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-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/')
```

```
--2024-03-05 08:05:56--  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   156MB/s    in 0.4s

2024-03-05 08:05:56 (156 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 24.1.2
     Python 3.9.18
```

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

```
!conda install matplotlib --yes
```

```
Channels:
 - defaults
 - conda-forge
Platform: linux-64
Collecting package metadata (repodata.json): done
Solving environment: done

## Package Plan ##

  environment location: /usr/local

  added / updated specs:
    - matplotlib


The following packages will be downloaded:

    package                    |            build
    ---------------------------|-----------------
    matplotlib-3.8.0           |   py39h06a4308_0           8 KB
    matplotlib-base-3.8.0      |   py39h1128e8f_0         6.8 MB
    pyparsing-3.0.9            |   py39h06a4308_0         151 KB
    ------------------------------------------------------------
                                           Total:         6.9 MB

The following NEW packages will be INSTALLED:

  matplotlib         pkgs/main/linux-64::matplotlib-3.8.0-py39h06a4308_0

The following packages will be UPDATED:

  matplotlib-base    conda-forge::matplotlib-base-3.5.2-py~ --> pkgs/main::matplotlib-base-3.8.0-py39h1128e8f_0

The following packages will be SUPERSEDED by a higher-priority channel:

  certifi            conda-forge/noarch::certifi-2024.2.2-~ --> pkgs/main/linux-64::certifi-2024.2.2-py39h06a4308_0
  conda              conda-forge::conda-24.1.2-py39hf3d152~ --> pkgs/main::conda-24.1.2-py39h06a4308_0
  pyparsing          conda-forge/noarch::pyparsing-3.1.1-p~ --> pkgs/main/linux-64::pyparsing-3.0.9-py39h06a4308_0



Downloading and Extracting Packages:
matplotlib-base-3.8. | 6.8 MB    | :   0% 0/1 [00:00<?, ?it/s]
pyparsing-3.0.9      | 151 KB    | :   0% 0/1 [00:00<?, ?it/s]

matplotlib-base-3.8. | 6.8 MB    | :  12% 0.12435465623668675/1 [00:00<00:00,  1.24it/s]
pyparsing-3.0.9      | 151 KB    | : 100% 1.0/1 [00:00<00:00,  9.61it/s]
pyparsing-3.0.9      | 151 KB    | : 100% 1.0/1 [00:00<00:00,  9.61it/s]

matplotlib-3.8.0     | 8 KB      | : 100% 1.0/1 [00:00<00:00,  9.21it/s]




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

```
#!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 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
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]
```

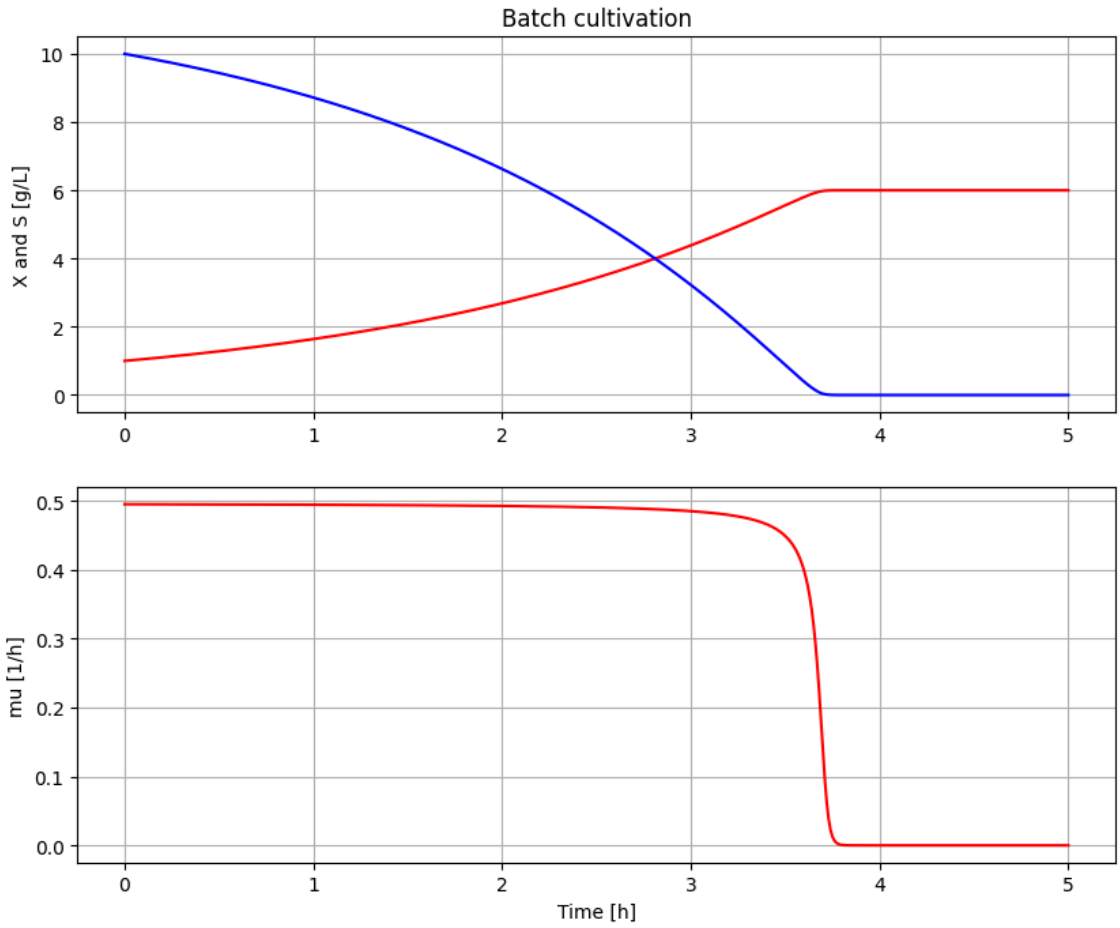
```
import warnings
warnings.filterwarnings("ignore")
```

BPL_TEST2_Batch - demo

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

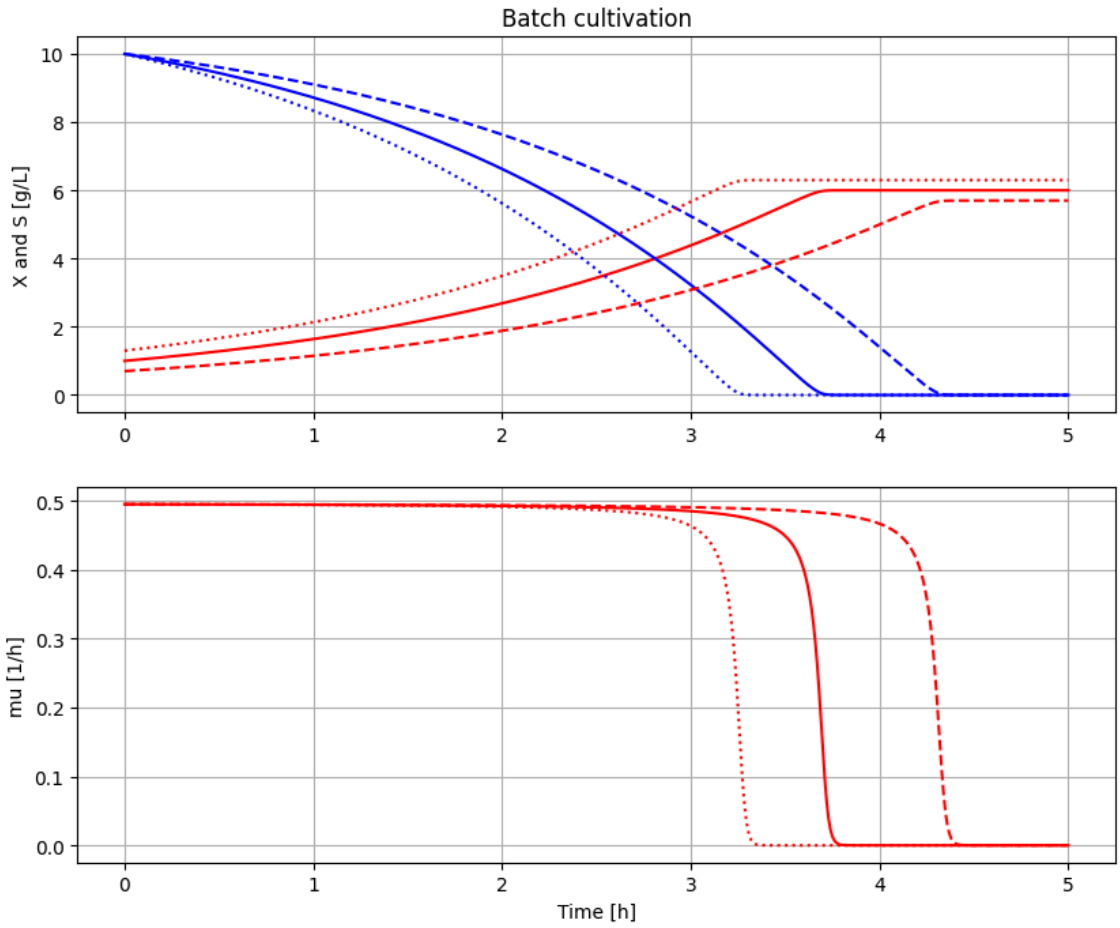
```
Simplified text book model - only substrate S and cell concentration X
```

```
# 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 were 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)
```

Batch cultivation

```
# 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)
```