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 PYTH0NPATH=

```
⇒ env: PYTHONPATH=
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
!chmod +x Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
!bash ./Miniconda3-py312_24.3.0-0-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.12/site-packages/')
```

```
--2024-05-21 06:21:12-- <a href="https://repo.anaconda.com/miniconda/Miniconda3-py312 24.3.0-0-Linux-x86 64.sh">https://repo.anaconda.com/miniconda/Miniconda3-py312 24.3.0-0-Linux-x86 64.sh</a> Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.191.158, 104.16.32.241, 2606:4700::6810:20f1, ... Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.191.158|:443... connected. HTTP request sent, awaiting response... 200 0K Length: 143351488 (137M) [application/octet-stream] Saving to: 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh'
```

Miniconda3-py312 24 100%[===========] 136.71M 158MB/s in 0.9s

2024-05-21 06:21:13 (158 MB/s) - 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh' saved [143351488/143351488]

PREFIX=/usr/local Unpacking payload ...

Installing base environment...

Preparing transaction: ...working... done Executing transaction: ...working... done installation finished.

!conda update -n base -c defaults conda --yes

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

Package Plan

environment location: /usr/local

added / updated specs:
 - conda

The following packages will be downloaded:

package	build		
conda-24.5.0 frozendict-2.4.2 openssl-3.0.13	py312h06a4308_0 py312h06a4308_0 py312h06a4308_0 h7f8727e_1	1.2 36 5.2	KB
	Total:	6.5	 МВ

The following NEW packages will be INSTALLED:

```
frozendict pkgs/main/linux-64::frozendict-2.4.2-py312h06a4308_0
```

The following packages will be UPDATED:

```
onda 24.3.0-py312h06a4308_0 --> 24.5.0-py312h06a4308_0
```

openssl

```
Downloading and Extracting Packages:
                   | 5.2 MB
| 1.2 MB
openssl-3.0.13
                                        |:
                                               0% 0/1 [00:00<?, ?it/s]
conda-24.5.0
                                               0% 0/1 [00:00<?, ?it/s]
openssl-3.0.13
                         | 5.2 MB
                                              0% 0.002997347135570501/1 [00:00<00:53, 53.55s/it]
                                        | : 44% 0.43853215920344746/1 [00:00<00:00, 2.48it/s]
| : 1% 0.01293349794914382/1 [00:00<00:13, 13.92s/it]
frozendict-2.4.2
                          | 36 KB
conda-24.5.0
                          1.2 MB
                                        | : 100% 1.0/1 [00:00<00:00, 2.48it/s]
| : 100% 1.0/1 [00:00<00:00, 1.78it/s]
frozendict-2.4.2
                         | 36 KB
conda-24.5.0
                         i 1.2 MB
```

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

!conda --version
!python --version

⇒ conda 24.5.0 Python 3.12.2

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

₹

```
Preparing transaction: done
Verifying transaction: done
Executing transaction: done
#!conda install matplotlib ---yes

#!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

Simulation with default values of the process

newplot(plotType='TimeSeries')

simu()

```
%%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
Fr Linux - run FMU pre-compiled OpenModelica 1.23.0-dev
    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

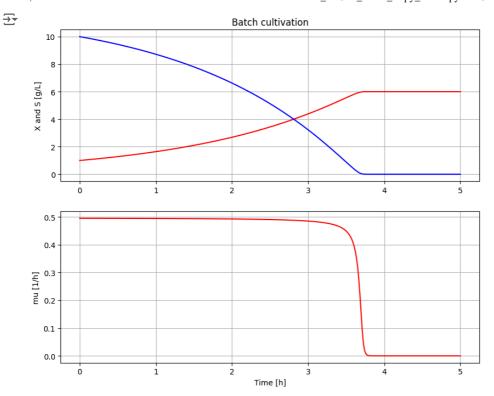
     - show()

    show plot from previous simulation

     - disp()
                    - display parameters and initial values from the last simulation

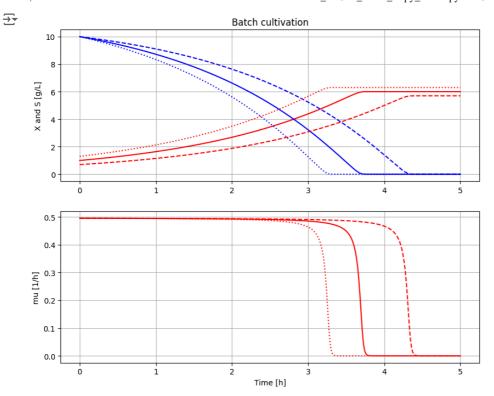
    describe() - describe culture, broth, parameters, variables with values/units

    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 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)

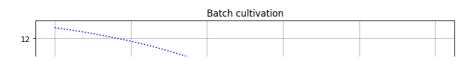
Restore default value of VX_start
init(VX_start=1.0)



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)

 $\overline{\pm}$

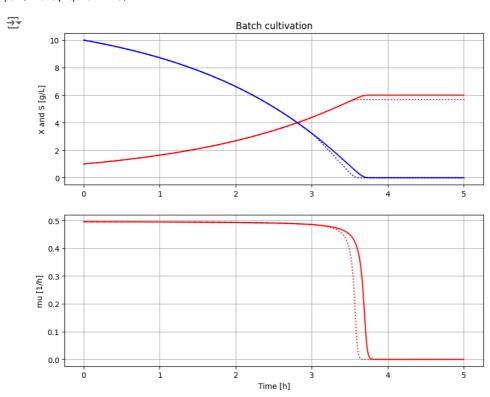


Simulation where metabolism is changed after 3 hours
newplot(plotType='TimeSeries')
simu(5)

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

# Growth rate variable at the end of the cultivation 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()

Control of the cultivation of the cultivation
```