

▼ BPL_TEST2_Batch script with PyFMI

The key library PyFMI is installed.

After the installation a small application BPL_TEST2_Batch 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-py39_23.1.0-1-Linux-x86_64.sh
!chmod +x Miniconda3-py39_23.1.0-1-Linux-x86_64.sh
!bash ./Miniconda3-py39_23.1.0-1-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.9/site-packages/')

--2023-04-20 09:14:19--  https://repo.anaconda.com/miniconda/Miniconda3-py39_23.1.0-1-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.130.3, 104.16.131.3, 2606:4700::6810:8303, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.130.3|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 69888122 (67M) [application/x-sh]
Saving to: 'Miniconda3-py39_23.1.0-1-Linux-x86_64.sh'

Miniconda3-py39_23. 100%[=====] 66.65M  144MB/s   in 0.5s

2023-04-20 09:14:19 (144 MB/s) - 'Miniconda3-py39_23.1.0-1-Linux-x86_64.sh' saved [69888122/69888122]

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 23.3.1  
Python 3.9.16
```

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

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

▼ 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_explore.me.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_explore.py

Linux - run FMU pre-comiled 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]

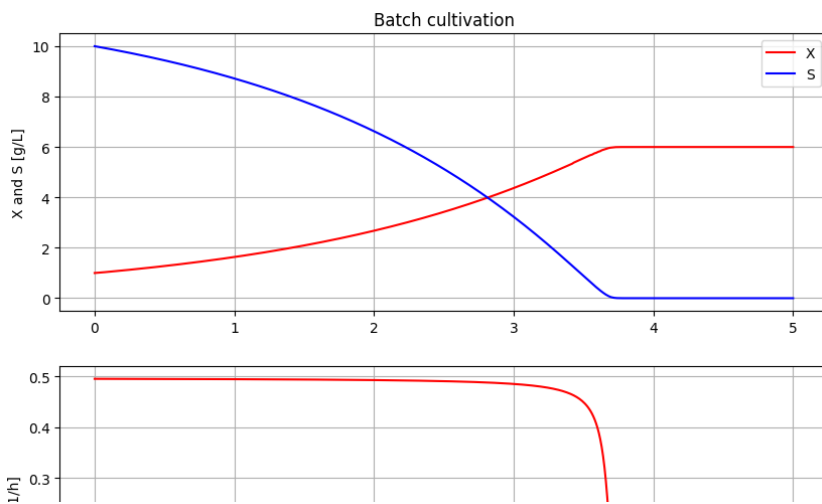
import warnings
warnings.filterwarnings("ignore")
```

▼ BPL_TEST2_Batch - demo

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

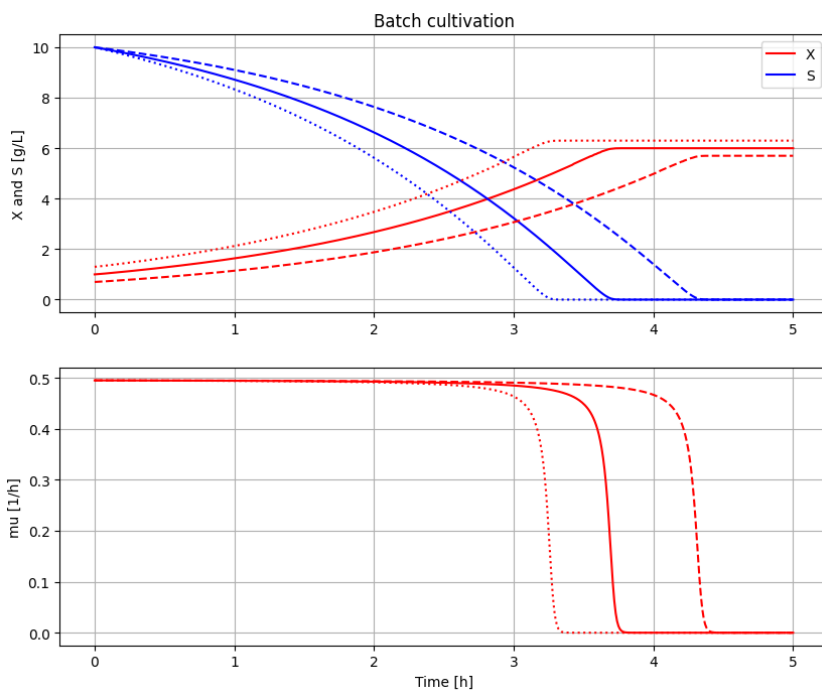
Simplified text book model - only substrate S and cell concentration X

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



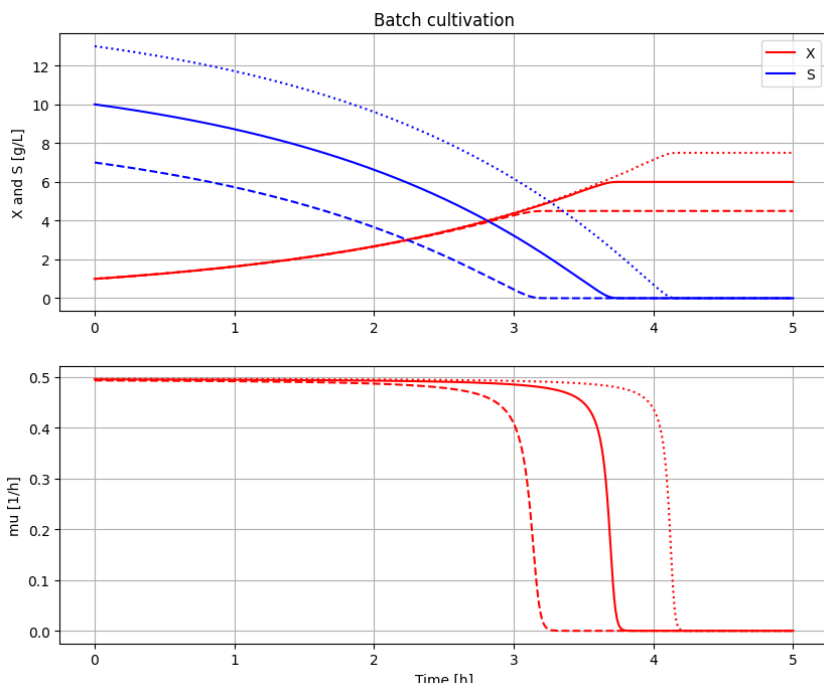
```
# Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_0=value); simu(5)

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



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

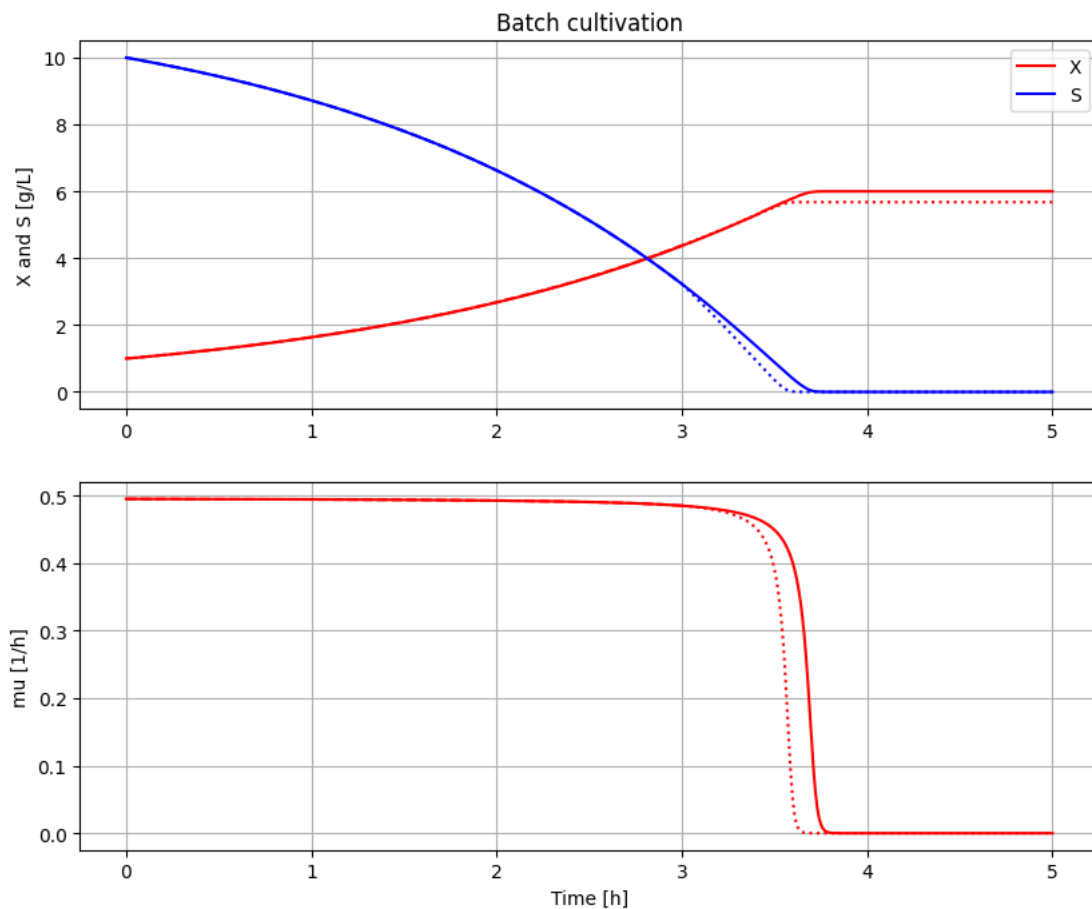
# Restore default value of VS_0
init(VS_0=10)
```



```
# 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 : 0.4
qSmax : 1.25
Ks : 0.1
```

```
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
-PyFMI: 2.10.2
-FMU by: OpenModelica Compiler OpenModelica 1.21.0
-FMI: 2.0
-Type: FMUModelME2
-Name: BPL_TEST2.Batch
-Generated: 2023-04-19T18:37:26Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.1.1
-Interaction: FMU-explore version 0.9.7
```

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✓ 0s completed at 11:16

