

## ▼ BPL\_TEST2\_Batch script with FMPy ver 0.3.15

The key library FMPy ver 0.3.15 is installed.

After the installation a small application BPL\_TEST2\_Batch 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-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/')

--2023-03-23 13:48:22--  https://repo.anaconda.com/miniconda/Miniconda3-py38\_22.11.1-1-Linux-x86\_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.131.3, 104.16.130.3, 2606:4700::6810:8303, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.131.3|: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  168MB/s   in 0.4s

2023-03-23 13:48:23 (168 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
```

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

```
!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
```

```
libbrotlicommon-1.0. | 70 KB | : 100% 1.0/1 [00:00<00:00, 2.00it/s]
fonttools-4.25.0 | 632 KB | : 100% 1.0/1 [00:00<00:00, 1.71it/s]
fonttools-4.25.0 | 632 KB | : 100% 1.0/1 [00:00<00:00, 1.71it/s]
```

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

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

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

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

## ▼ BPL\_TEST2\_Batch setup

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

- FMU - BPL\_TEST2\_Batch\_linux\_om\_me.fmu
- Setup-file - BPL\_TEST2\_Batch\_fmpy\_explore.py

```

%%bash
git clone https://github.com/janpeter19/BPL_TEST2_Batch

Cloning into 'BPL_TEST2_Batch'...

%cd BPL_TEST2_Batch

/content/BPL_TEST2_Batch/BPL_TEST2_Batch

run -i BPL_TEST2_Batch_fmpy_explore.py

Linux - run FMU pre-compiled OpenModelica 1.21.x

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 simula
- describe() - describe culture, broth, parameters, variables with values

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()
<Figure size 708.661x566.929 with 0 Axes>

%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]

import warnings
warnings.filterwarnings("ignore")

```

## ▼ BPL\_TEST2\_Batch - demo

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

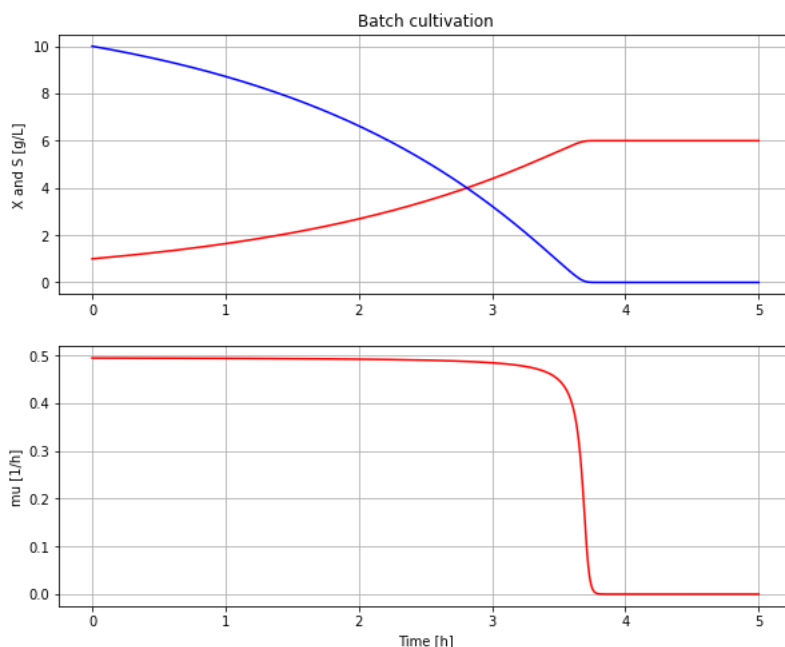
```
# Pump schedule parameter
```

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

```

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

```

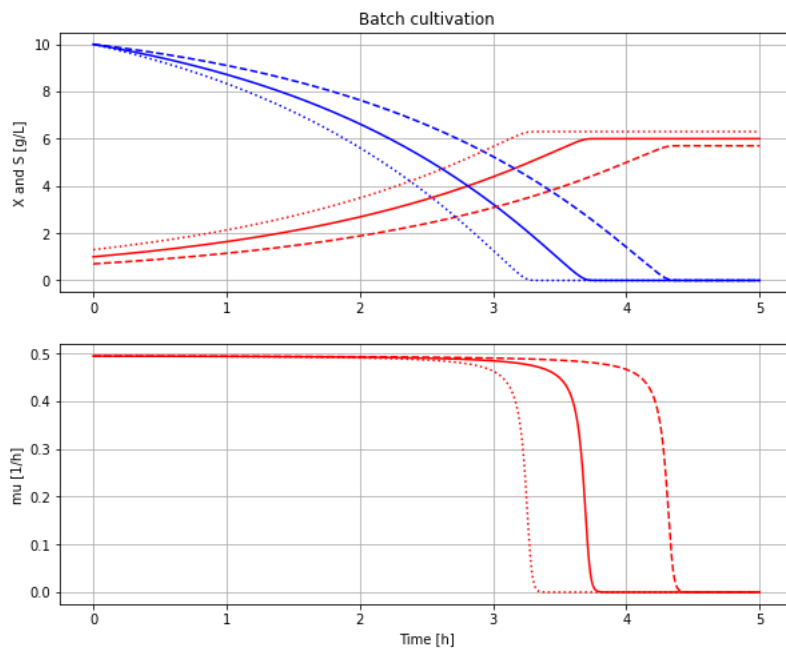


```

# Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_0=value); simu(5)

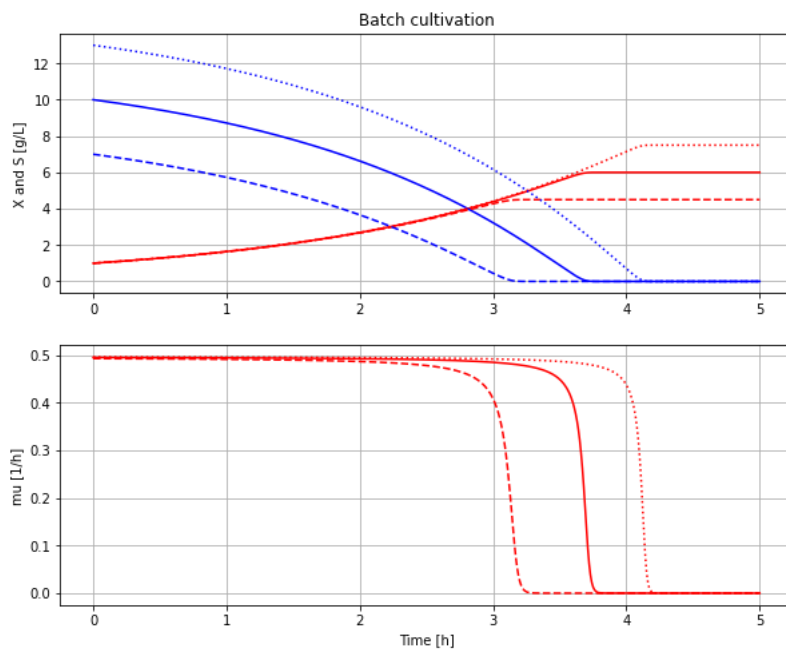
```

```
# Restore default value of VX_0
init(VX_0=1.0)
```



```
# Simulation where initial value of substrate VS_0 is varied
newplot(plotType='TimeSeries')
for value in [10, 7, 13]: init(VS_0=value); simu(5)

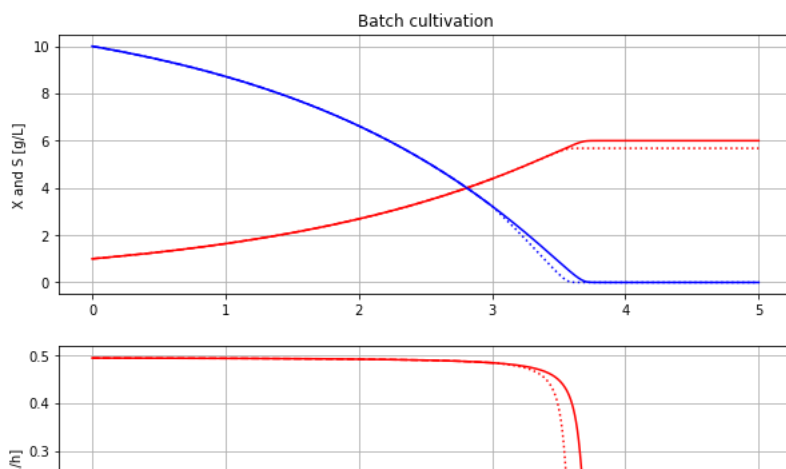
# Restore default value of VS_0
init(VS_0=10)
```



```
# Simulation where metabolism is changed after 3 hours
newplot(plotType='TimeSeries')
simu(5)

simu(3)
par(Y=0.4, qSmax=1.0/(0.4/0.5)); simu(2, 'cont')

# Restore default value of Y and qSmax
par(Y=0.5, qSmax=1.0)
```



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

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

```
0 1 2 3 4 5
```

```
# Growth rate variable at the end of the cultivation
```

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

```
Cell specific growth rate variable : 0.0 [ 1/h ]
```

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

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

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

```
MSL: 3.2.3 - used components: none
```

```
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.Batch
-Generated: 2023-01-19T09:34:26Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.1.1-beta
-Interaction: FMU-explore for FMPy version 0.9.7c
```