

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]`

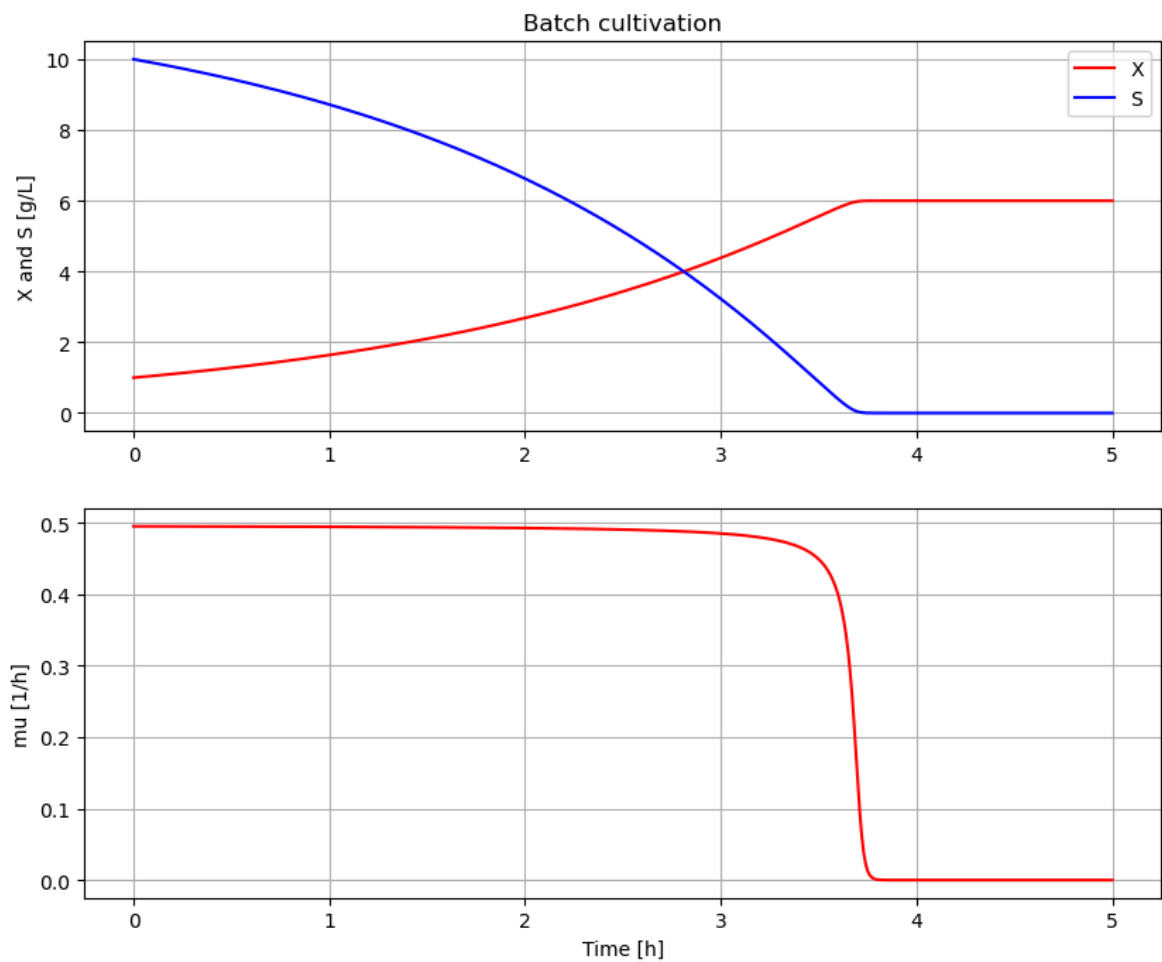
In [3]: `process_diagram()`

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



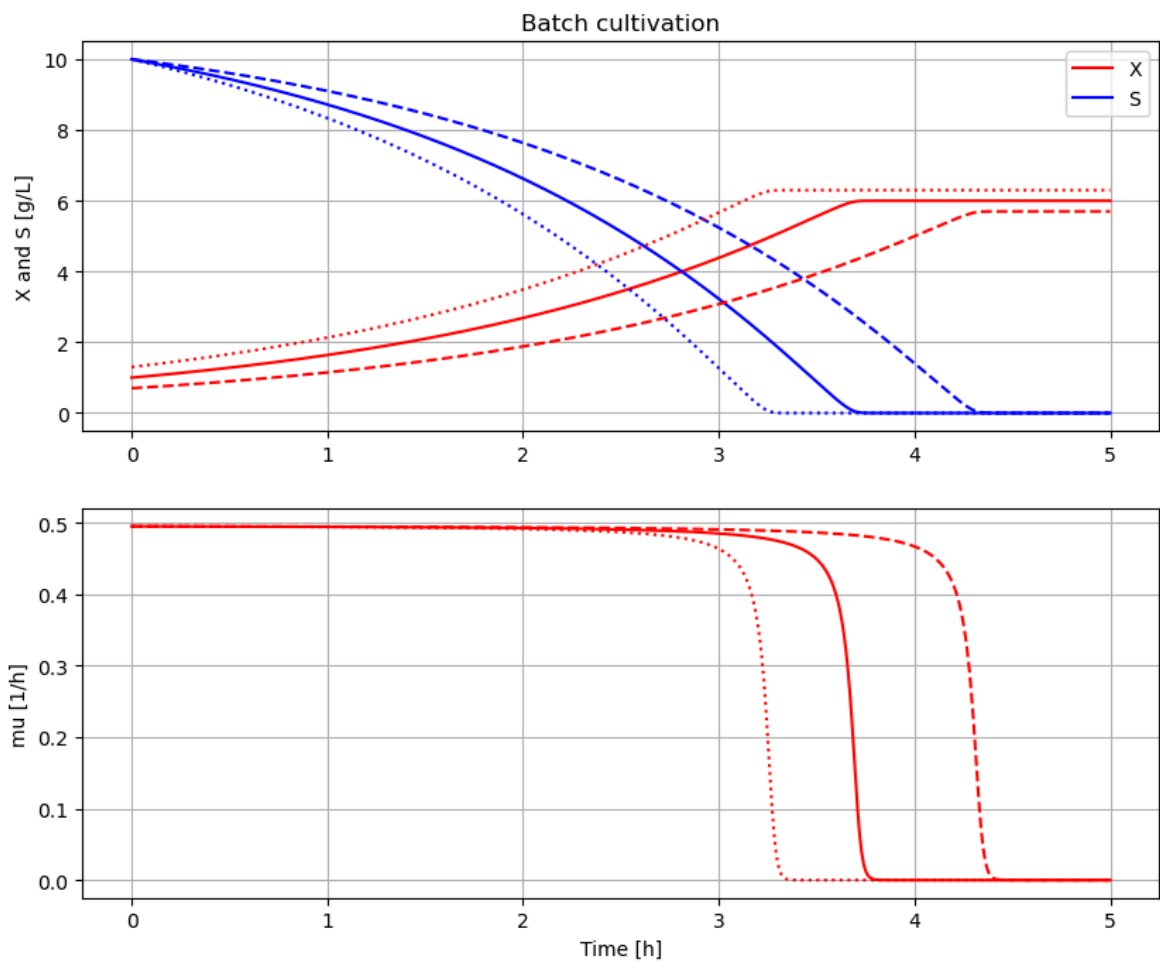
`disp('bioreactor', mode='long')`

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



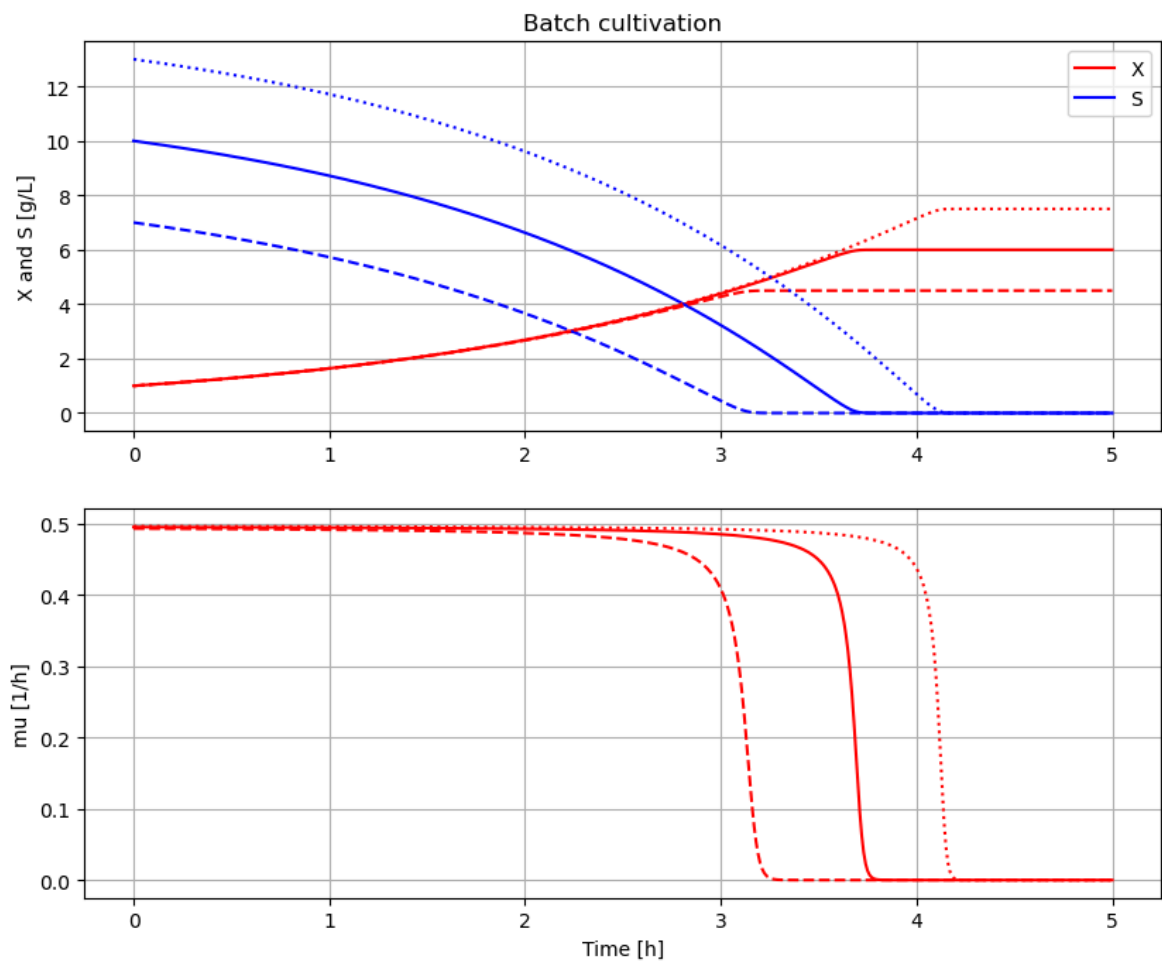
```
In [5]: # Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

# 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)

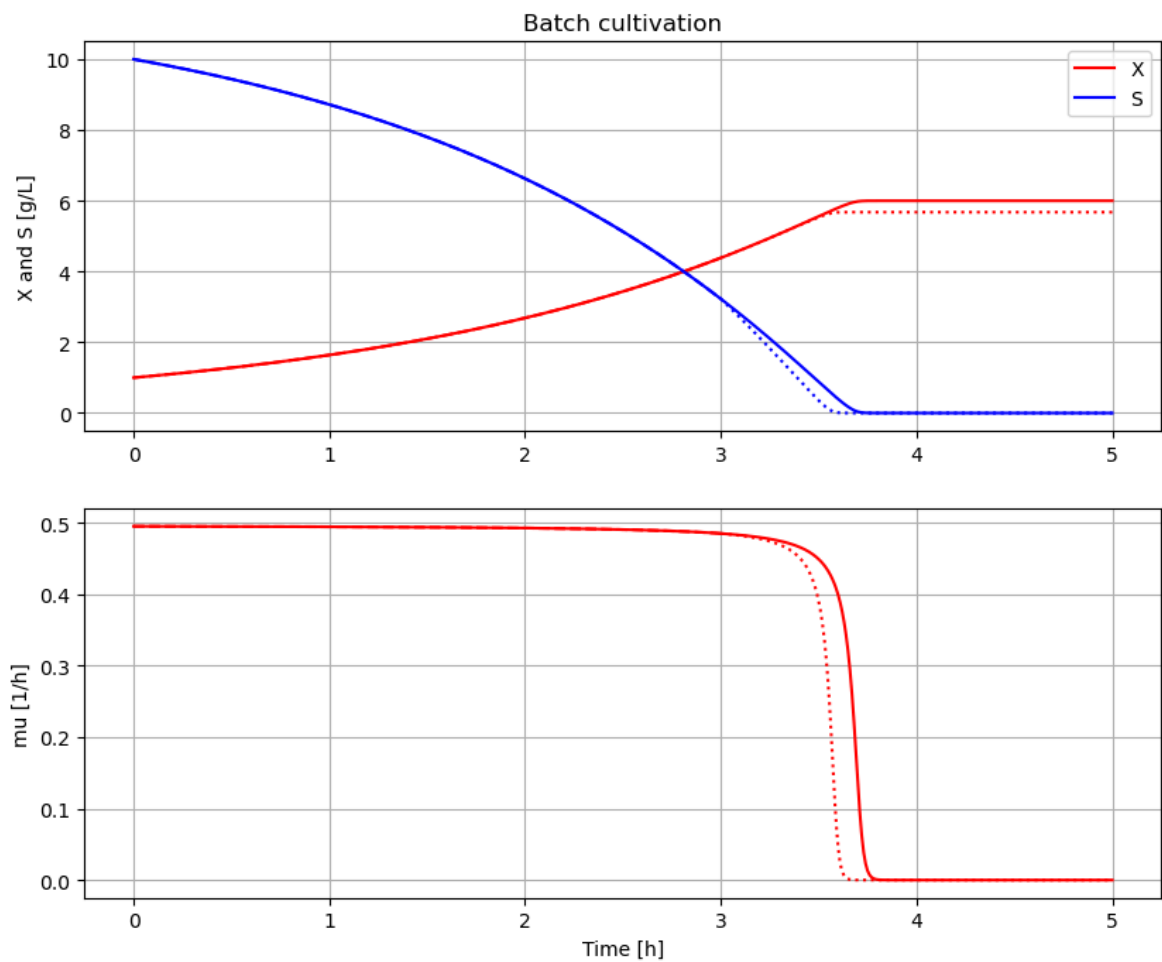
# Restore default value of VS_start
init(VS_start=10)
```



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

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

```
MSL: none
```

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

System information

-OS: Windows
-Python: 3.10.13
-Scipy: not installed in the notebook
-PyFMI: 2.12.0
-FMU by: JModelica.org
-FMI: 2.0
-Type: FMUModelCS2
-Name: BPL_TEST2.Batch
-Generated: 2024-05-12T20:44:19
-MSL: 3.2.2 build 3
-Description: Bioprocess Library version 2.2.0
-Interaction: FMU-explore version 1.0.0

In [13]: !conda list xz

```
# packages in environment at C:\Users\janpa\miniconda3\envs\pyfmi2120:
#
# Name                          Version                      Build      Channel
xz                              5.2.6                      h8d14728_0  conda-forge
```

In [14]: !conda list xz-utils

```
# packages in environment at C:\Users\janpa\miniconda3\envs\pyfmi2120:
#
# Name                          Version                      Build      Channel
```

In []: