

# BPL\_TEST2\_Fedbatch - demo

```
In [1]: run -i BPL_TEST2_Fedbatch_fmpy_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

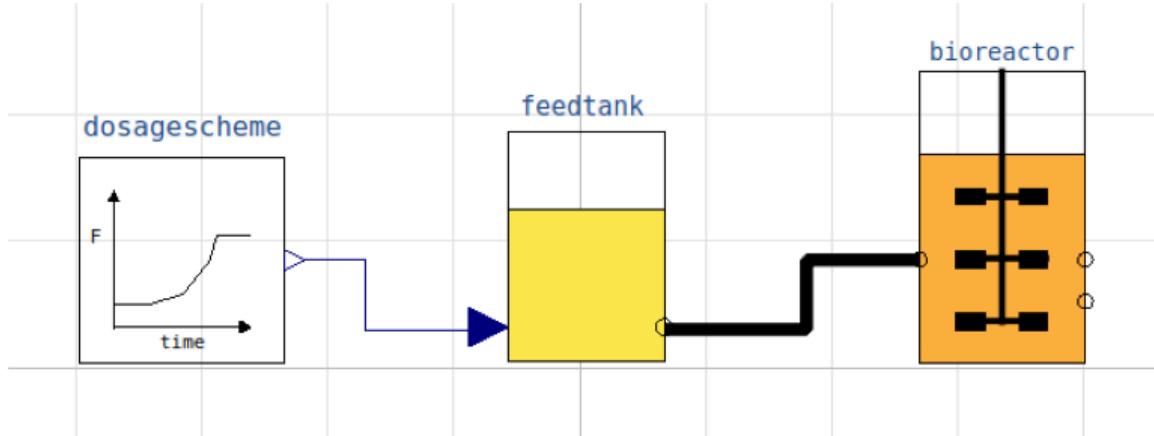
Note that both disp() and describe() takes values from the last simulation and the command process\_diagram() brings up the main configuration

Brief information about a command by help(), eg help(simu)  
Key system information is listed with the command system\_info()

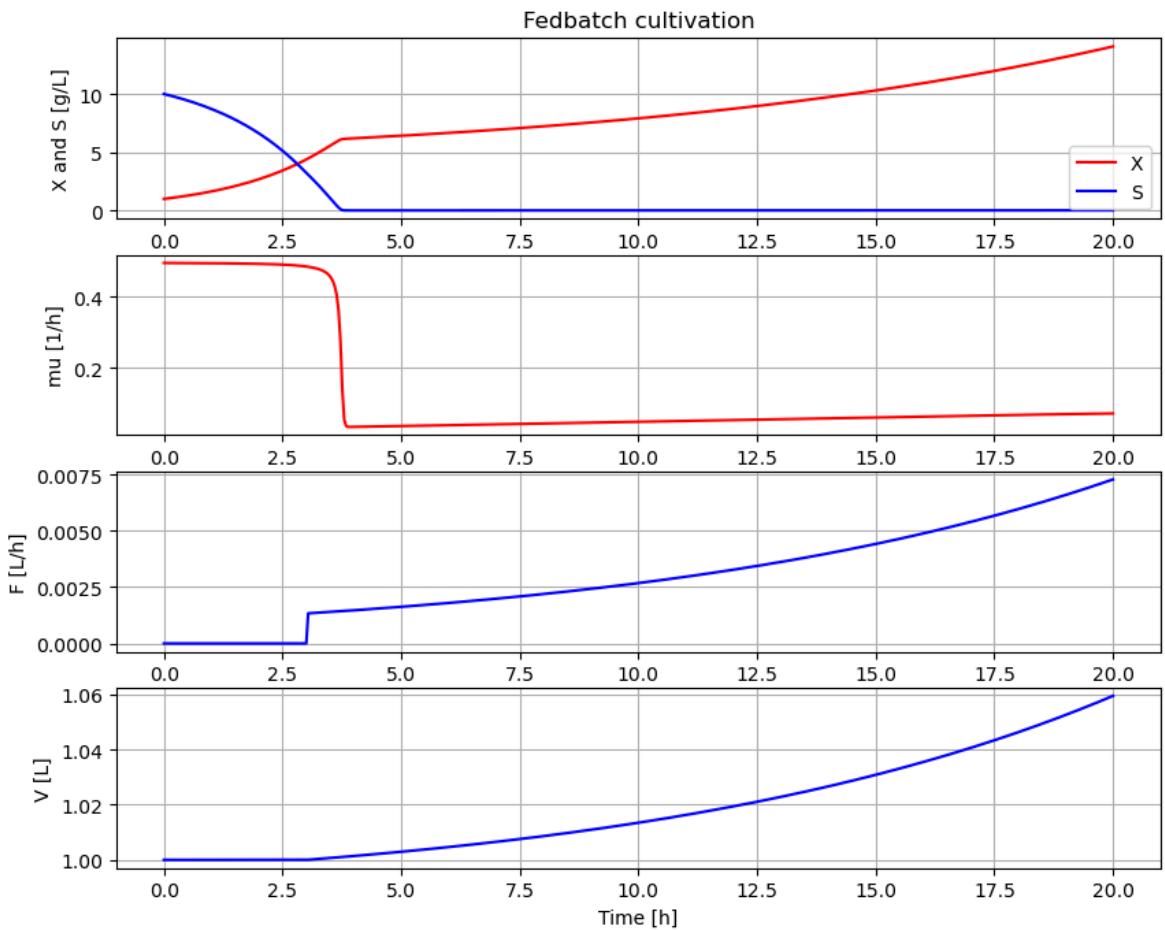
```
In [2]: %matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

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



```
In [4]: # Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)
```



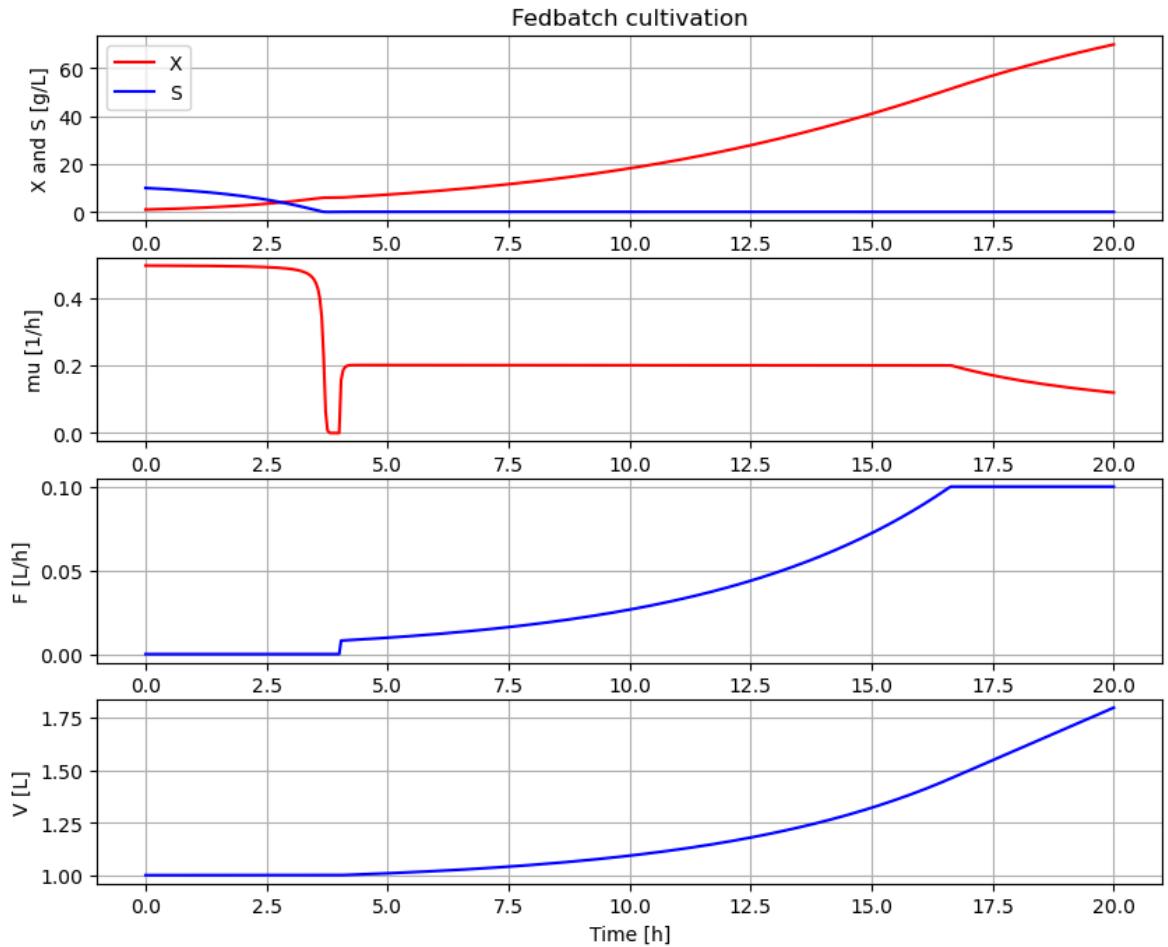
```
In [5]: disp(mode='long')
```

```

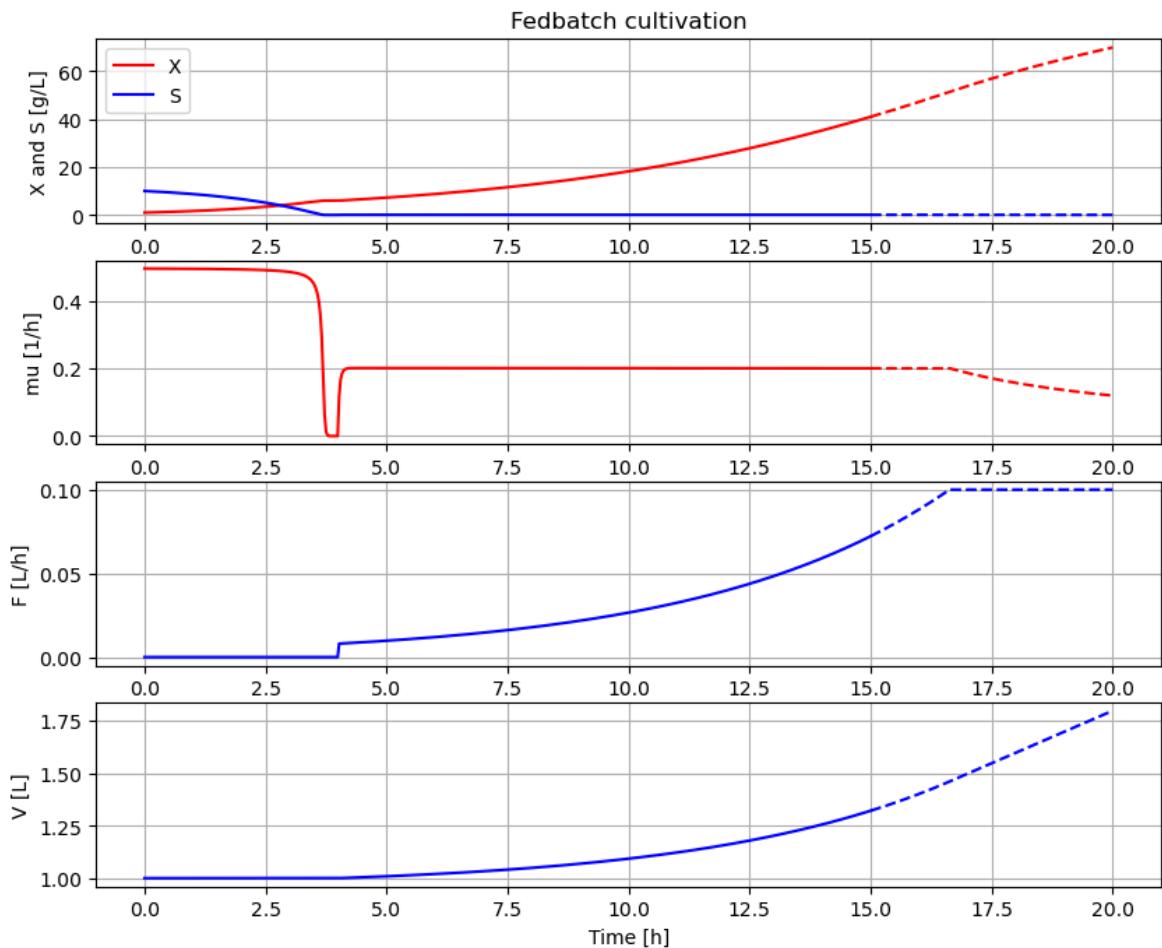
bioreactor.V_start : V_start : 1.0
bioreactor.m_start[1] : VX_start : 1.0
bioreactor.m_start[2] : VS_start : 10.0
bioreactor.culture.Y : Y : 0.5
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1
feedtank.c_in[2] : feedtank.S_in : 300.0
feedtank.V_start : feedtank.V_start : 10.0
dosagescheme.mu_feed : mu_feed : 0.1
dosagescheme.t_startExp : t_startExp : 3.0
dosagescheme.F_startExp : F_startExp : 0.001
dosagescheme.F_max : F_max : 0.3

```

```
In [6]: # A more typical feed scheme for the culture at hand
newplot(plotType='TimeSeries')
par(t_startExp=4, F_startExp=0.008, mu_feed=0.2, F_max=0.1)
simu(20)
```



```
In [7]: # Test function simu(mode='cont')
newplot()
simu(15)
simu(5, 'cont')
```



```
In [8]: disp('culture')
```

```
Y : 0.5
qSmax : 1.0
Ks : 0.1
```

```
In [9]: disp('Y', mode='long')
```

```
bioreactor.culture.Y : Y : 0.5
```

```
In [10]: describe('mu')
```

```
Cell specific growth rate variable : 0.12 [ 1/h ]
```

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

```
['bioreactor', 'bioreactor.culture', 'dosagescheme', 'feedtank', 'MSL']
```

```
In [12]: describe('MSL')
```

```
MSL: RealInput, RealOutput
```

```
In [13]: system_info()
```

```
System information
-OS: Windows
-Python: 3.12.11
-Scipy: not installed in the notebook
-FMPy: 0.3.25
-FMU by: JModelica.org
-FMI: 2.0
-Type: CS
-Name: BPL.Examples_TEST2.Fedbatch
-Generated: 2025-07-26T09:38:43
-MSL: 3.2.2 build 3
-Description: Bioprocess Library version 2.3.1
-Interaction: FMU-explore for FMPy version 1.0.2
```

In [14]: `!lsb_release -a`

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