

## ▼ 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 20.04.5 LTS
Release:      20.04
Codename:     focal
```

```
%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/')
```

```
--2023-06-01 06:23:39-- https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-Linux-;
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.130.3, 104.16.131.3, 2606:4700::6810
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.130.3|: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 195MB/s in 0.4s
```

```
2023-06-01 06:23:39 (195 MB/s) - 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh' saved [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
```

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

```
conda 23.5.0
Python 3.10.9
```

```
!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 1.21.0
```

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

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")
```

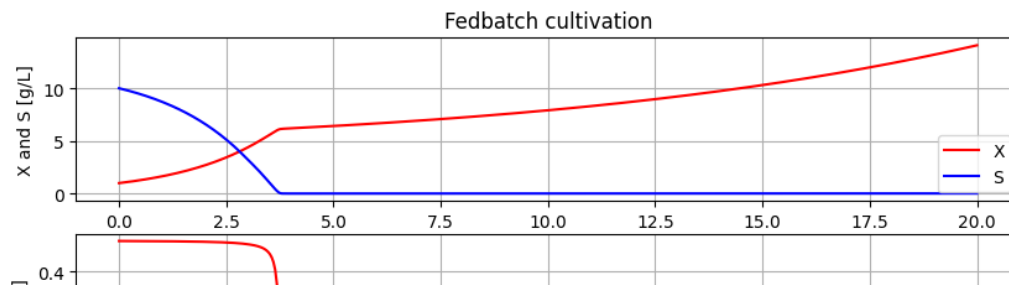
## ▼ BPL\_TEST2\_Fedbatch - demo

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

# Pump sche

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_0 : V_0 : 1.0
bioreactor.m_0[1] : VX_0 : 1.0
bioreactor.m_0[2] : VS_0 : 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_0 : feedtank.V_0 : 10.0
dosagescheme.mu_feed : mu_feed : 0.1
dosagescheme.t_start : t_start : 3.0
dosagescheme.F_start : F_start : 0.001
dosagescheme.F_max : F_max : 0.3
```

```
# A more typical feed scheme for the culture at hand
newplot(plotType='TimeSeries')
par(t_start=4, F_start=0.008, mu_feed=0.2, F_max=0.1)
simu(20)
```

## Fedbatch cultivation

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

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

0.0 2.5 5.0 7.5 10.0 12.5 15.0 17.5 20.0

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

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

| | | | | | | | | | | |

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

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

0.05 | | | | | | | | | | | |

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

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

| | | | | | | | | | | |

```
system_info()
```

```
System information
```

```
-OS: Linux
-Python: 3.10.11
-Scipy: not installed in the notebook
-PyFMI: 2.10.3
-FMU by: OpenModelica Compiler OpenModelica 1.21.0
-FMI: 2.0
-Type: FMUModelME2
-Name: BPL_TEST2.Fedbatch
-Generated: 2023-04-20T12:24:29Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.1.1
-Interaction: FMU-explore version 0.9.7
```