

BPL_TEST2_Batch - demo

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

Windows - run FMU pre-compiled JModelica 2.14

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 simulation
- describe() - describe culture, broth, parameters, variables with values/units

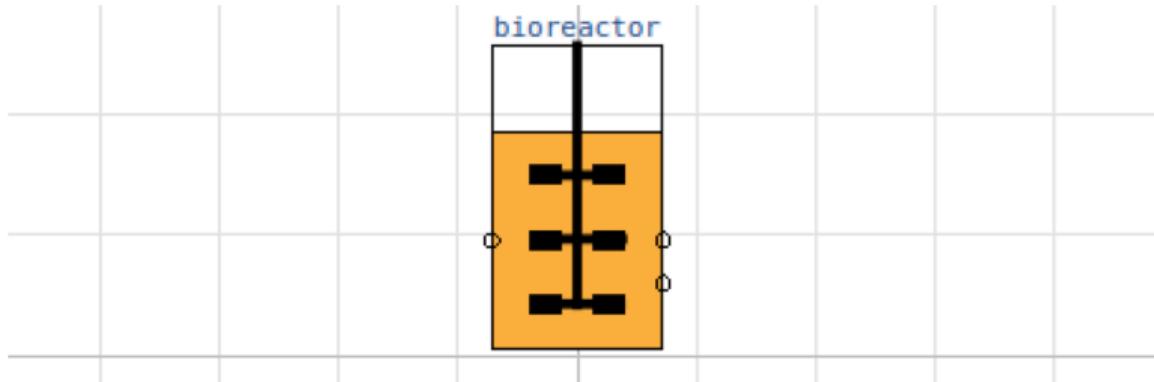
Note that both disp() and describe() takes values from the last simulation and the command process_diagram() brings up the main configuration

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]
```

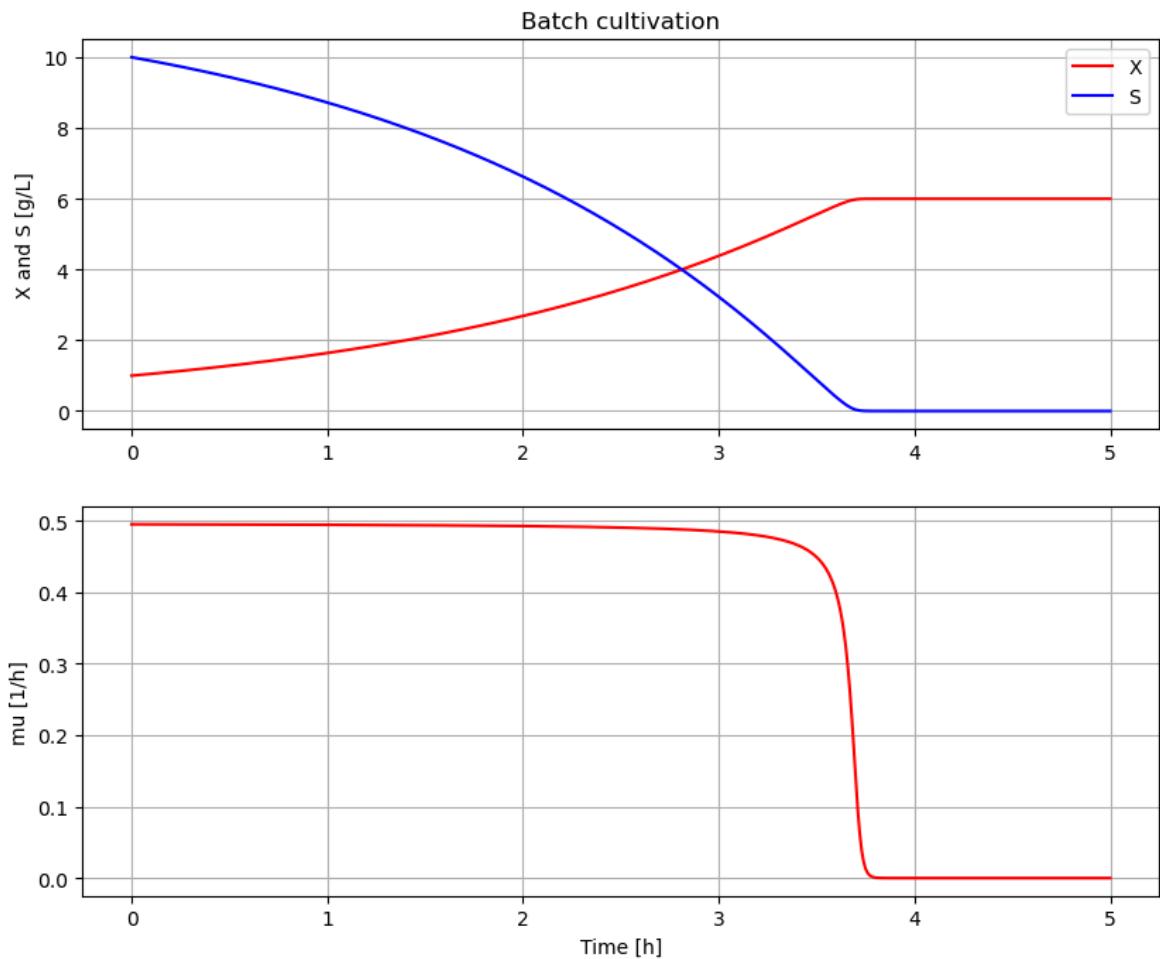
```
In [3]: process_diagram()
```

No processDiagram.png file in the FMU, but try the file on disk.



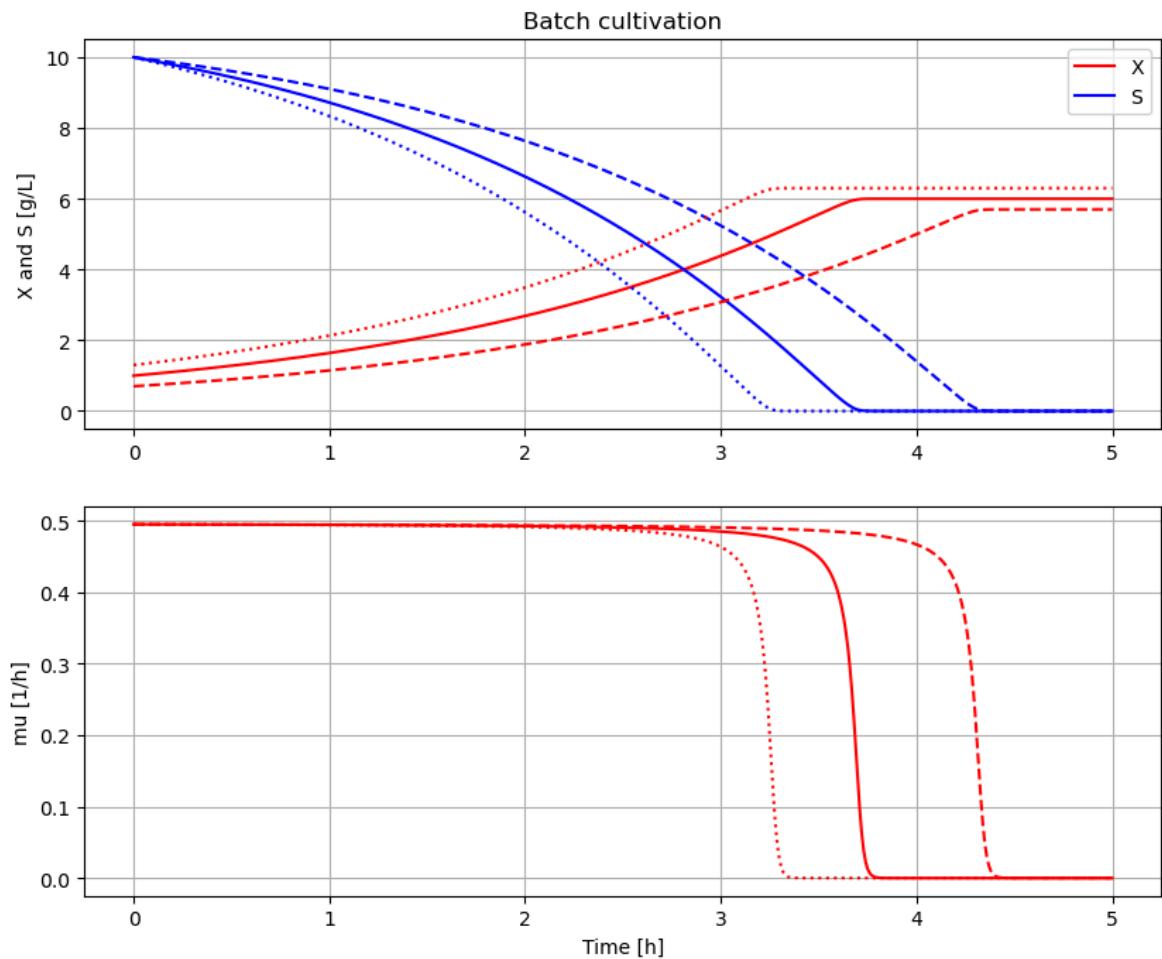
```
disp('bioreactor', mode='long')
```

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



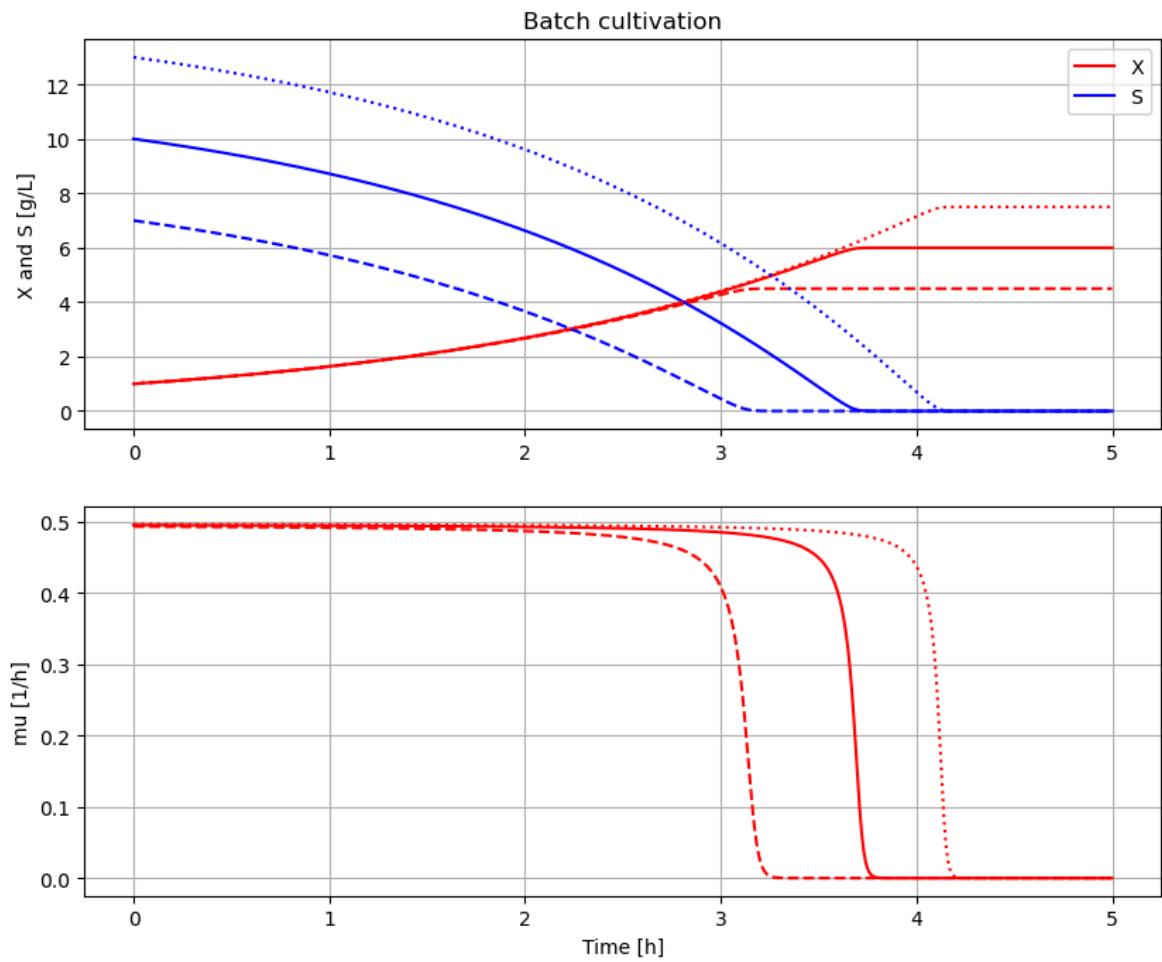
```
In [5]: # Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

# 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)

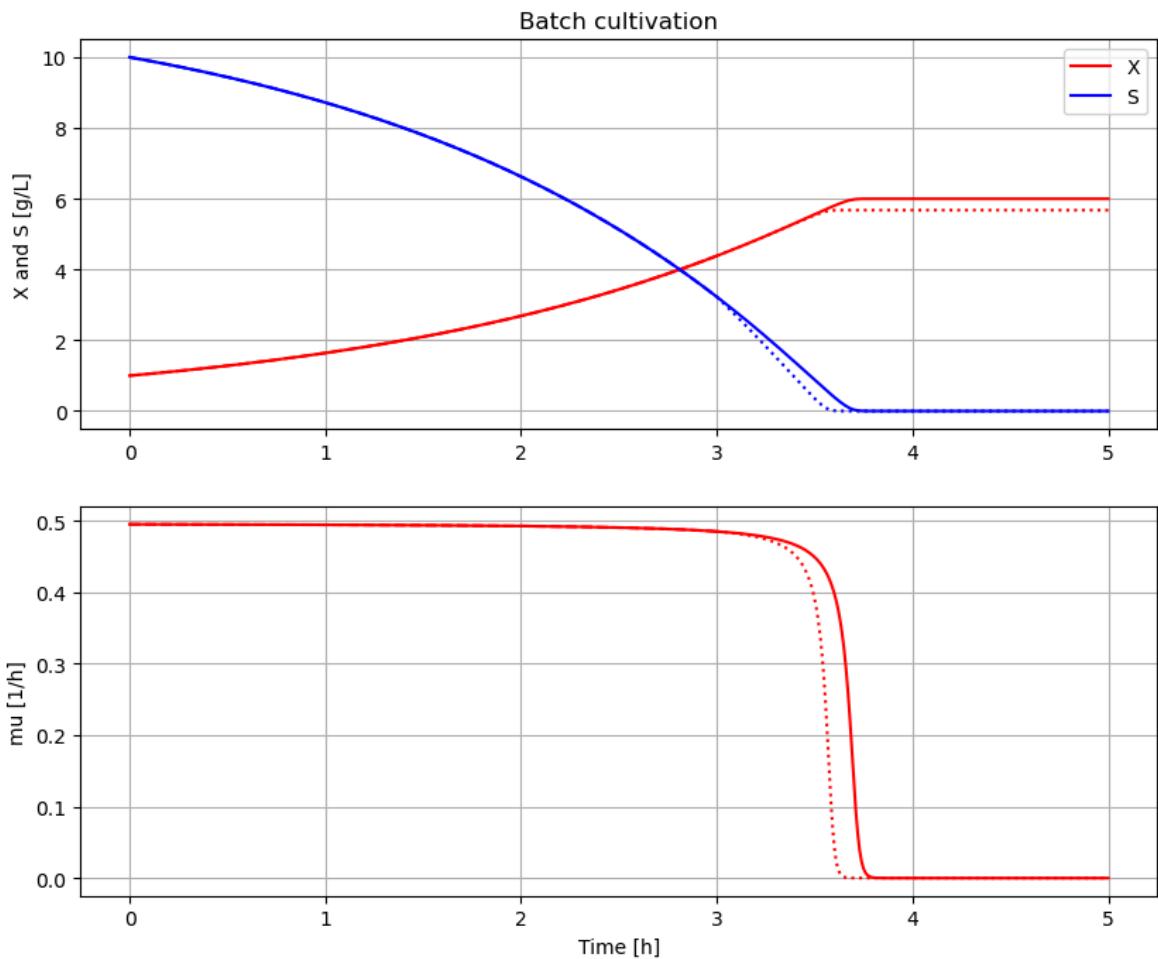
# Restore default value of VS_start
init(VS_start=10)
```



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

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

```
MSL: none
```

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

System information

- OS: Windows
- Python: 3.12.11
- Scipy: not installed in the notebook
- PyFMI: 2.19.0
- FMU by: JModelica.org
- FMI: 2.0
- Type: FMUModelCS2
- Name: BPL.Examples_TEST2.Batch
- Generated: 2025-07-26T09:37:39
- MSL: 3.2.2 build 3
- Description: Bioprocess Library version 2.3.1
- Interaction: FMU-explore version 1.0.2

In [13]: `!lsb_release -a`

```
'lsb_release' is not recognized as an internal or external command,  
operable program or batch file.
```

In []: