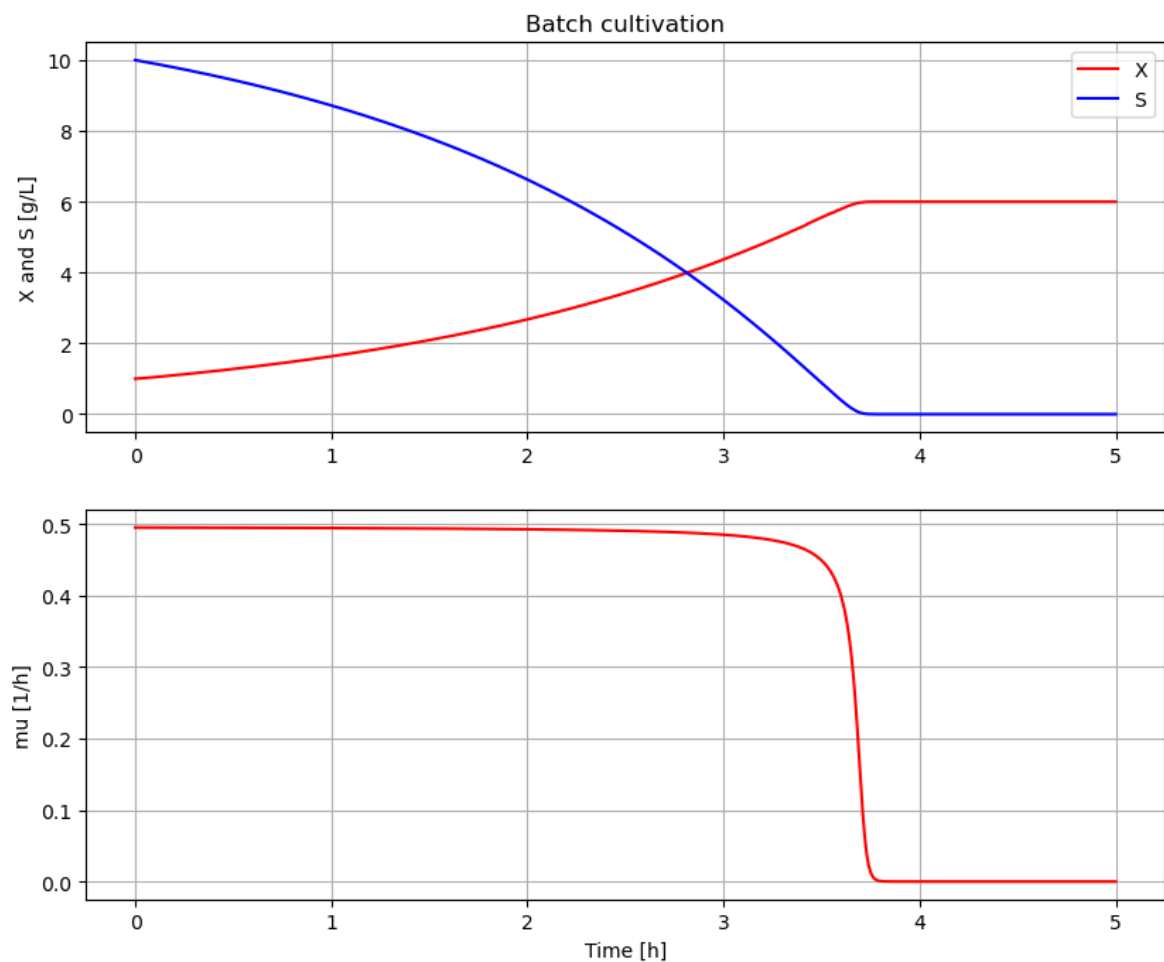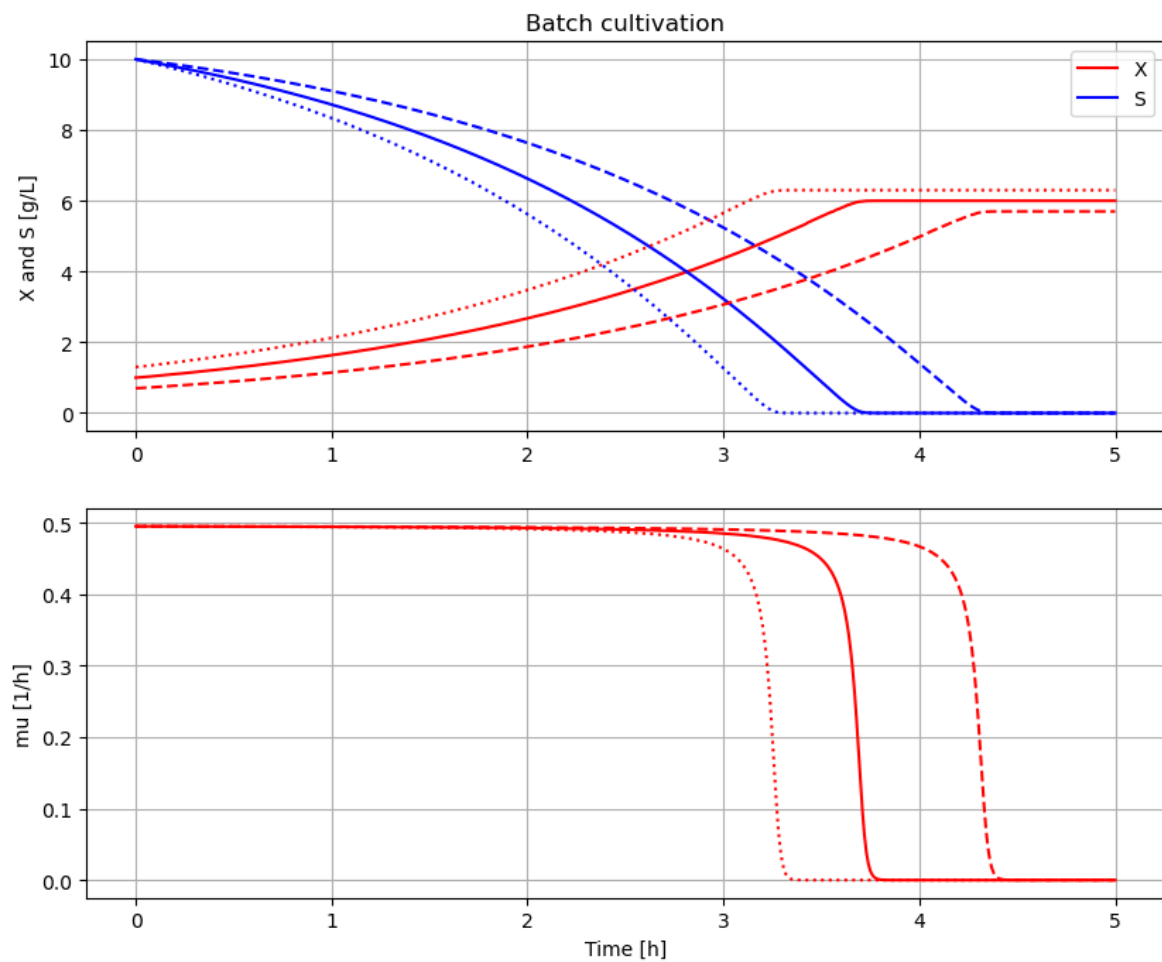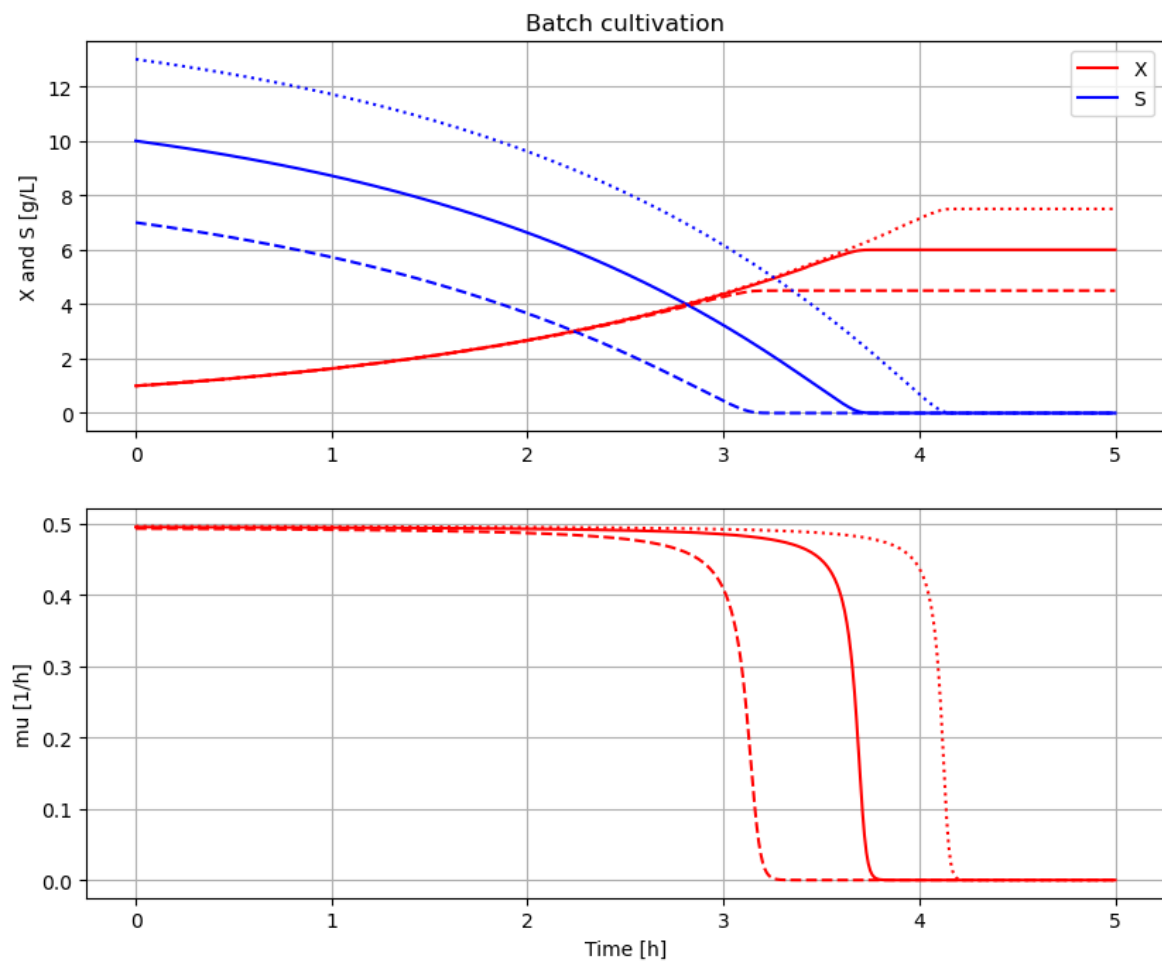

In [5]:
```python
# Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

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

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

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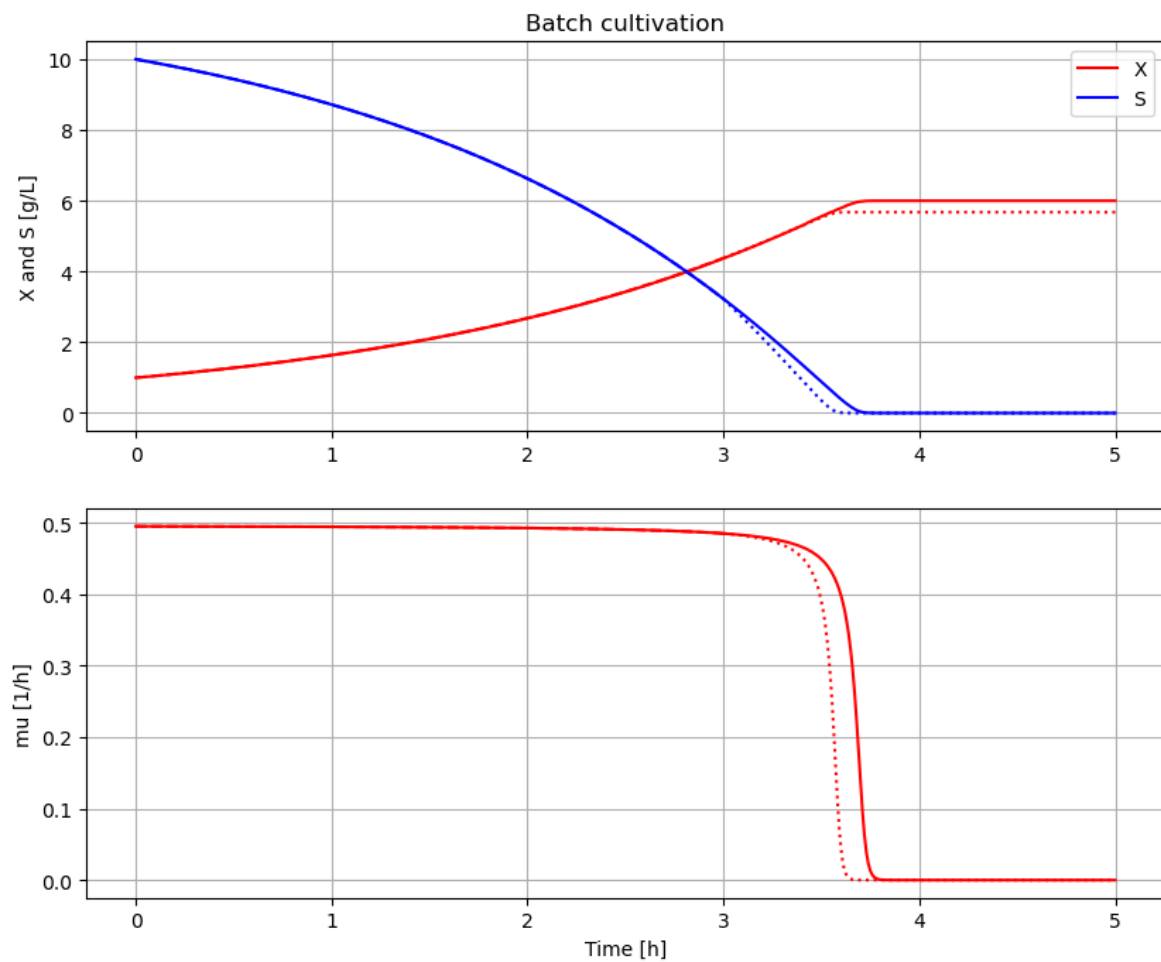
Batch cultivation

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)
```

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']

In [11]: describe('MSL')

        MSL: 4.1.0 - used components: none

In [12]: system_info()
```

```
System information
 -OS: Linux
 -Python: 3.12.9
 -Scipy: not installed in the notebook
 -PyFMI: 2.18.0
 -FMU by: OpenModelica Compiler OpenModelica 1.26.0~dev-200-gcb3254b
 -FMI: 2.0
 -Type: FMUModelME2
 -Name: BPL.Examples_TEST2.Batch
 -Generated: 2025-07-28T07:58:02Z
 -MSL: 4.1.0
 -Description: Bioprocess Library version 2.3.1
 -Interaction: FMU-explore version 1.0.0
```

In [13]: `!lsb_release -a`

```
No LSB modules are available.
Distributor ID: Ubuntu
Description:    Ubuntu 24.04.3 LTS
Release:        24.04
Codename:       noble
```

In [ ]: