

## ▼ BPL\_TEST2\_Batch script with PyFMI ver 2.9.8

The key library PyFMI ver 2.9.8 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/')

--2023-02-13 09:48:22--  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::6810:8203, ...
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  145MB/s   in 0.4s

2023-02-13 09:48:23 (145 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
```

```

package setuptools conflicts for:
wheel -> setuptools
pip -> setuptools
python=3.8 -> pip -> setuptools
conda[version='>=22.11.1'] -> ruamel.yaml[version='>=0.11.14,<0.18'] -> setuptools
conda[version='>=22.11.1'] -> setuptools[version='>=31.0.1']

Package suitesparse conflicts for:
assimulo -> sundials[version='>=6.4.0,<6.5.0a0'] -> suitesparse[version='>=5.10.1,<6.0a0']
sundials -> suitesparse[version='>=5.10.1,<6.0a0']

```

```

Package scipy conflicts for:
assimulo -> scipy
pyfmi -> scipyThe following specifications were found to be incompatible with your system:

```

```

- feature:/linux-64::__glibc==2.31=0
- feature:|@/linux-64::__glibc==2.31=0
- assimulo -> libgfortran-ng -> __glibc[version='>=2.17']
- libopenblas -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
- numpy -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
- openssl -> libgcc-ng[version='>=7.5.0'] -> __glibc[version='>=2.17']
- python=3.8 -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
- scipy -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
- tbb -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']

```

Your installed version is: 2.31

```

!conda --version
!python --version

conda 22.11.1
Python 3.8.15

```

```

!conda install -c conda-forge pyfmi --yes # Install the key package
- conda-forge/linux-64::libblas==3.9.0=16_linux64_openblasdone

```

```

==> WARNING: A newer version of conda exists. <==
current version: 22.11.1
latest version: 23.1.0

```

Please update conda by running

```
$ conda update -n base -c defaults conda
```

Or to minimize the number of packages updated during conda update use

```
conda install conda=23.1.0
```

## Package Plan ##

```

environment location: /usr/local

added / updated specs:
- pyfmi

```

The following packages will be downloaded:

package	build		
conda-22.11.1	py38h578d9bd_1	905 KB	conda-forge
Total:		905 KB	

The following packages will be REMOVED:

Downloading and Extracting Packages

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/BPL_TEST2_Batch

run -i BPL_TEST2_Batch_explore_me.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 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>

fmu_model

'xBPL_TEST2_Batch_linux_om_me.fmu'

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

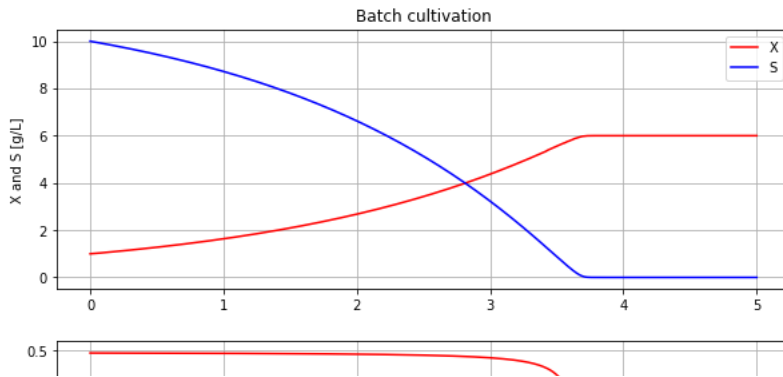
import warnings
warnings.filterwarnings("ignore")
```

## ▼ BPL\_TEST2\_Batch - demo

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

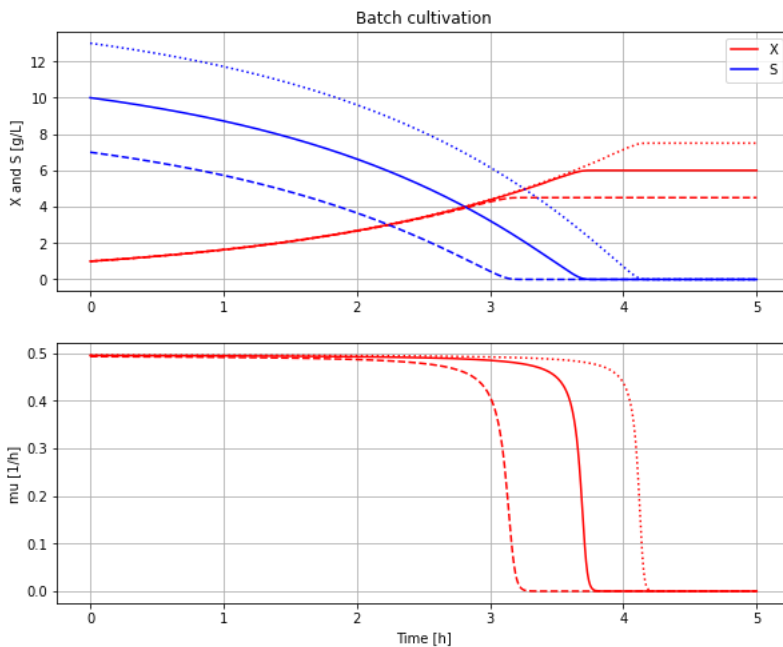
Simplified text book model - only substrate S and cell concentration X

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



```
# Simulation were initial value of 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)
```



```
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']
```

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

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

```
system_info()
```



```
System information
-OS: Linux
-Python: 3.8.10
-Scipy: not installed in the notebook
-PyFMI: 2.9.8
-FMU by: OpenModelica Compiler OpenModelica 1.21.0~dev-185-g9d983b8
-FMI: 2.0
-Type: FMUModelME2
-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 version 0.9.6
```

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✓ 0s completed at 10:54

