

## BPL\_TEST2\_Batch - demo

```
In [1]: run -i BPL_TEST2_Batch_fmpy_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 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

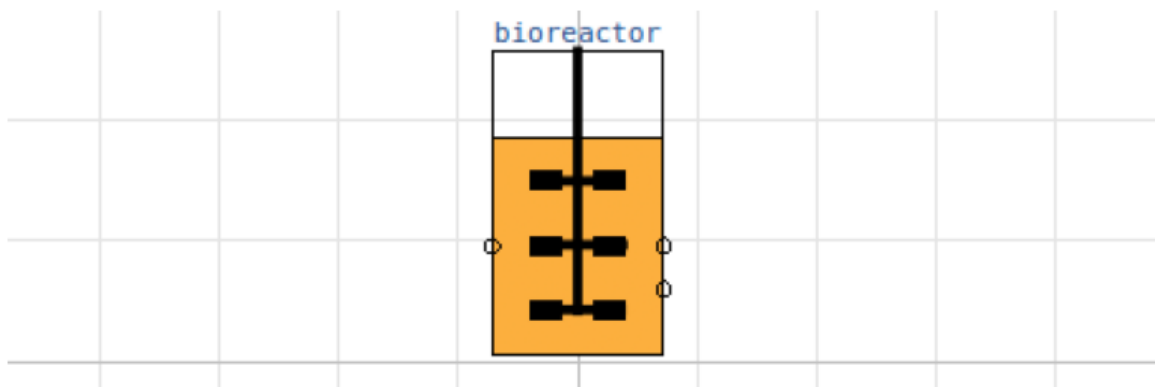
Brief information about a command by help(), eg help(simu)

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

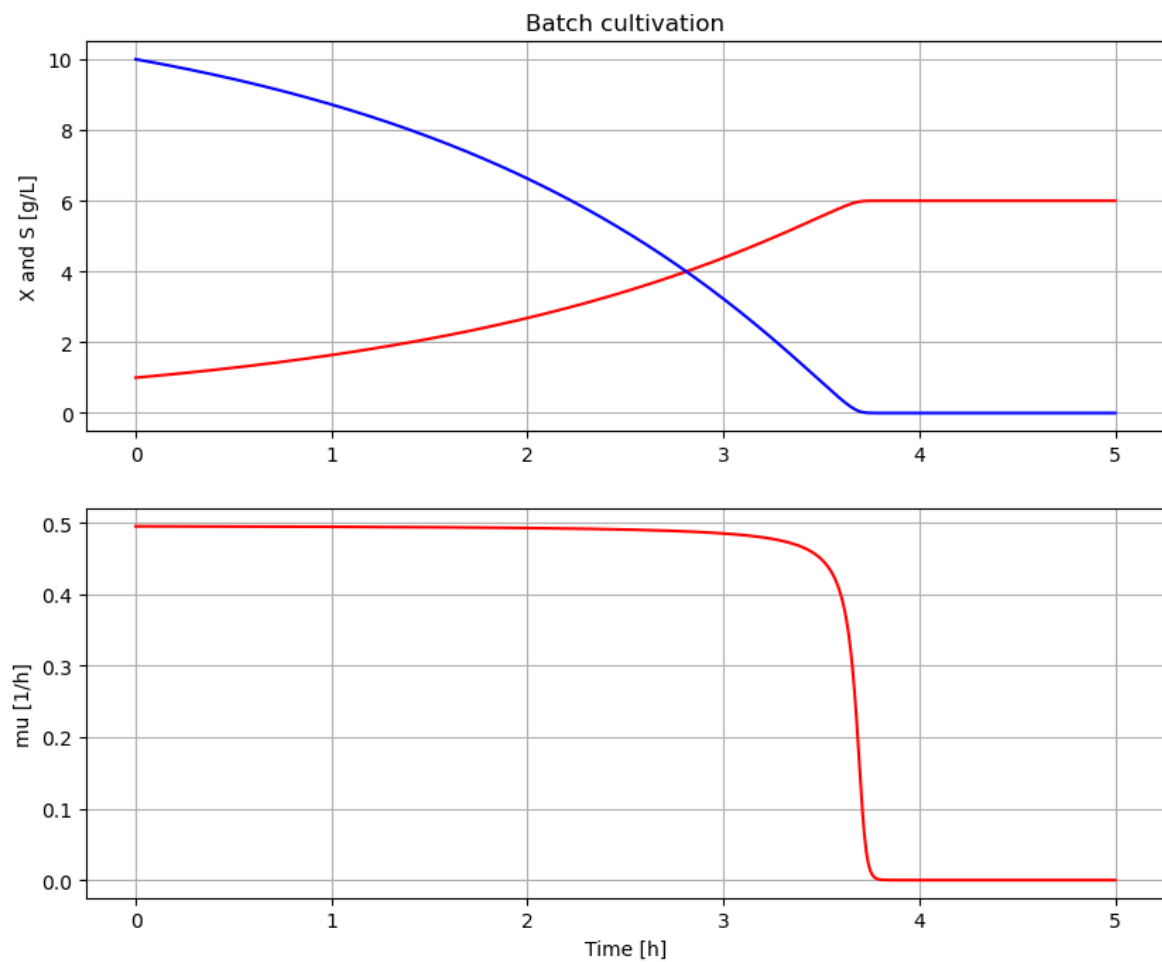
```
In [2]: %matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

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

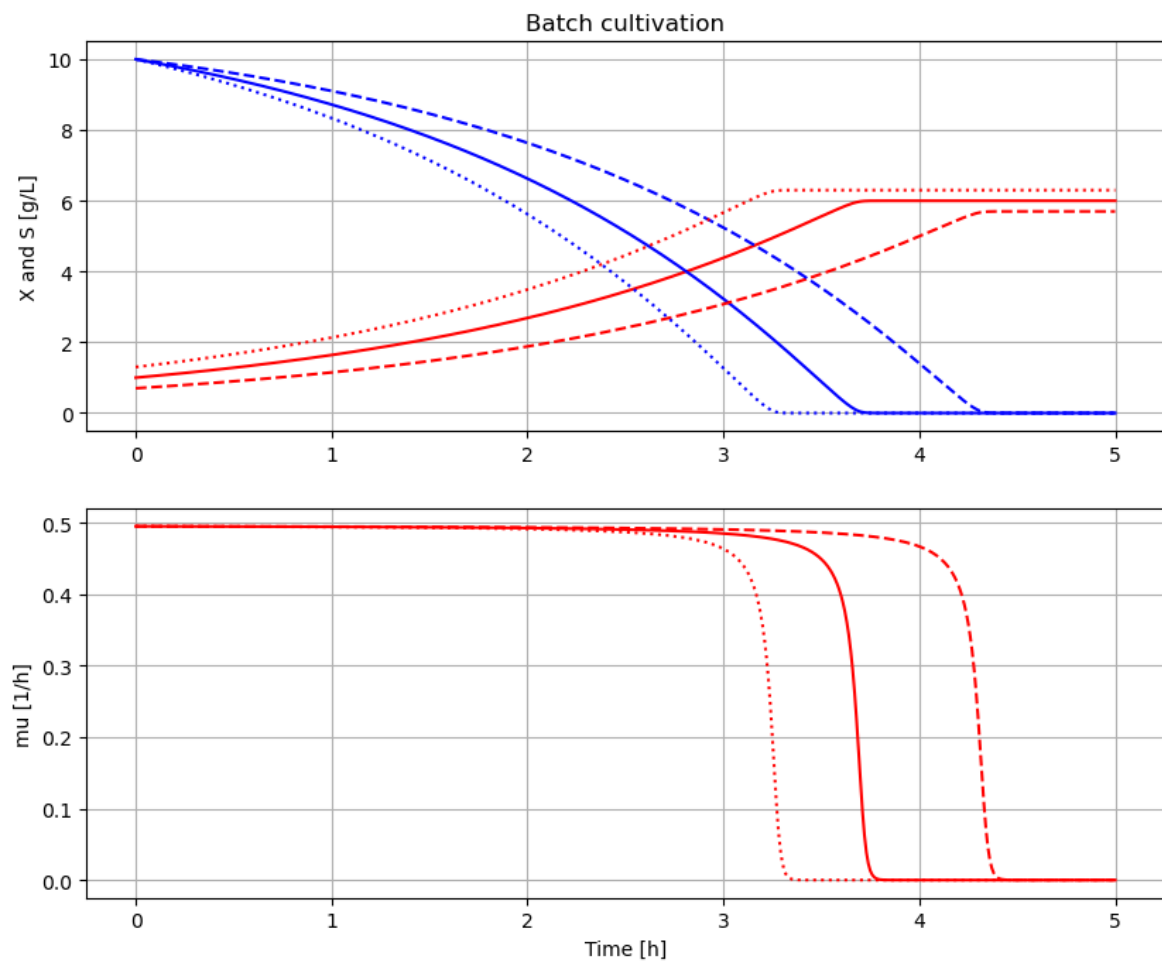


```
In [4]: # Simulation with default values of the process
newplot(plotType='TimeSeries')
simu()
```



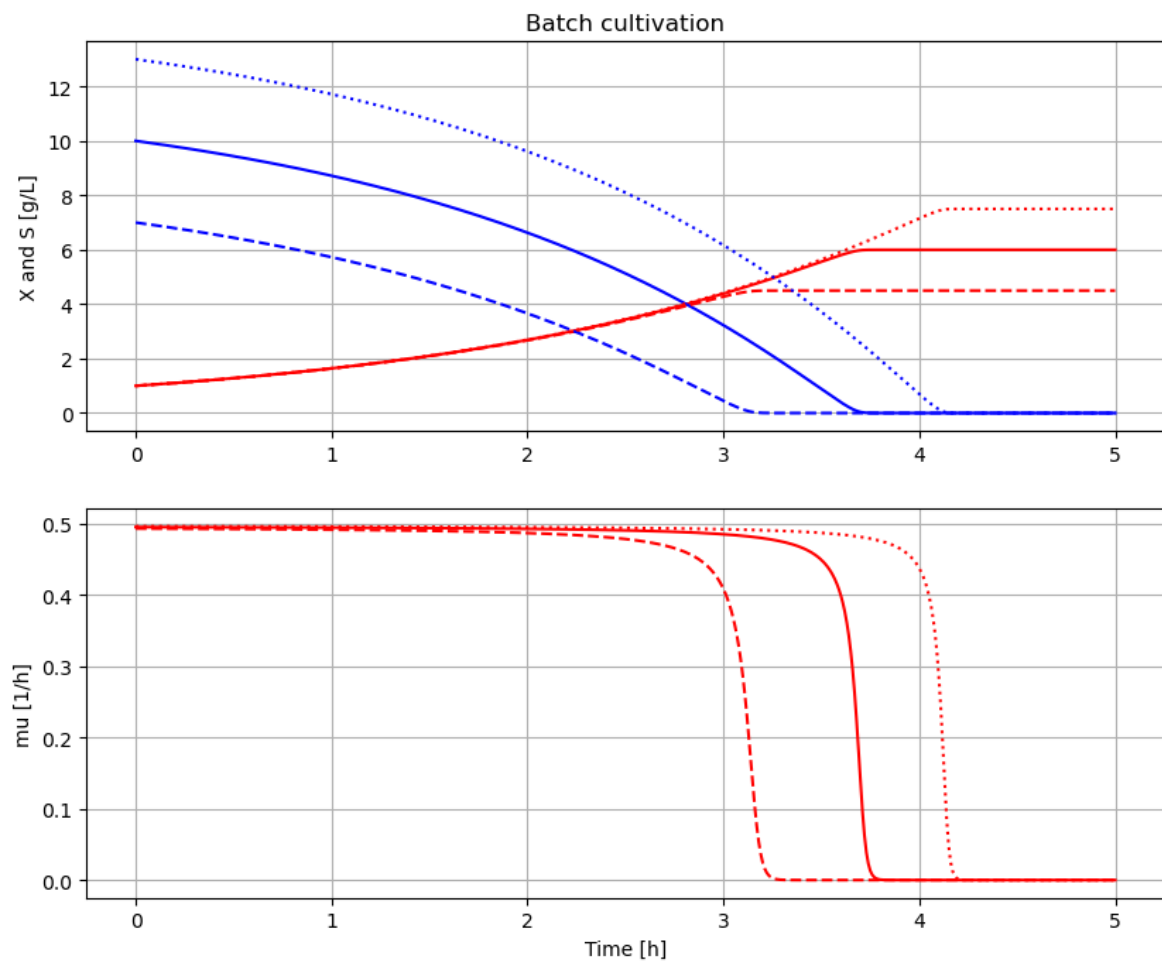
```
In [5]: # Simulation were initial value of biomass VX_start is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

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



```
In [6]: # Simulation were initial value of substrate VS_0 is varied
newplot(plotType='TimeSeries')
for value in [10, 7, 13]: init(VS_start=value); simu(5)

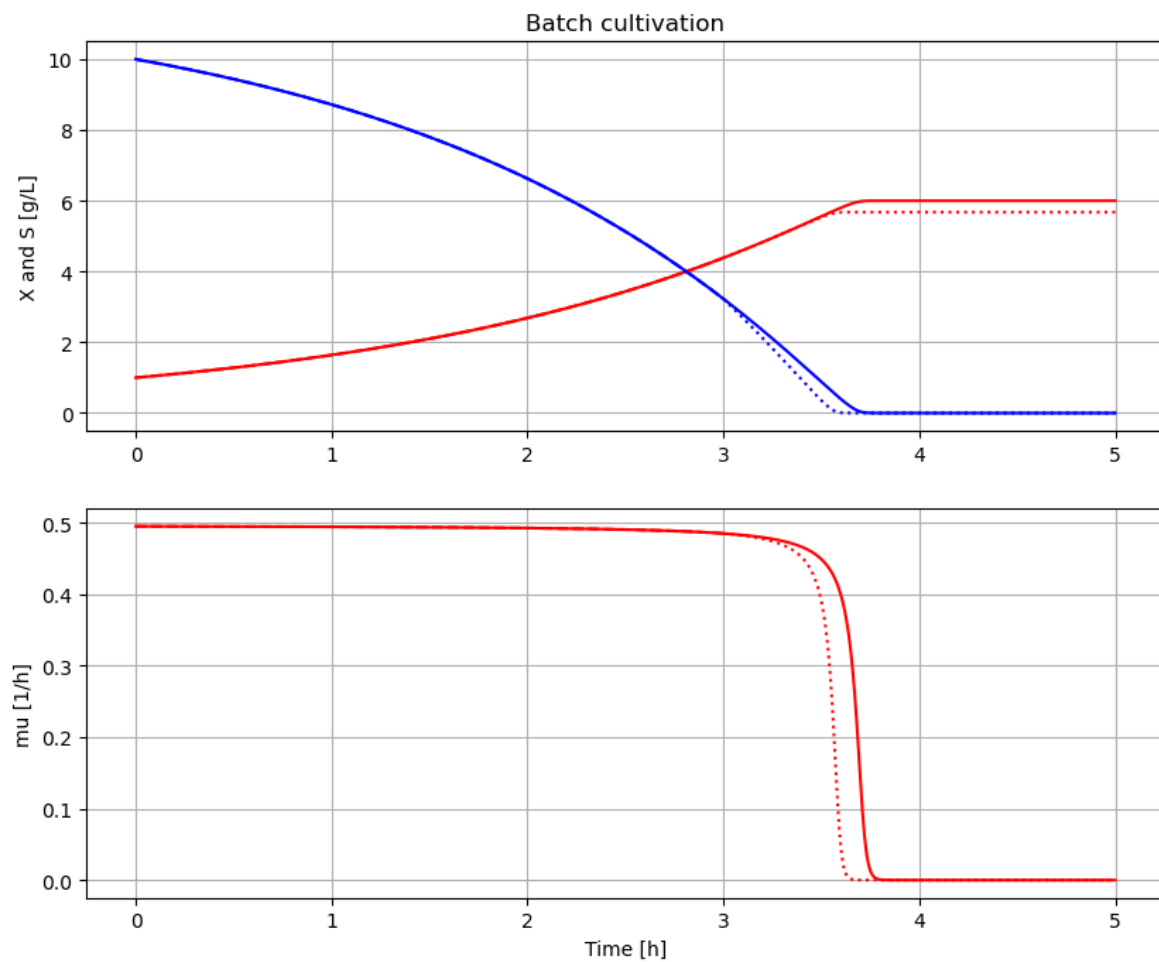
# Restore default value of VS_0
init(VS_start=10)
```



```
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 : 0.5  
qSmax : 1.0  
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: 3.12.11
- Scipy: not installed in the notebook
- FMPy: 0.3.26
- FMU by: OpenModelica Compiler OpenModelica 1.26.0~dev-200-gcb3254b
- FMI: 2.0
- Type: ME
- 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 for FMPy version 1.0.1

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 [ ]: