

# BPL\_TEST2\_Batch - demo

```
In [12]: 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

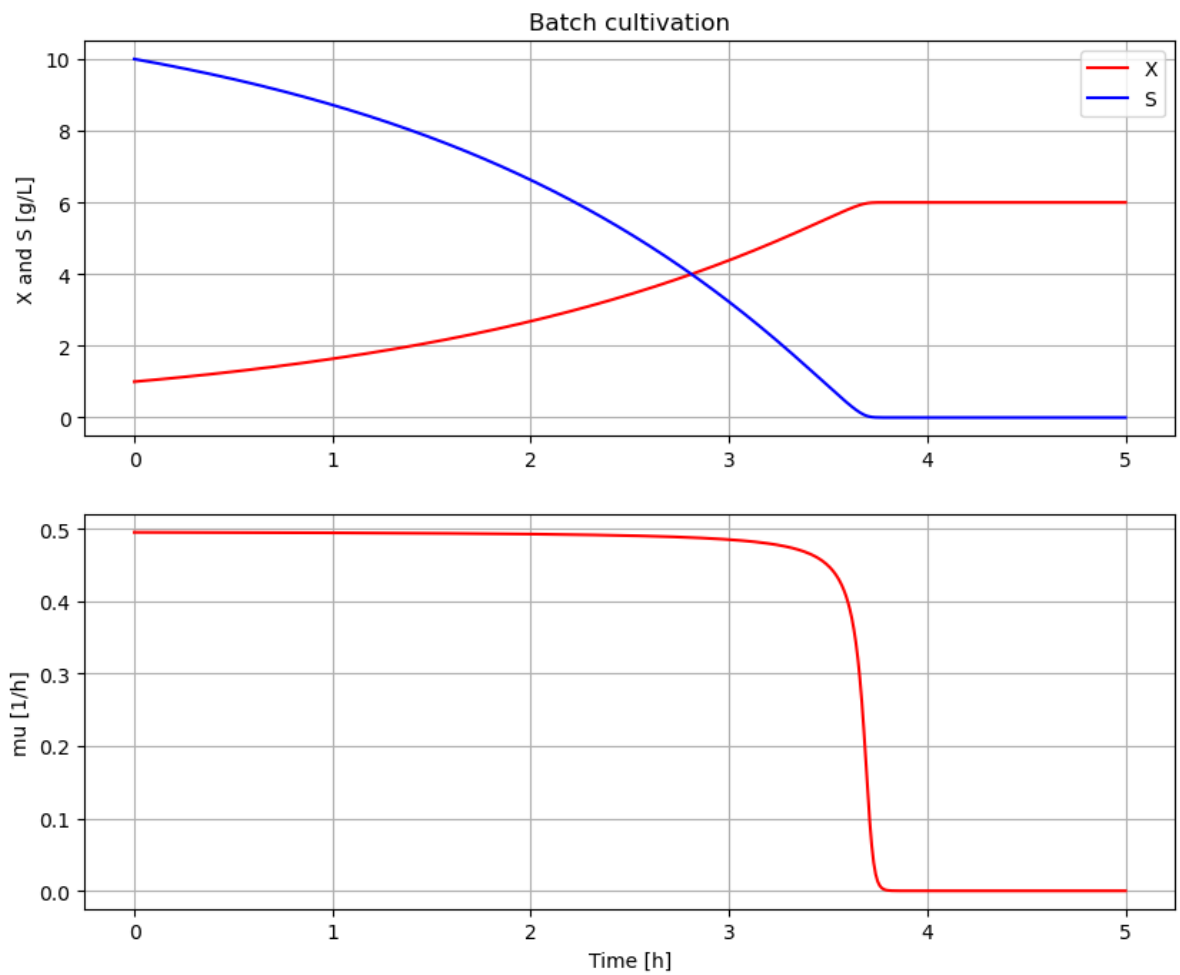
Brief information about a command by help(), eg help(simu)

Key system information is listed with the command system\_info()

<Figure size 984.252x787.402 with 0 Axes>

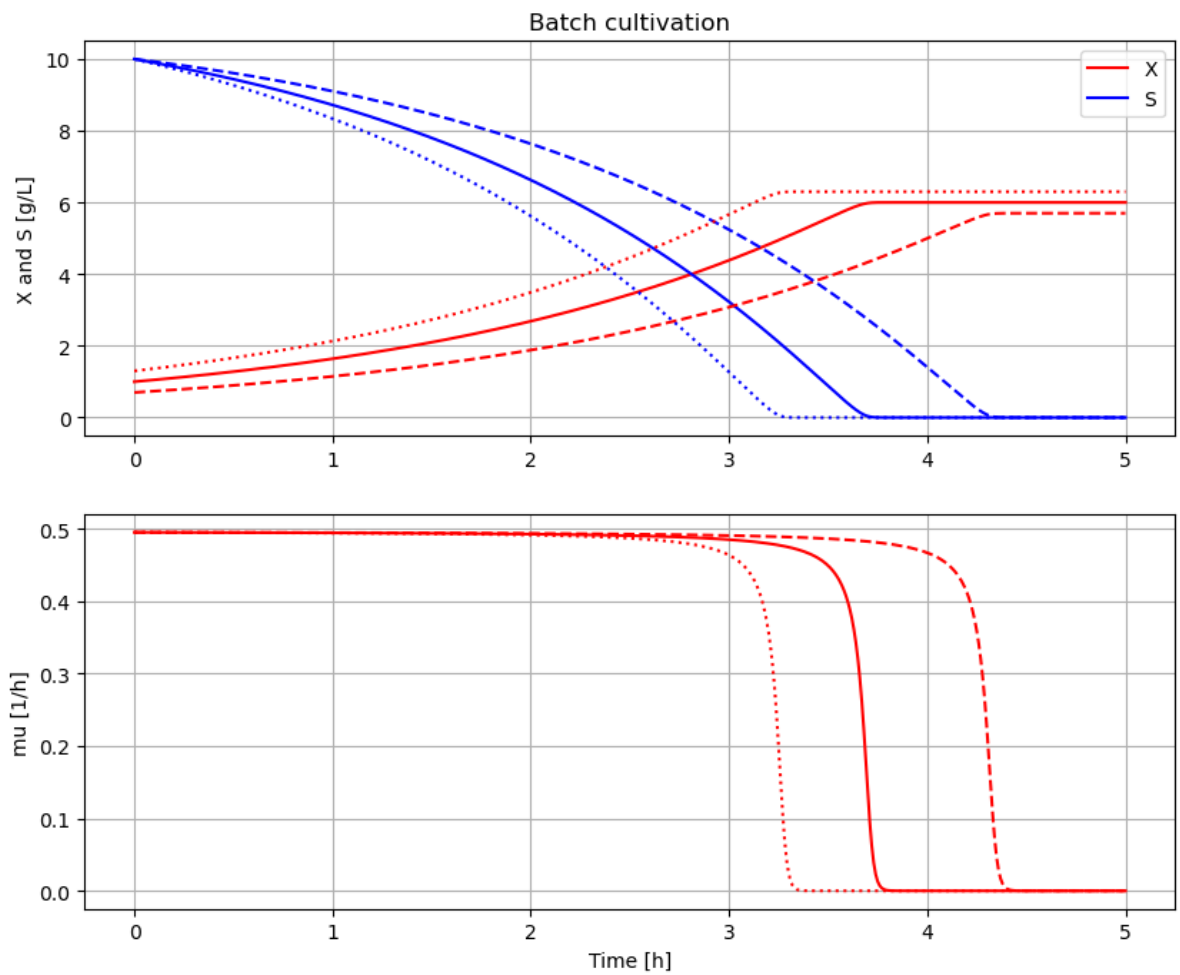
```
In [13]: %matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

```
In [14]: # Simulation with default values of the process
newplot(plotType='TimeSeries')
simu()
```



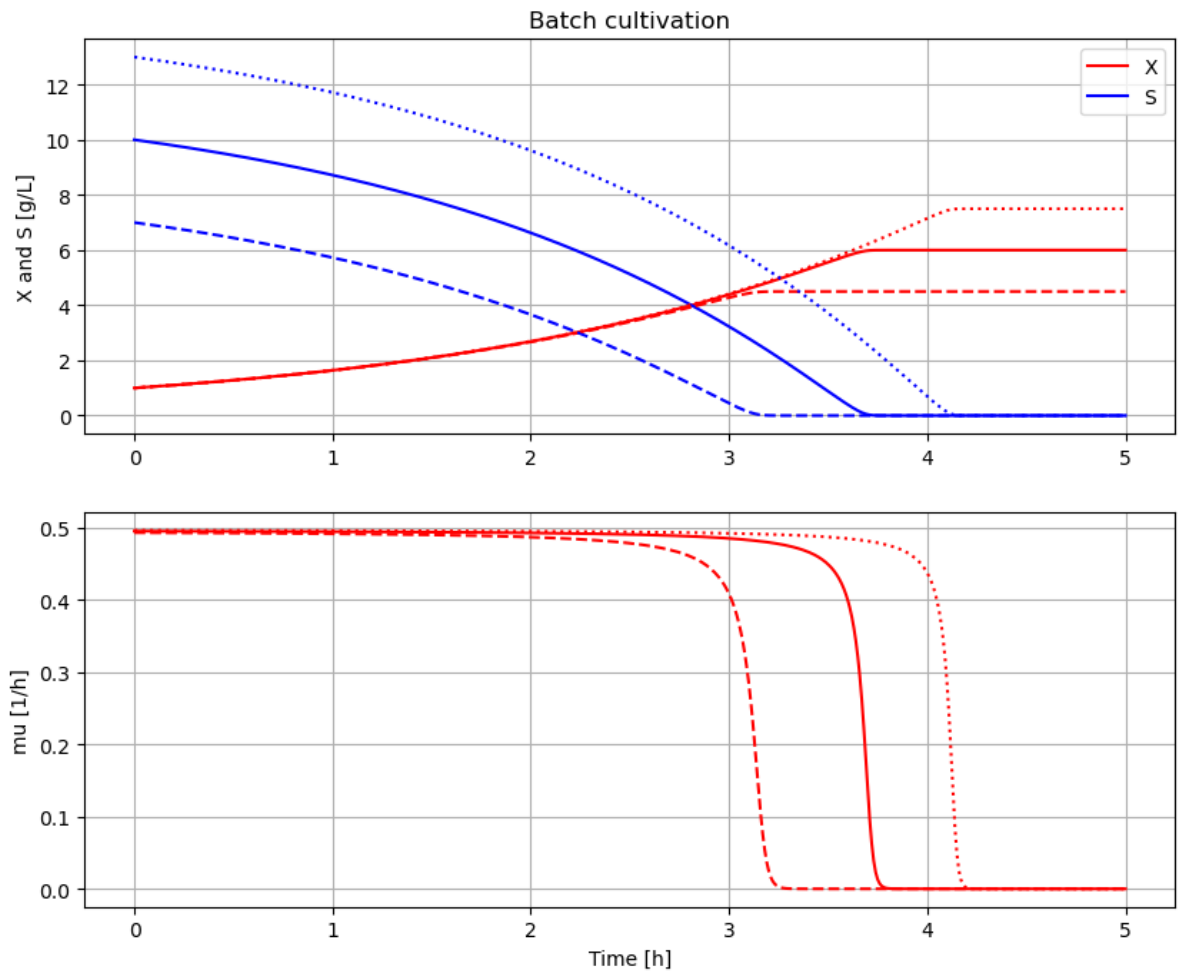
```
In [15]: # Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_0=value); simu(5)

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



```
In [16]: # 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)

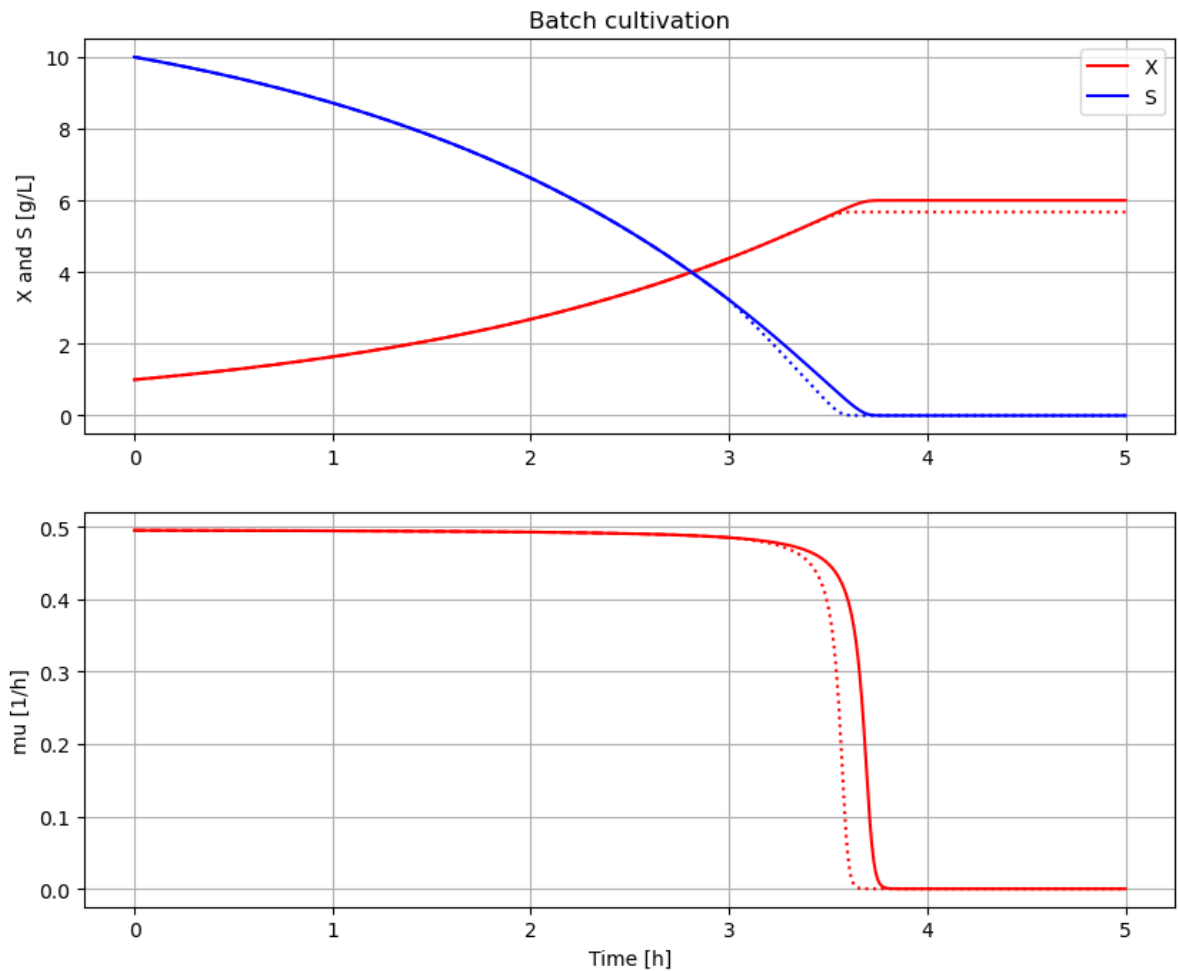
# Restore default value of VS_0
init(VS_0=10)
```



```
In [17]: # 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 [18]: disp('culture')
```

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

```
In [19]: describe('mu')
```

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

```
In [20]: describe('parts')
```

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

```
In [21]: describe('MSL')
```

```
MSL: none
```

```
In [22]: 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: 2023-03-30T09:07:34
-MSL: 3.2.2 build 3
-Description: Bioprocess Library version 2.1.1
-Interaction: FMU-explore version 0.9.7
```

In [ ]: