

▼ 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/')

--2023-01-19 10:43:03--  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  82.1MB/s   in 0.8s

2023-01-19 10:43:04 (82.1 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
```

```
sqlite-3.40.1      | 1.2 MB      | : 100% 1.0/1 [00:00<00:00, 1.85it/s]
```

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

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

```
conda 22.11.1  
Python 3.8.15
```

```
!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

```
# Filter out DeprecationWarnings for 'np.float as alias' is needed - wish I could make filter more narrow
#import warnings
#warnings.filterwarnings("ignore")
```

```
%%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_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 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]
```

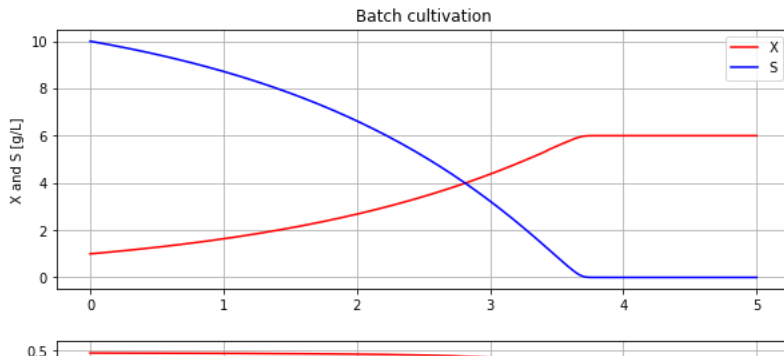
```
import warnings
warnings.filterwarnings("ignore")
```

▼ BPL_TEST2_Batch - demo

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

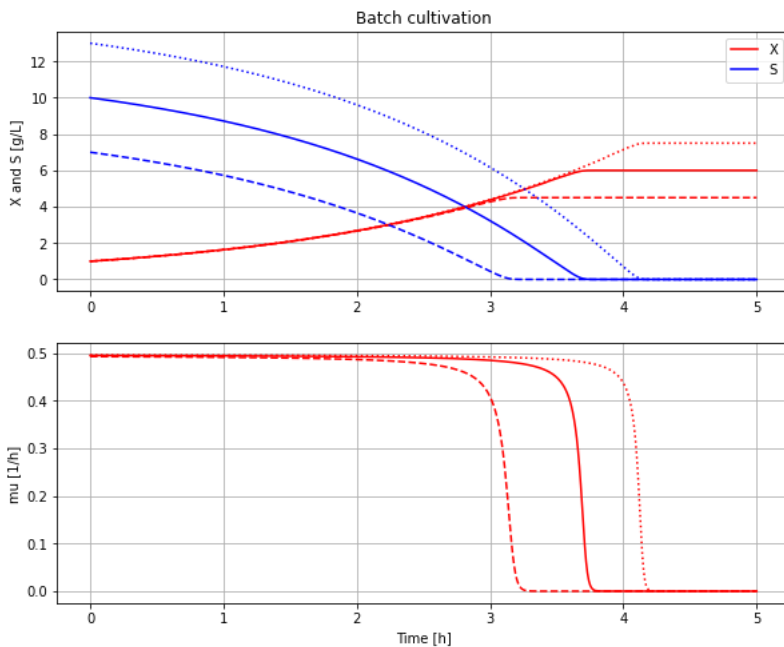
```
Simplified text book model - only substrate S and cell concentration X
```

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



```
# Simulation were initial value of 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: information not accessible from this FMU
```

```
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: MSL.version information not accessible
```

-Description: BPL.version information not accessible
-Interaction: FMU-explore version 0.9.6d

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✓ 0s completed at 11:44

