

## ✓ BPL\_TEST2\_Fedbatch script with PyFMI

The key library PyFMI is installed.

After the installation a small application BPL\_TEST2\_Fedbatch is loaded and run. You can continue with this example if you like.

```
!lsb_release -a # Actual VM Ubuntu version used by Google
```

```
➤ No LSB modules are available.  
Distributor ID: Ubuntu  
Description:    Ubuntu 22.04.3 LTS  
Release:        22.04  
Codename:       jammy
```

```
%env PYTHONPATH=
```

```
➤ env: PYTHONPATH=
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-Linux-x86_64.sh  
!chmod +x Miniconda3-py310_23.1.0-1-Linux-x86_64.sh  
!bash ./Miniconda3-py310_23.1.0-1-Linux-x86_64.sh -b -f -p /usr/local  
import sys  
sys.path.append('/usr/local/lib/python3.10/site-packages/')
```

```
➤ --2024-05-23 11:17:36-- https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-Linux-x86_64.sh  
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.158, 2606:4700::6810:bf9e, ...  
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... connected.  
HTTP request sent, awaiting response... 200 OK  
Length: 74403966 (71M) [application/x-sh]  
Saving to: 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh'
```

```
Miniconda3-py310_23 100%[=====] 70.96M 221MB/s in 0.3s
```

```
2024-05-23 11:17:36 (221 MB/s) - 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh' saved [74403966/74403966]
```

```
PREFIX=/usr/local  
Unpacking payload ...
```

```
Installing base environment...
```

```
Downloading and Extracting Packages
```

```
Downloading and Extracting Packages
```

```
Preparing transaction: done  
Executing transaction: done  
installation finished.
```

```
!conda update -n base -c defaults conda --yes
```

```
➤
```

```
Preparing transaction: done  
Verifying transaction: done  
Executing transaction: done
```

```
!conda --version  
!python --version
```

```
🔄 conda 23.1.0  
Python 3.10.14
```

```
!conda install -c conda-forge pyfmi --yes # Install the key package
```

```
🔄
```

```
Preparing transaction: done
Verifying transaction: done
Executing transaction: done
```

## ✓ BPL\_TEST2\_Fedbatch setup

Now specific installation and the run simulations. Start with connecting to Github. Then upload the two files:

- FMU - BPL\_TEST2\_Fedbatch\_linux\_om\_me.fmu
- Setup-file - BPL\_TEST2\_Fedbatch\_explore.me.py

```
%%bash
```

```
git clone https://github.com/janpeter19/BPL_TEST2_Fedbatch
```

```
➦ Cloning into 'BPL_TEST2_Fedbatch'...
```

```
%cd BPL_TEST2_Fedbatch
```

```
➦ /content/BPL_TEST2_Fedbatch
```

```
run -i BPL_TEST2_Fedbatch_explore.py
```

```
➦ Linux - run FMU pre-compiled OpenModelica 1.23.0-dev
```

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()

```
%matplotlib inline
```

```
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

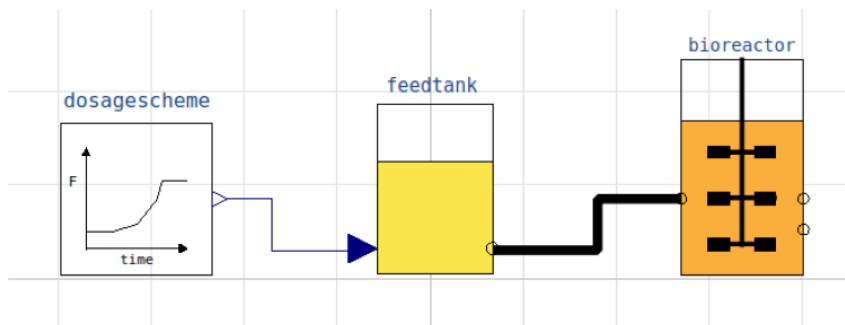
```
import warnings
```

```
warnings.filterwarnings("ignore")
```

## ✓ BPL\_TEST2\_Fedbatch - demo

```
process_diagram()
```

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

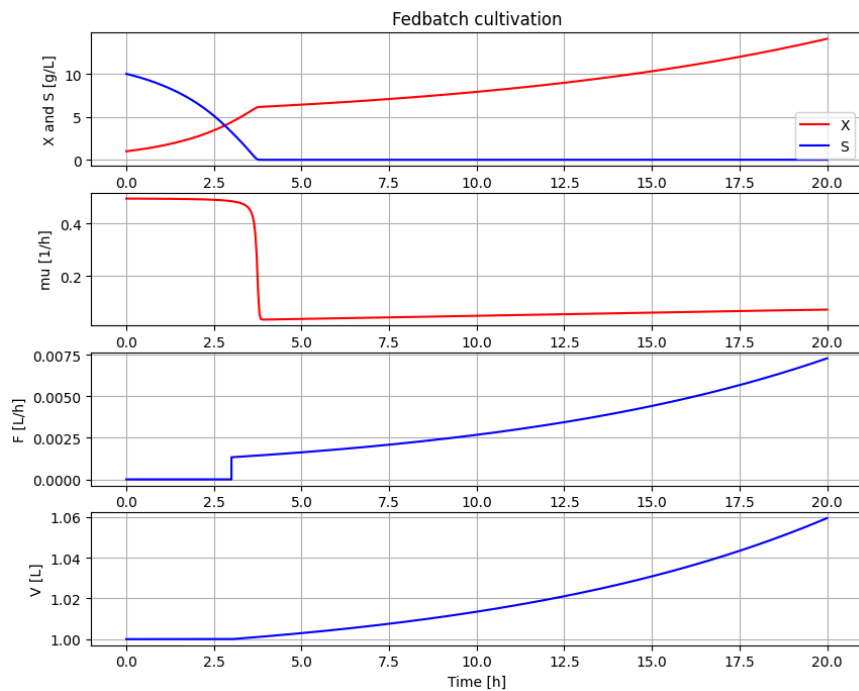


```
describe('culture'); print(); #describe('liquidphase')
```

```
# Pump schedule parameter
```

```
➦ Simplified text book model - only substrate S and cell concentration X
```

```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)
```

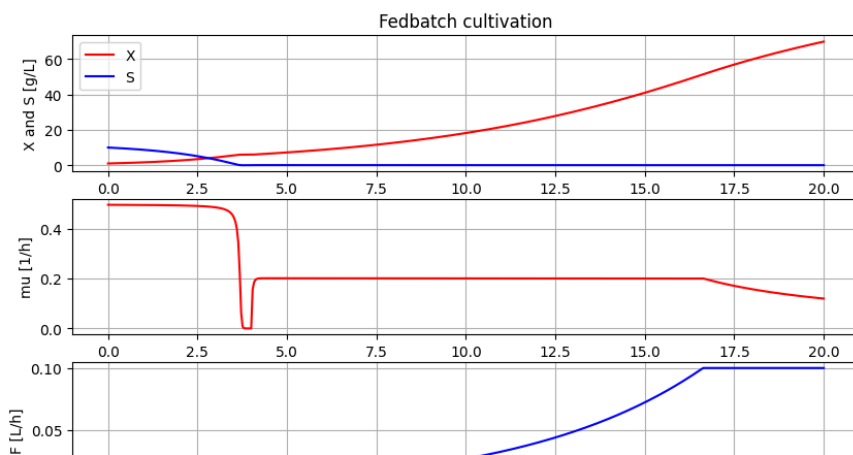


```
disp(mode='long')
```



```
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
```

```
# 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)
```



```
disp('culture')
```



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



```
describe('mu')
```



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

```
describe('parts')
```



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

```
describe('MSL')
```



```
MSL: 3.2.3 - used components: RealInput, RealOutput
```

```
system_info()
```



```
System information
-OS: Linux
-Python: 3.10.12
-Scipy: not installed in the notebook
-PyFMI: 2.13.0
-FMU by: OpenModelica Compiler OpenModelica 1.23.0~dev.beta.1-1-g379f714
-FMI: 2.0
-Type: FMUModelME2
-Name: BPL_TEST2.Fedbatch
-Generated: 2024-05-20T13:38:03Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.2.0
-Interaction: FMU-explore version 1.0.0
```