

# BPL\_TEST2\_Fedbatch - demo

```
In [1]: run -i BPL_TEST2_Fedbatch_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

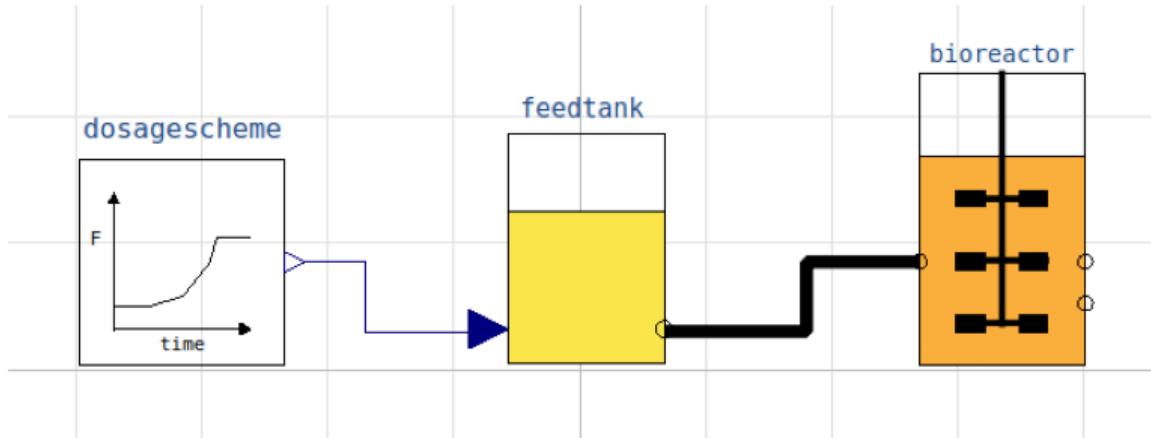
Note that both disp() and describe() takes values from the last simulation and the command process\_diagram() brings up the main configuration

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.



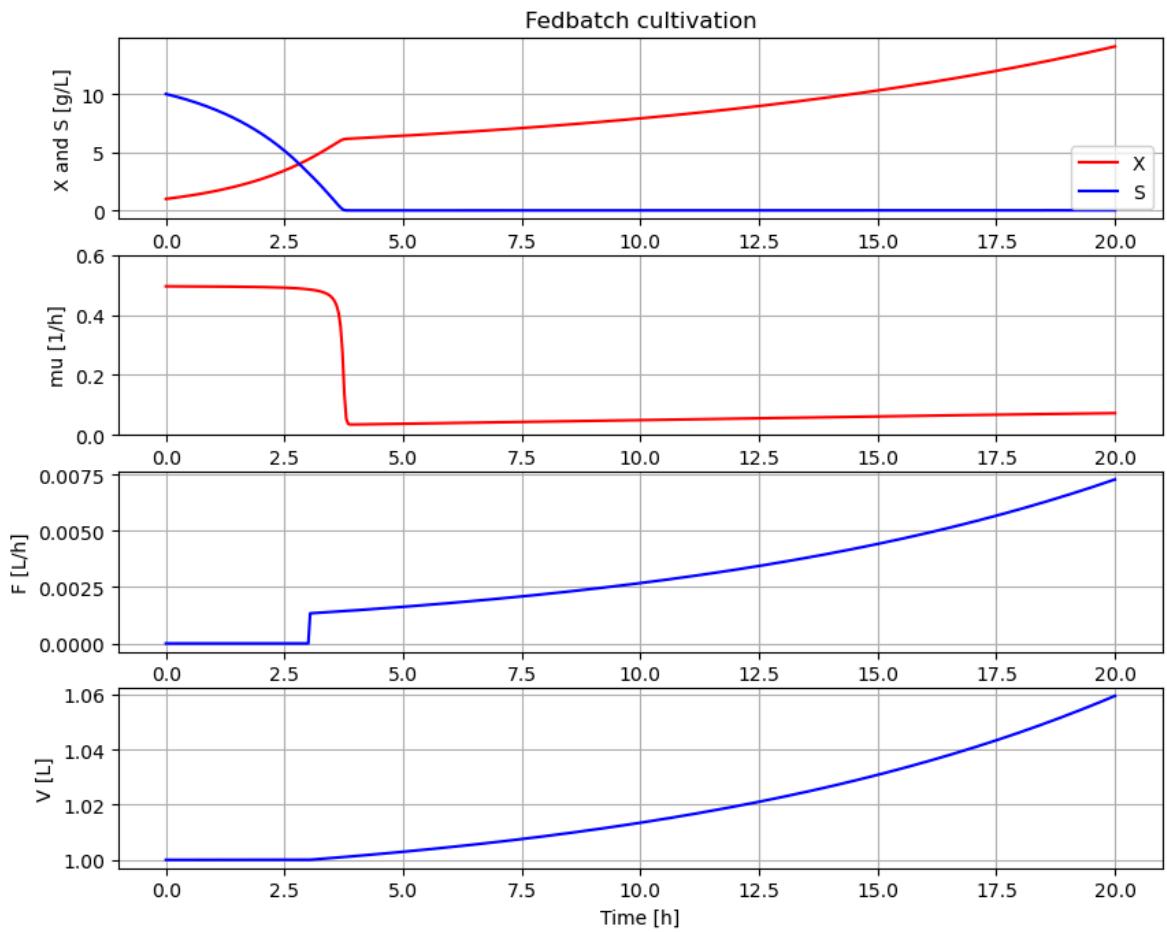
```
disp('dosagescheme')
```

```
In [4]: #disp('feedtank')
```

```
In [5]: #disp('bioreactor', mode='Long')
```

```
In [6]: # Simulation with default values of the process
newplot(plotType='TimeSeries'); ax2.set_ylim(0,0.6)

simu(20)
```



```
In [7]: # Let us display and then save the feedprofile
disp('dosagescheme')
```

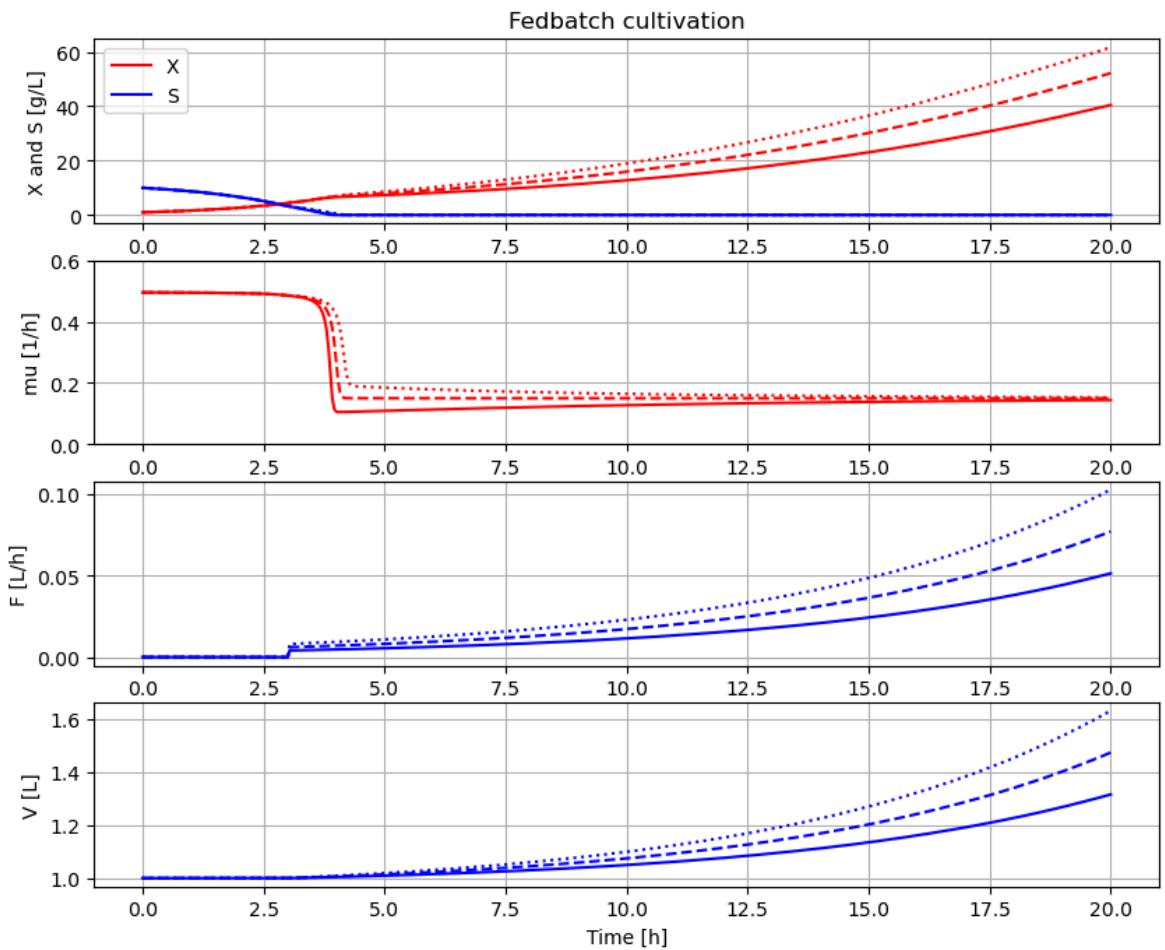
```
F_start : 0.0
mu_feed : 0.1
t_startExp : 3.0
F_startExp : 0.001
F_max : 0.3
```

```
In [8]: feedprofile_1={'F_start':0, 'mu_feed':0.1, 't_startExp':3, 'F_startExp':0.001, '
```

```
In [9]: # Let us develop a feedprofile with mu_feed=0.15 1/h instead
newplot(plotType='TimeSeries'); ax2.set_ylim(0,0.6)

# Choose mu_feed
par(mu_feed=0.15)

# Tune F_startExp value to get a stable culture growth rate at mu 0.15 1/h
for value in [0.004, 0.006, 0.008]:
    par(F_startExp=value)
    simu(20)
```

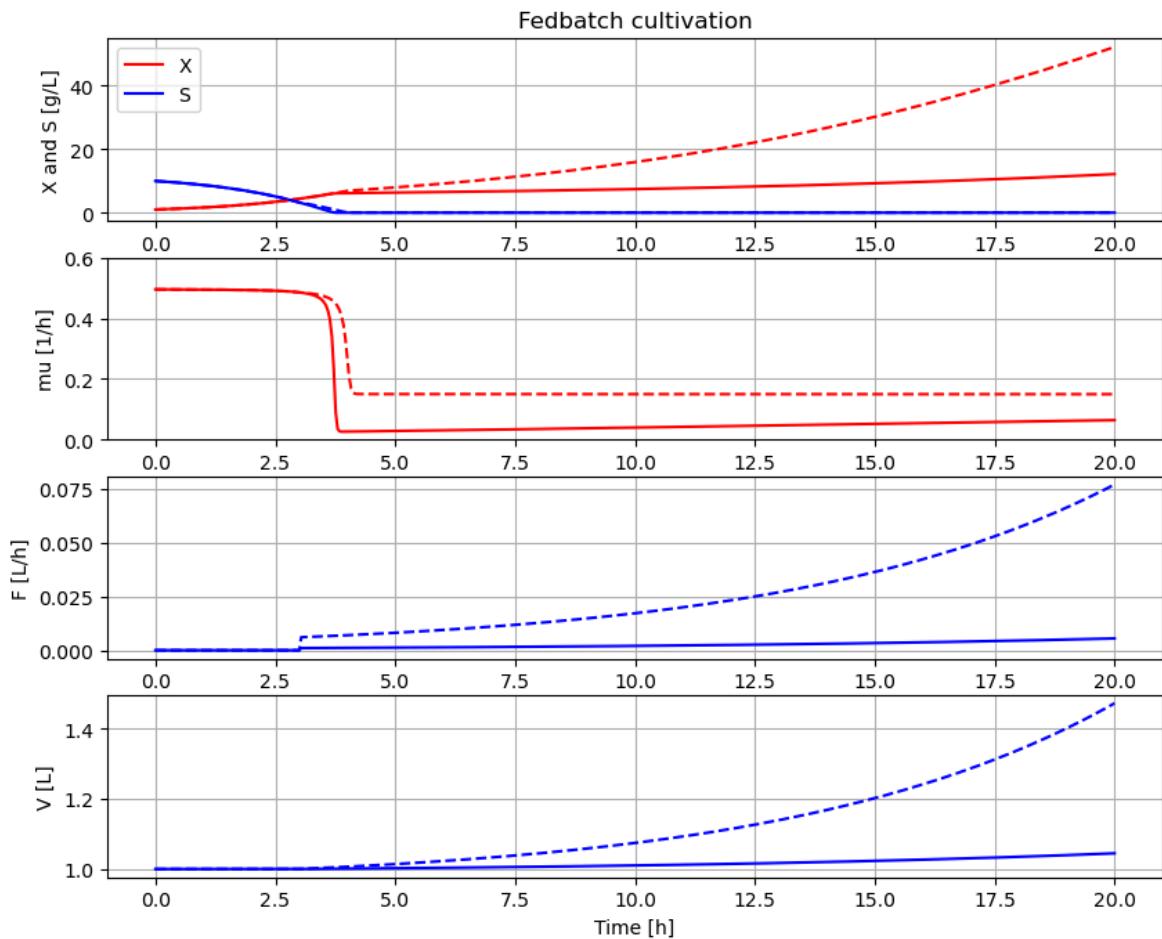


```
In [10]: # We choose F_startExp = 0.008 and save the new feedprofile
feedprofile_2={'F_start':0, 'mu_feed':0.15, 't_startExp':3, 'F_startExp':0.006,
```

```
In [11]: # Compare the result of ot the two
newplot(plotType='TimeSeries'); ax2.set_ylim(0,0.6)

for feedprofile in [feedprofile_1, feedprofile_2]:
    par(feedprofile)
    simu(20)

# Restore the original feedprofile
par(feedprofile_2)
```



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

Cell specific growth rate variable : 0.15 [ 1/h ]

```
In [13]: describe('parts')
```

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

```
In [14]: describe('MSL')
```

MSL: RealInput, RealOutput

```
In [15]: system_info()
```

System information  
 -OS: Windows  
 -Python: 3.12.11  
 -Scipy: not installed in the notebook  
 -PyFMI: 2.19.0  
 -FMI by: JModelica.org  
 -FMI: 2.0  
 -Type: FMUModelCS2  
 -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 version 1.0.2

```
In [16]: !lsb_release -a
```

'lsb\_release' is not recognized as an internal or external command,  
 operable program or batch file.

In [ ]: