

✓ BPL_TEST2_Batch script with FMPy

The key library FMPy 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 22.04.3 LTS
  Release:       22.04
  Codename:      jammy
```

```
%env PYTHONPATH=
```

```
➤ env: PYTHONPATH=
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
```

```
!chmod +x Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
```

```
!bash ./Miniconda3-py312_24.3.0-0-Linux-x86_64.sh -b -f -p /usr/local
```

```
import sys
```

```
sys.path.append('/usr/local/lib/python3.12/site-packages/')
```

```
➤ --2024-11-07 07:32:06-- https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
  Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.191.158, 104.16.32.241, 2606:4700::6810:20f1, ...
  Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.191.158|:443... connected.
  HTTP request sent, awaiting response... 200 OK
  Length: 143351488 (137M) [application/octet-stream]
  Saving to: 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh'
```

```
Miniconda3-py312_24 100%[=====] 136.71M 113MB/s in 1.2s
```

```
2024-11-07 07:32:07 (113 MB/s) - 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh' saved [143351488/143351488]
```

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

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

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

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

```
➤
  ca-certificates                2024.3.11-h06a4308_0 --> 2024.9.24-h06a4308_0
  certifi                       2024.2.2-py312h06a4308_0 --> 2024.8.30-py312h06a4308_0
  conda                         24.3.0-py312h06a4308_0 --> 24.9.2-py312h06a4308_0
  openssl                       3.0.13-h7f8727e_0 --> 3.0.15-h5eee18b_0
```

```
frozendict-2.4.2      | 36 KB      | : 100% 1.0/1 [00:00<00:00, 2.86it/s]
```

```
frozendict-2.4.2      | 36 KB      | : 100% 1.0/1 [00:00<00:00, 2.86it/s]  
conda-24.9.2          | 1.1 MB     | : 100% 1.0/1 [00:00<00:00, 1.55it/s]
```

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

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

```
🔄 conda 24.9.2  
   Python 3.12.2
```

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

```
🔄
```

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

```

#!conda install matplotlib --yes

#!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

```

run -i BPL_TEST2_Batch_fmpy_explore.py

```

 Linux - run FMU pre-compiled OpenModelica

```

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_Batch - demo

```

describe('culture'); print(); #describe('liquidphase')                                # Pump schedule parameter

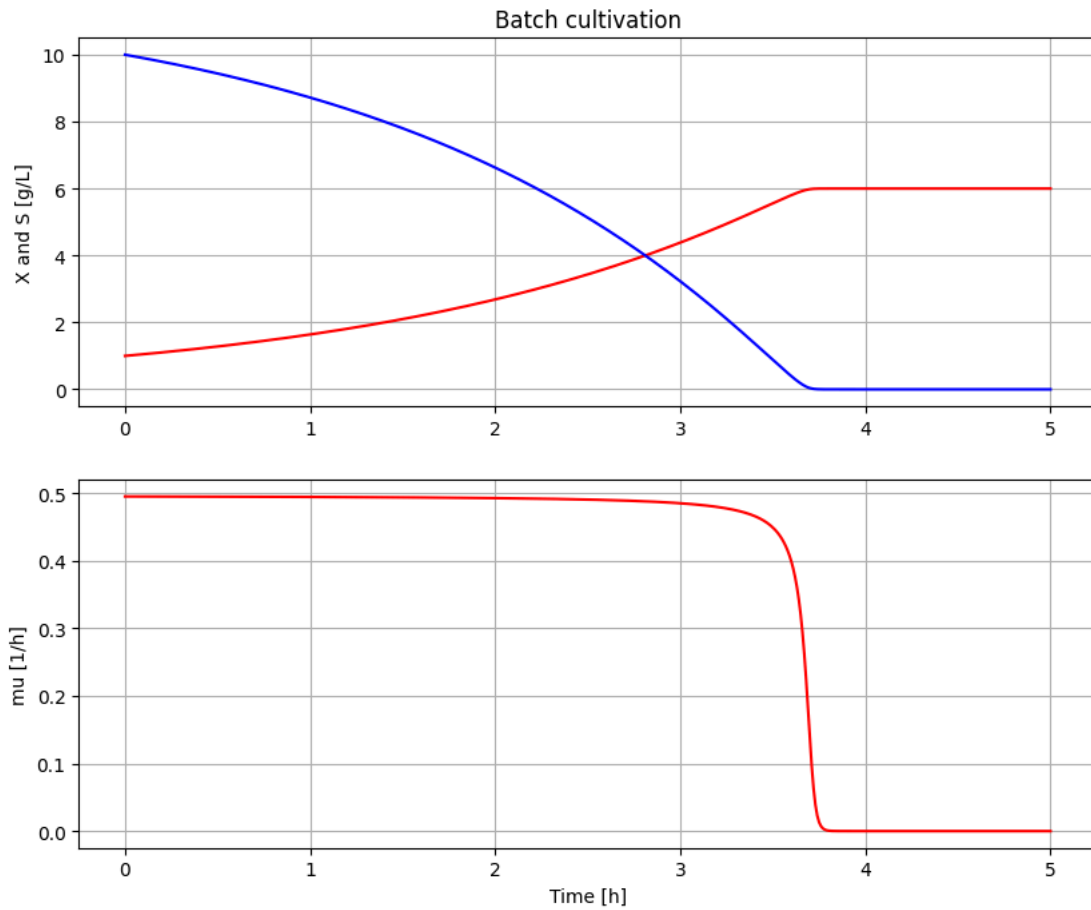
```

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

```

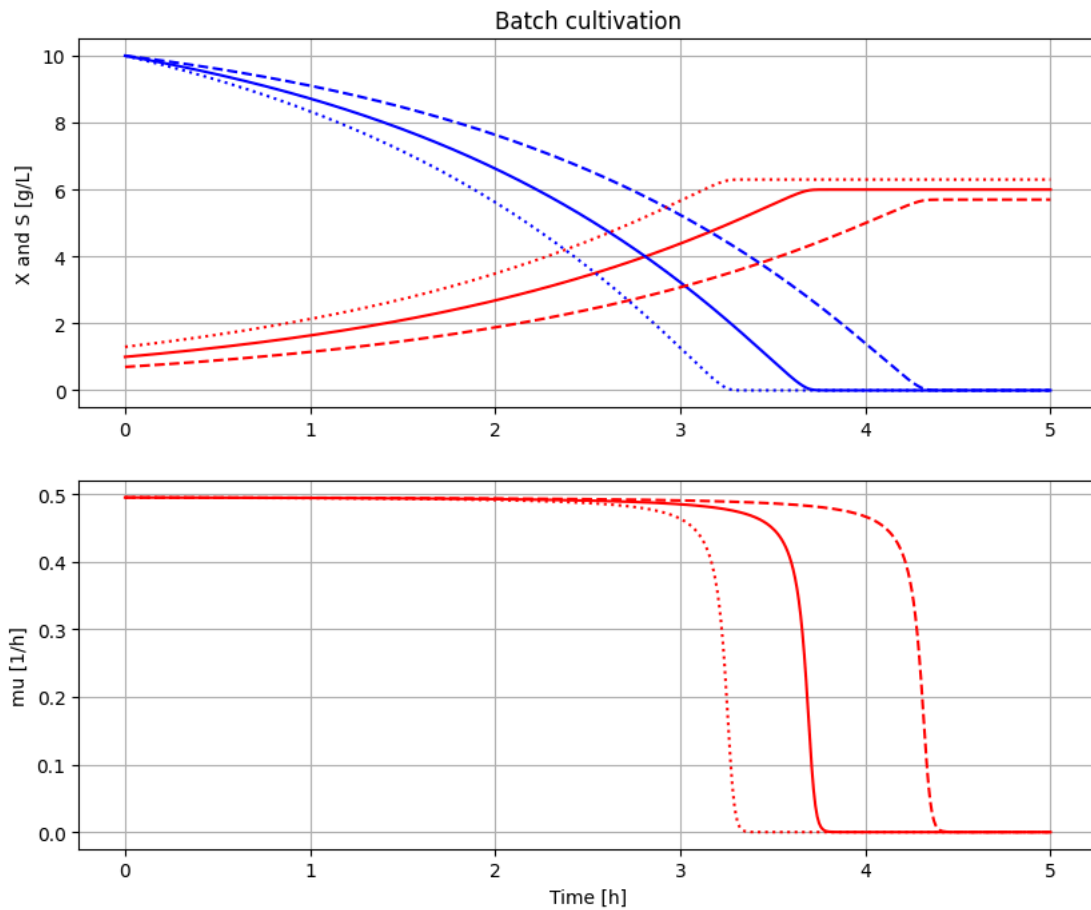
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu()

```



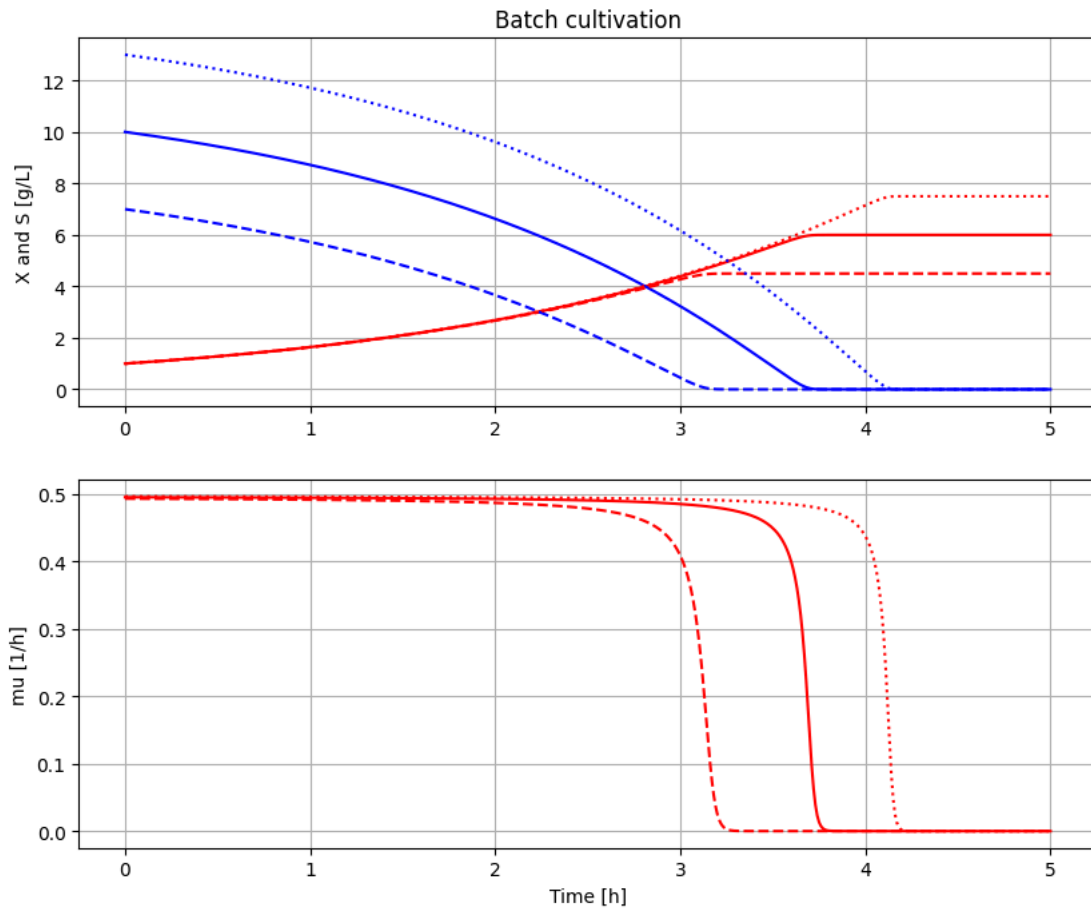
```
# Simulation were initial value of biomass VX_start is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

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



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

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



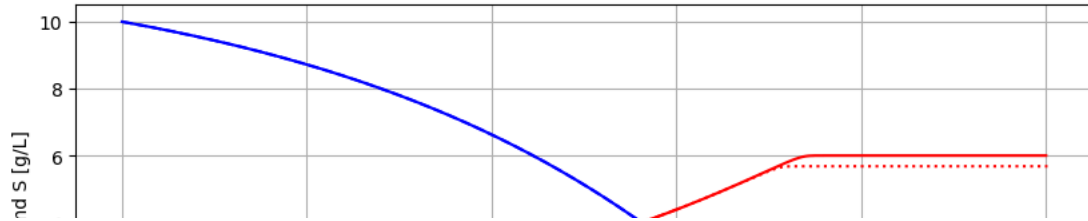
```
# Simulation where metabolism is changed after 3 hours
newplot(plotType='TimeSeries')
simu(5)

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)
```



Batch cultivation



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



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

```
# 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: 3.10.12
-Scipy: not installed in the notebook
-FMPy: 0.3.20
-FMU by: OpenModelica Compiler OpenModelica 1.25.0~dev-133-ga5470be
-FMI: 2.0
-Type: ME
-Name: BPL.Examples_TEST2.Batch
-Generated: 2024-11-06T21:35:34Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.3.0
-Interaction: FMU-explore for FMPy version 1.0.1
```

Start coding or [generate](#) with AI.