



## ▼ BPL\_TEST2\_Fedbatch script with FMPy 0.3.15

The key library FMPy ver 0.3.15 is installed.

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

```
lslsb_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-py38_22.11.1-1-Linux-x86_64.sh
!chmod +x Miniconda3-py38_22.11.1-1-Linux-x86_64.sh
!bash ./Miniconda3-py38_22.11.1-1-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.8/site-packages/')

--2023-03-21 12:56:19-- https://repo.anaconda.com/miniconda/Miniconda3-py38_22.11.1-1-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.130.3, 104.16.131.3, 2606:4700::6810:8203, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.130.3|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 64630241 (62M) [application/x-sh]
Saving to: 'Miniconda3-py38_22.11.1-1-Linux-x86_64.sh'

Miniconda3-py38_22. 100%[=====] 61.64M  129MB/s   in 0.5s

2023-03-21 12:56:20 (129 MB/s) - 'Miniconda3-py38_22.11.1-1-Linux-x86_64.sh' saved [64630241/64630241]

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
```

```
sqlite-3.41.1      | 1.2 MB      | : 100% 1.0/1 [00:00<00:00, 2.24it/s]
```

```
sqlite-3.41.1      | 1.2 MB      | : 100% 1.0/1 [00:00<00:00, 2.24it/s]
```

```
xz-5.2.10          | 429 KB      | : 100% 1.0/1 [00:00<00:00, 2.30it/s]
```

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

```
conda 23.1.0  
Python 3.8.15
```

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

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

```
!conda install matplotlib --yes
```

```
fonttools-4.25.0      | 632 KB      | : 100% 1.0/1 [00:00<00:00, 2.01it/s]
```

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

```
#!conda install scipy --yes
```

```
#!conda install xlrd --yes
```

```
#!conda install openpyxl --yes
```

## ▼ 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\_fmpy\_explore.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_fmipy_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 schedule parameter

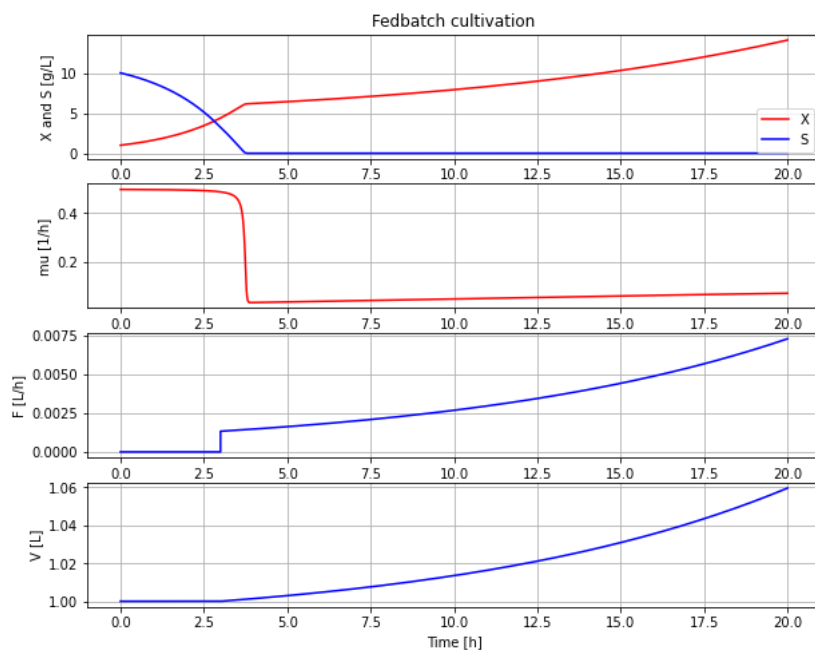
```

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_0 : V_0 : 1.0
bioreactor.m_0[1] : VX_0 : 0.0
bioreactor.m_0[2] : VS_0 : 0.0

```

```

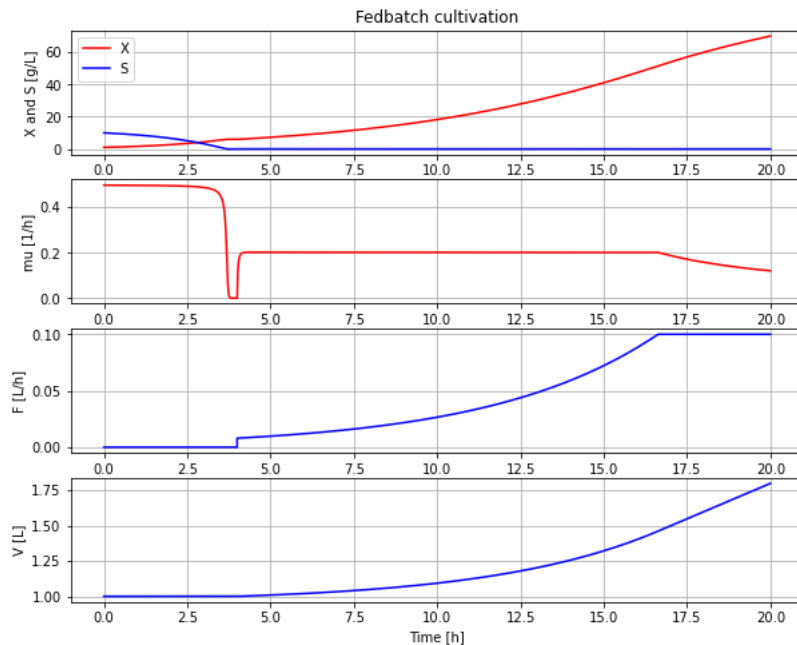
bioreactor.culture.Y : Y : 0.5
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1
feedtank.c_in[2] : feedtank.S_in : 0.0
feedtank.V_0 : feedtank.V_0 : 100.0
dosagescheme.mu_feed : mu_feed : 0.2
dosagescheme.t_start : t_start : 2.0
dosagescheme.F_start : F_start : 0.12
dosagescheme.F_max : F_max : 3.0

```

```

# 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)

```



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

```

Y : 0.5
qSmax : 1.0
Ks : 0.1

```

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

```
Cell specific growth rate variable : 0.0 [ 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: 3.9.16
-Scipy: not installed in the notebook
-FMPy: 0.3.15
-FMU by: OpenModelica Compiler OpenModelica 1.21.0-dev-185-g9d983b8
-FMI: 2.0
-Type: ME
-Name: BPL_TEST2.Fedbatch
-Generated: 2023-01-19T09:29:14Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.1.1-beta
-Interaction: FMU-explore for FMPy version 0.9.7b

```

✓ 0s completed at 14:03

● ×