

## ▼ 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/')

--2023-01-20 12:46:05--  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  307MB/s   in 0.2s

2023-01-20 12:46:05 (307 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
```

```
pyrmi -> assimulo[version='>=5.0'] -> sundials[version='>=6.4.0,<6.5.0a0']
assimulo -> sundials[version='>=6.4.0,<6.5.0a0']
```

Package mpfr conflicts for:

```
sundials -> suitesparse[version='>=5.10.1,<6.0a0'] -> mpfr[version='>=4.0.2,<5.0a0|>=4.1.0,<5.0a0']
suitesparse -> mpfr[version='>=4.0.2,<5.0a0|>=4.1.0,<5.0a0']
```

Package scipy conflicts for:

```
assimulo -> scipy
pyfmi -> scipy
```

Package enum34 conflicts for:

```
conda-content-trust -> cryptography -> enum34
```

conda -> enum34The 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
```

Collecting package metadata (current\_repodata.json): done

Solving environment: /

The environment is inconsistent, please check the package plan carefully

The following packages are causing the inconsistency:

```
- conda-forge/linux-64::numpy==1.24.1=py38hab0fcb9_0
- conda-forge/linux-64::tbb==2021.7.0=h924138e_1
- conda-forge/linux-64::suitesparse==5.10.1=h9e50725_1
- conda-forge/linux-64::scipy==1.10.0=py38h10c12cc_0
- conda-forge/linux-64::pyfmi==2.9.8=py38h26c90d9_1
- conda-forge/linux-64::assimulo==3.3=py38h71f17ff_1
- conda-forge/linux-64::libcblas==3.9.0=16_linux64_openblas
- conda-forge/linux-64::sundials==6.4.1=h89a52a3_0
- conda-forge/linux-64::liblapack==3.9.0=16_linux64_openblas
- conda-forge/linux-64::libhwloc==2.8.0=h32351e8_1
- conda-forge/linux-64::libopenblas==0.3.21=pthreads_h78a6416_3
- conda-forge/linux-64::fmilib==2.4.1=h27087fc_0
- conda-forge/linux-64::libblas==3.9.0=16_linux64_openblasdone
```

## Package Plan ##

environment location: /usr/local

added / updated specs:

```
- pyfmi
```

The following packages will be REMOVED:

```
libgomp-11.2.0-h1234567_1
```

The following packages will be UPDATED:

```
ca-certificates    pkgs/main::ca-certificates-2022.10.11~ --> conda-forge::ca-certificates-2022.12.7-ha878542_0
libgcc-ng          pkgs/main::libgcc-ng-11.2.0-h1234567_1 --> conda-forge::libgcc-ng-12.2.0-h65d4601_19
libstdcxx-ng       pkgs/main::libstdcxx-ng-11.2.0-h12345~ --> conda-forge::libstdcxx-ng-12.2.0-h46fd767_19
openssl            pkgs/main::openssl-1.1.1s-h7f8727e_0 --> conda-forge::openssl-1.1.1s-h0b41bf4_1
```

The following packages will be SUPERSEDED by a higher-priority channel:

```
_libgcc_mutex      pkgs/main::_libgcc_mutex-0.1-main --> conda-forge::_libgcc_mutex-0.1-conda_forge
_openmp_mutex      pkgs/main::_openmp_mutex-5.1-1_gnu --> conda-forge::_openmp_mutex-4.5-2_kmp_llvm
certifi            pkgs/main/linux-64::certifi-2022.12.7~ --> conda-forge/noarch::certifi-2022.12.7-pyhd8ed1ab_0
conda              pkgs/main::conda-22.11.1-py38h06a4308~ --> conda-forge::conda-22.11.1-py38h578d9bd_1
```

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/BPL_TEST2_Batch

run -i BPL_TEST2_Batch_explore_me.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 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

'BPL_TEST2_Batch_linux_om_me.fmu'

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

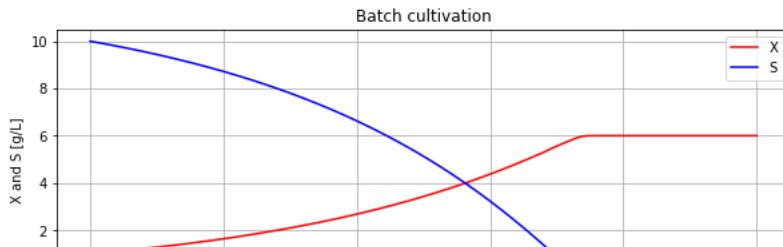
import warnings
warnings.filterwarnings("ignore")
```

## ▼ BPL\_TEST2\_Batch - demo

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

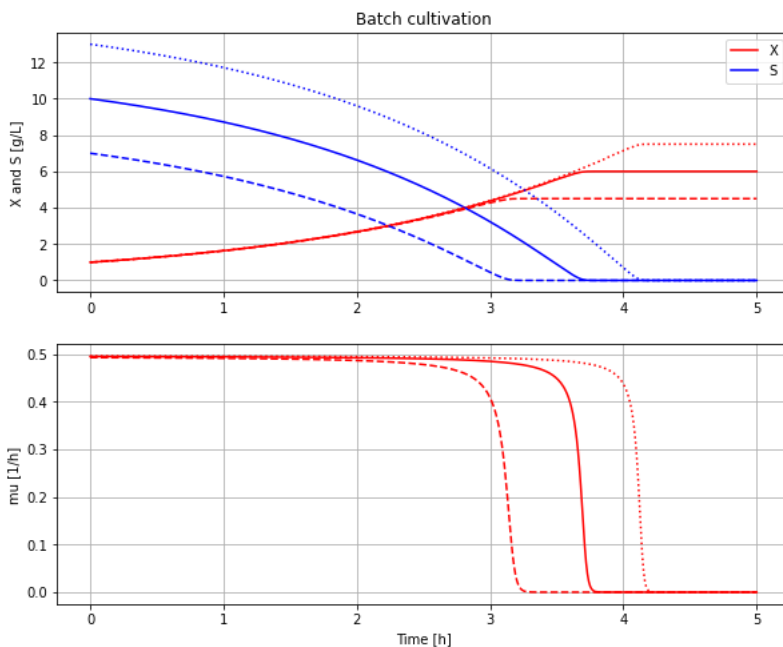
Simplified text book model - only substrate S and cell concentration X

# 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 0.9.6e
```

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✓ 0s completed at 13:50

