

# BPL\_TEST2\_Fedbatch - demo

In [1]: `run -i BPL_TEST2_Fedbatch_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

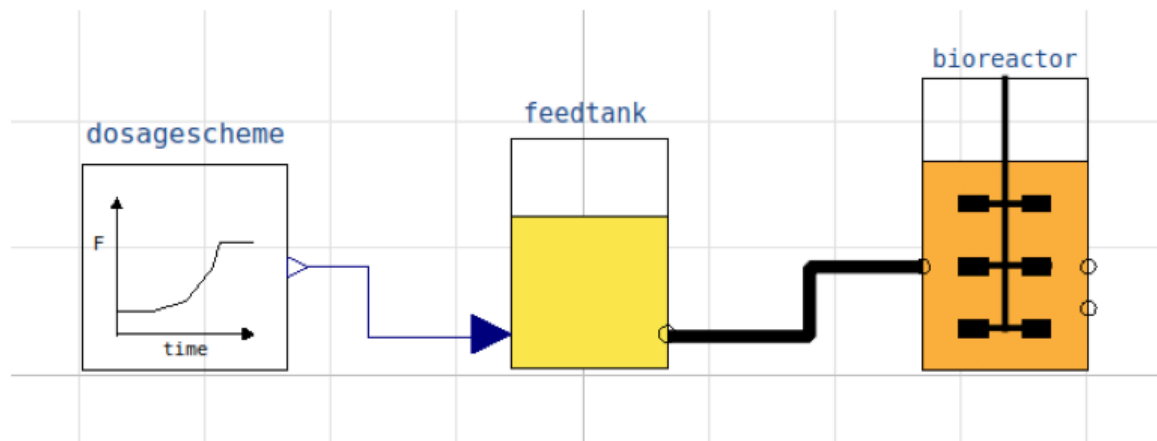
Brief information about a command by `help()`, eg `help(simu)`

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.

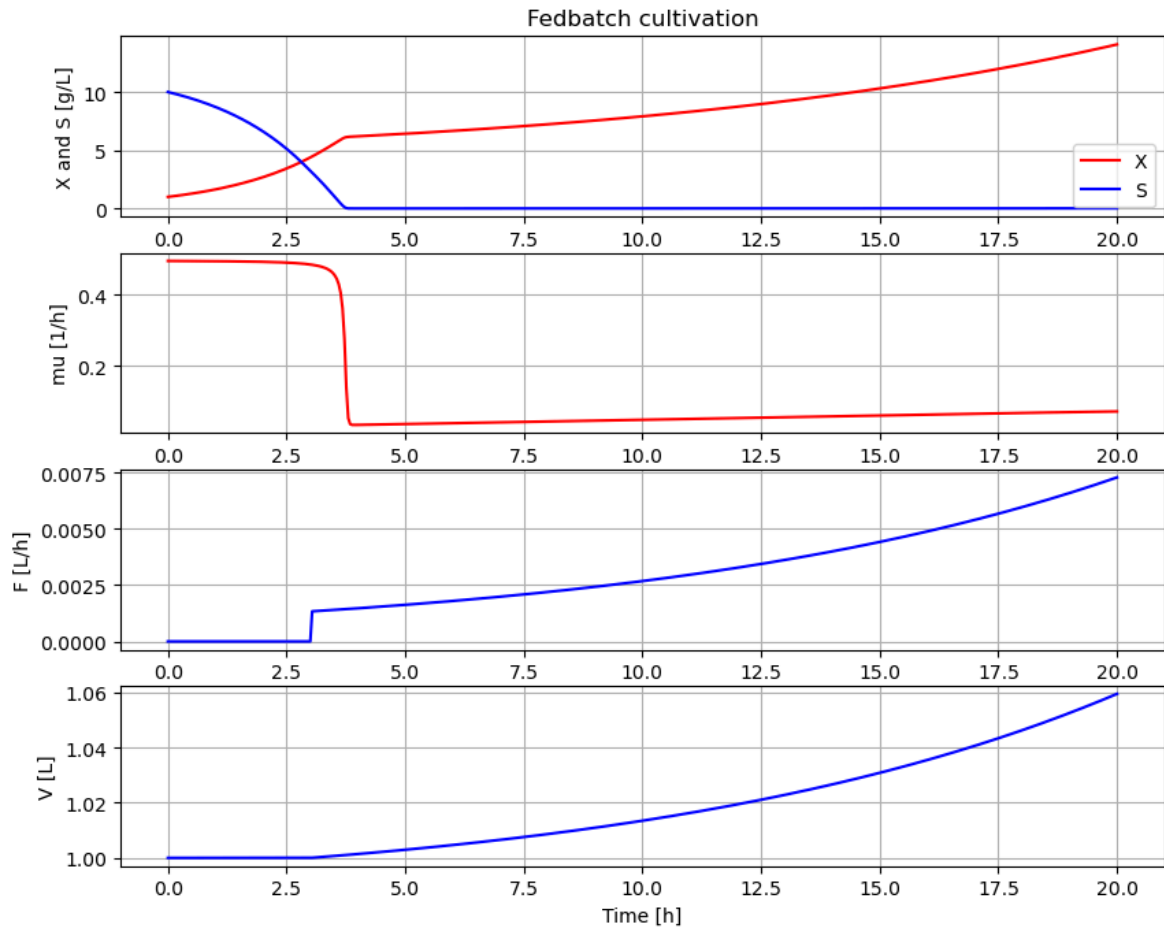


`disp('dosagescheme')`

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

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

In [6]: `# Simulation with default values of the process`  
`newplot(plotType='TimeSeries')`  
`simu(20)`



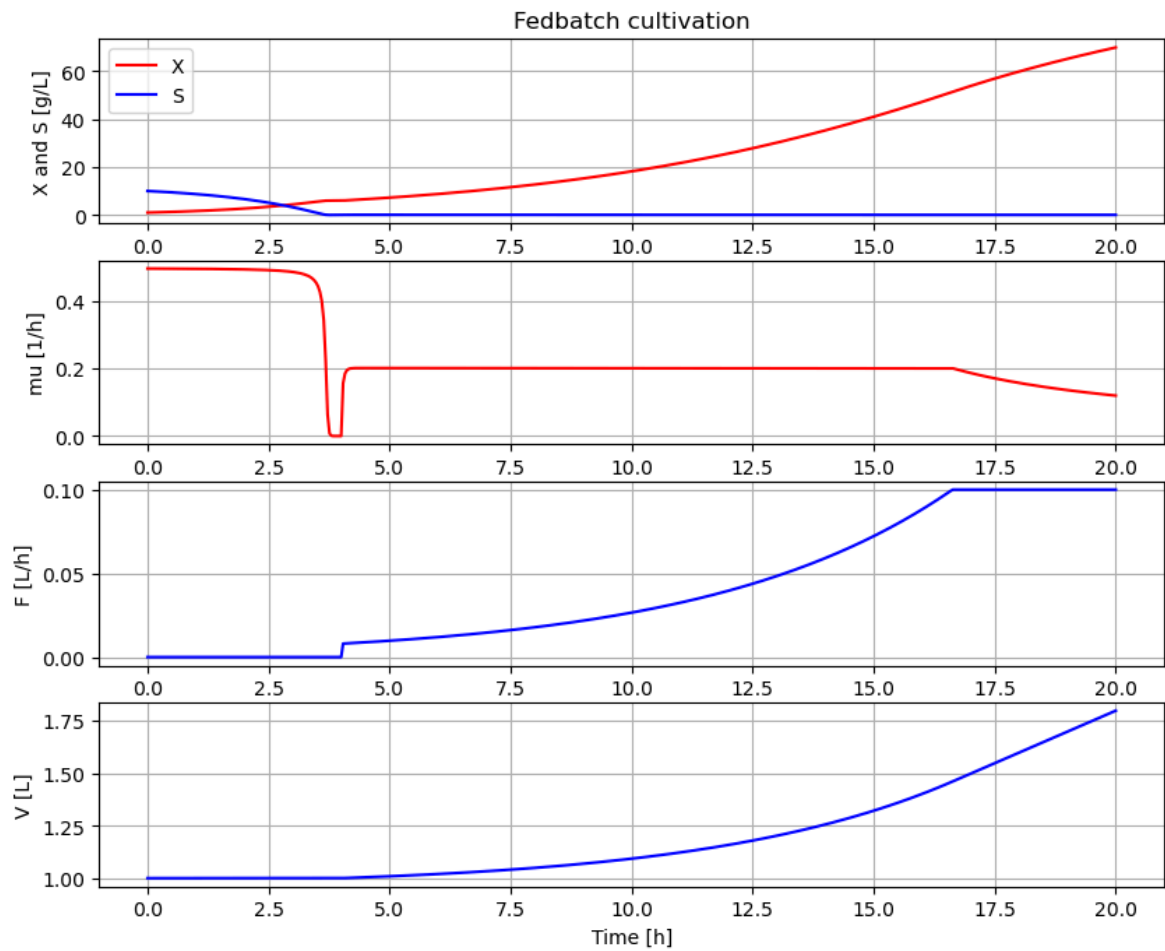
In [7]: `disp(mode='long')`

```

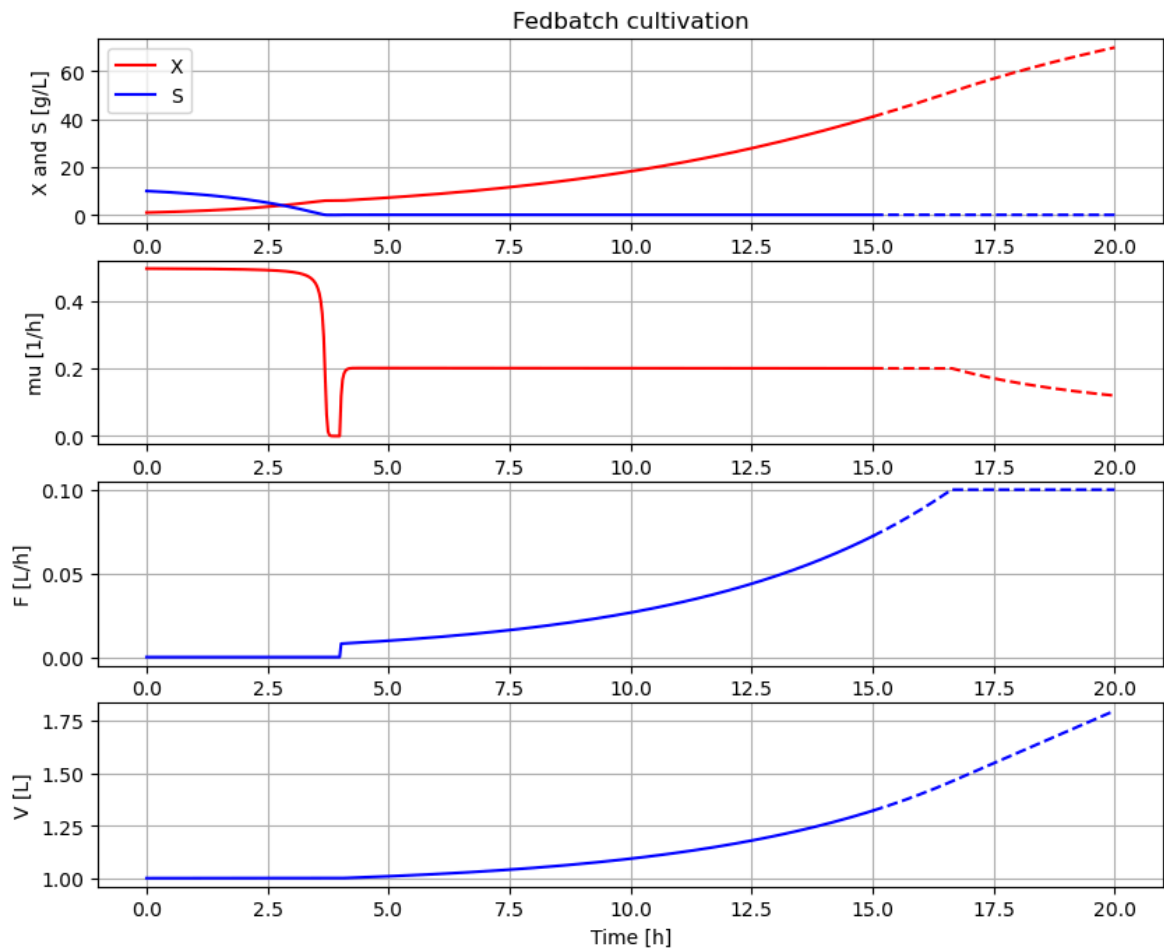
bioreactor.V_start : V_start : 1.0
bioreactor.m_start[1] : VX_start : 1.0
bioreactor.m_start[2] : VS_start : 10.0
bioreactor.culture.Y : Y : 0.5
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1
feedtank.c_in[2] : feedtank.S_in : 300.0
feedtank.V_start : feedtank.V_start : 10.0
dosagescheme.F_start : F_start : 0.0
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 [8]: `# 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 [9]: # Test function simu(mode='cont')
newplot()
simu(15)
simu(5, 'cont')
```



```
In [10]: disp('culture')
```

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

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

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

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

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

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

```
MSL: RealInput, RealOutput
```

```
In [14]: system_info()
```

System information  
-OS: Windows  
-Python: 3.10.14  
-Scipy: not installed in the notebook  
-PyFMI: 2.13.0  
-FMU by: JModelica.org  
-FMI: 2.0  
-Type: FMUModelCS2  
-Name: BPL\_TEST2.Fedbatch  
-Generated: 2024-05-12T20:49:52  
-MSL: 3.2.2 build 3  
-Description: Bioprocess Library version 2.2.0  
-Interaction: FMU-explore version 1.0.0

```
In [15]: !conda list assimulo
```

```
# packages in environment at C:\Users\janpa\miniconda3\envs\pyfmi2130:
#
# Name                               Version                Build      Channel
assimulo                             3.5.1                  py310h75059c1_0  conda-forge
```

```
In [19]: !conda list xz
```

```
# packages in environment at C:\Users\janpa\miniconda3\envs\pyfmi2130:
#
# Name                               Version                Build      Channel
xz                                   5.2.6                  h8d14728_0    conda-forge
```

```
In [ ]:
```