

# 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

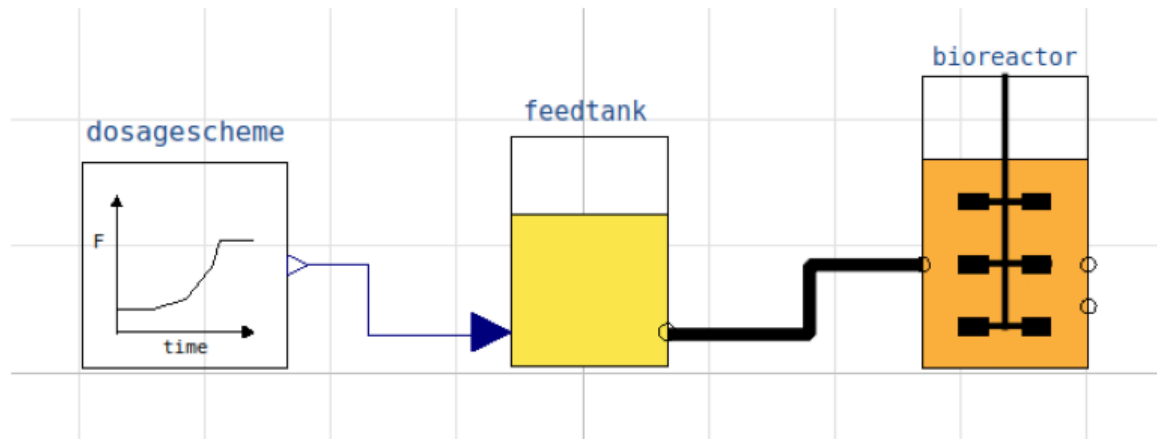
Brief information about a command by `help()`, eg `help(simu)`

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.



In [4]: `disp('dosagescheme')`

```
F_start : 0.0
mu_feed : 0.2
t_startExp : 2.0
F_startExp : 0.12
F_max : 3.0
```

In [5]: `disp('feedtank')`

```
feedtank.S_in : 0.0
feedtank.V_start : 100.0
```

In [6]: `disp('bioreactor', mode='long')`

```

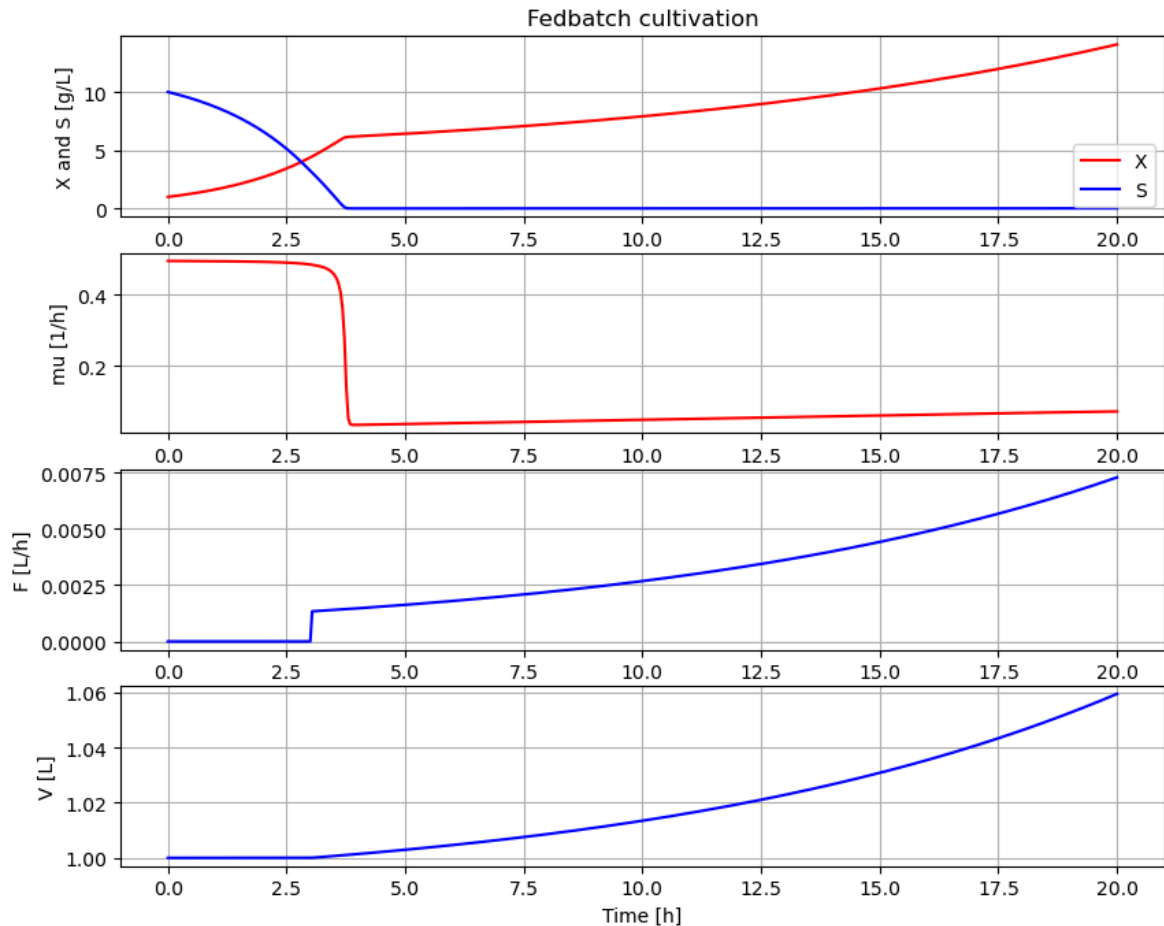
bioreactor.V_start : V_start : 1.0
bioreactor.m_start[1] : VX_start : 0.0
bioreactor.m_start[2] : VS_start : 0.0
bioreactor.culture.Y : Y : 0.5
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1

```

```

In [7]: # Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)

```



```

In [8]: disp(mode='long')

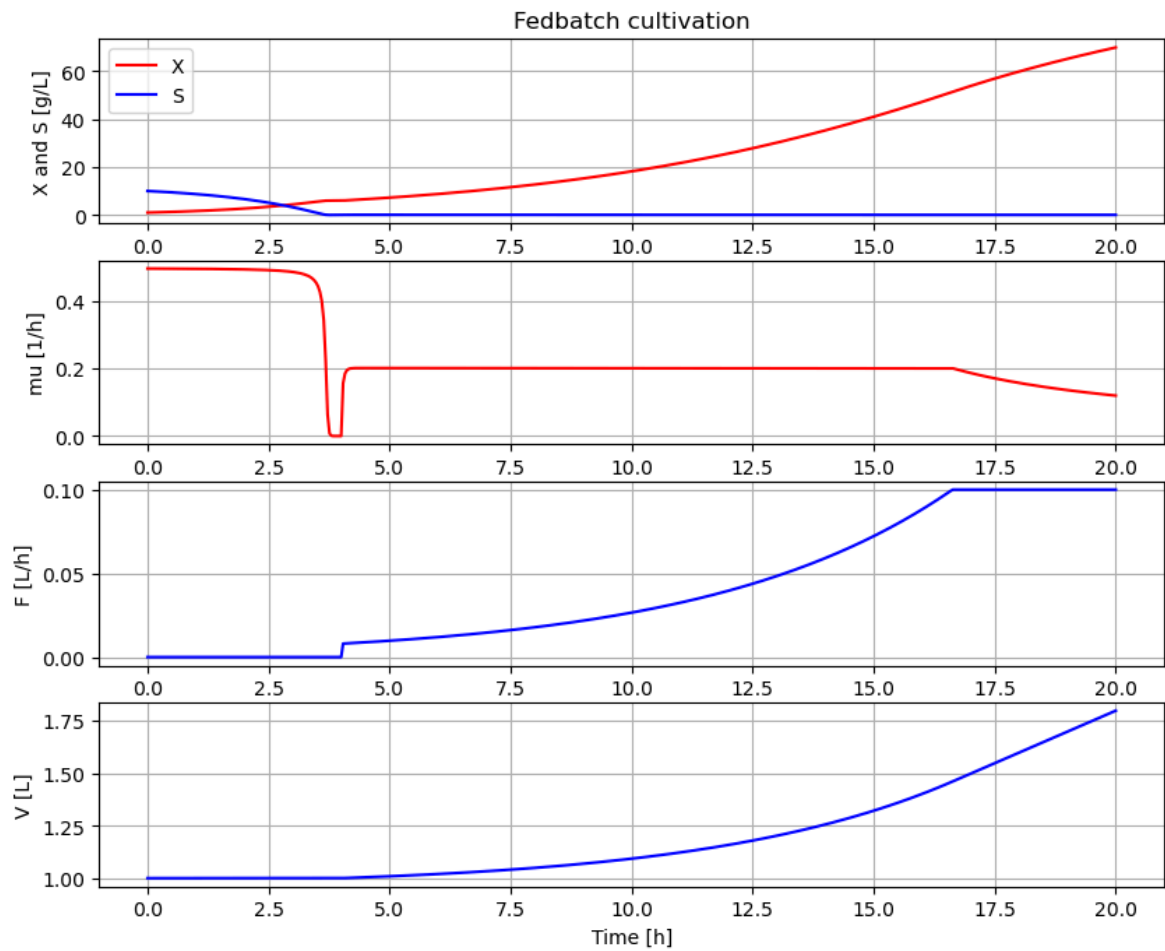
bioreactor.V_start : V_start : 1.0
bioreactor.m_start[1] : VX_start : 1.0
bioreactor.m_start[2] : VS_start : 10.0
bioreactor.culture.Y : Y : 0.5
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1
feedtank.c_in[2] : feedtank.S_in : 300.0
feedtank.V_start : feedtank.V_start : 10.0
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

```

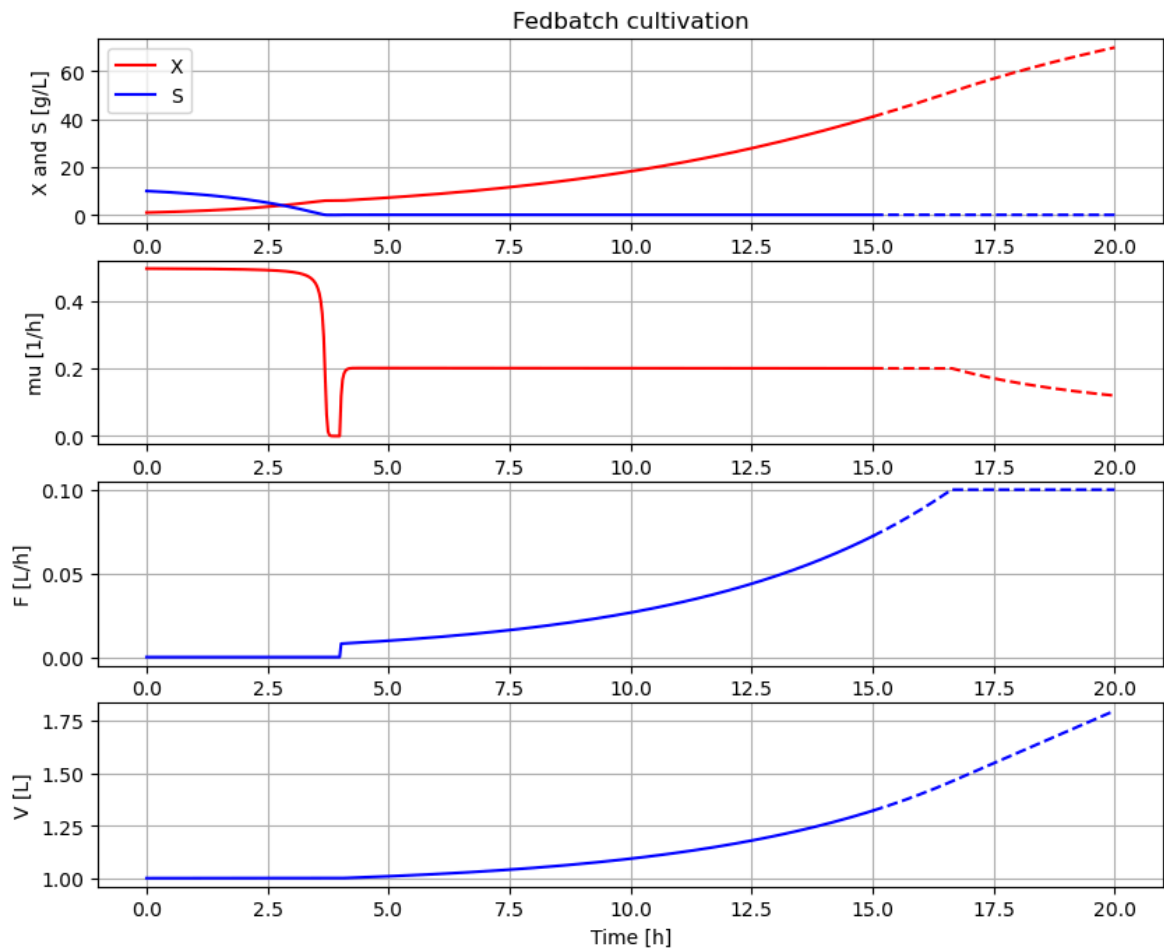
```

In [9]: # 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 [10]: # Test function simu(mode='cont')
newplot()
simu(15)
simu(5, 'cont')
```



```
In [11]: disp('culture')
```

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

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

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

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

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

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

```
MSL: RealInput, RealOutput
```

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

## System information

- OS: Windows
- Python: 3.10.13
- Scipy: not installed in the notebook
- PyFMI: 2.11.0
- FMU by: JModelica.org
- FMI: 2.0
- Type: FMUModelCS2
- Name: BPL\_TEST2.Fedbatch
- Generated: 2024-02-29T19:31:10
- MSL: 3.2.2 build 3
- Description: Bioprocess Library version 2.1.2 prel
- Interaction: FMU-explore version 0.9.9

In [ ]: