∨ 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-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/')
```

```
--2024-07-06 16:08:32--  https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.191.158, 104.16.32.241, 2606:4700::6810:bf9e, .
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.191.158|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 143351488 (137M) [application/octet-stream]
Saving to: 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh'

Miniconda3-py312_24 100%[===================>] 136.71M  93.4MB/s    in 1.5s

2024-07-06 16:08:34 (93.4 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
```

```
The following packages will be downloaded:

    package                    |            build
    ---------------------------|-----------------
    certifi-2024.6.2           | py312h06a4308_0          161 KB
    conda-24.5.0               | py312h06a4308_0          1.2 MB
    frozendict-2.4.2           | py312h06a4308_0           36 KB
    openssl-3.0.14             |       h5eee18b_0          5.2 MB
    ------------------------------------------------------------
                                           Total:          6.6 MB

The following NEW packages will be INSTALLED:
```

```
certifi-2024.6.2       | 161 KB    | :    0% 0/1 [00:00<?, ?it/s]


openssl-3.0.14         | 5.2 MB    | :    0% 0.0030006342237126712/1 [00:00<01:16, 76.58s/it]

openssl-3.0.14         | 5.2 MB    | :   54% 0.5441479449199349/1 [00:00<00:00,  2.07it/s]


frozendict-2.4.2       | 36 KB     | :   44% 0.43853215920344746/1 [00:00<00:00,  1.24it/s]
conda-24.5.0           | 1.2 MB    | :    1% 0.01293349794914382/1 [00:00<00:28, 29.31s/it]

certifi-2024.6.2       | 161 KB    | : 100% 1.0/1 [00:00<00:00,  2.78it/s]

certifi-2024.6.2       | 161 KB    | : 100% 1.0/1 [00:00<00:00,  2.78it/s]


frozendict-2.4.2       | 36 KB     | : 100% 1.0/1 [00:00<00:00,  2.25it/s]


openssl-3.0.14         | 5.2 MB    | : 100% 1.0/1 [00:01<00:00,  1.02s/it]
conda-24.5.0           | 1.2 MB    | : 100% 1.0/1 [00:01<00:00,  1.04it/s]
```

```
    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

```
%%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

```
    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")
```
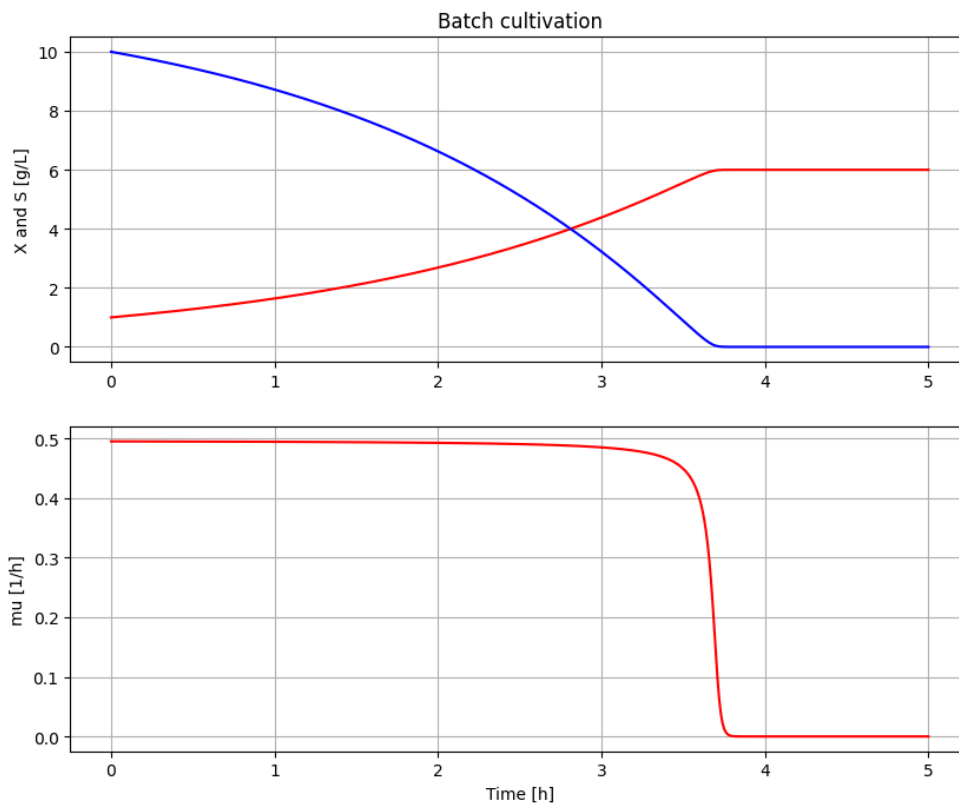
⌄ BPL_TEST2_Batch - demo

```
describe('culture'); print(); #describe('liquidphase')                              # Pump schedule parame
```
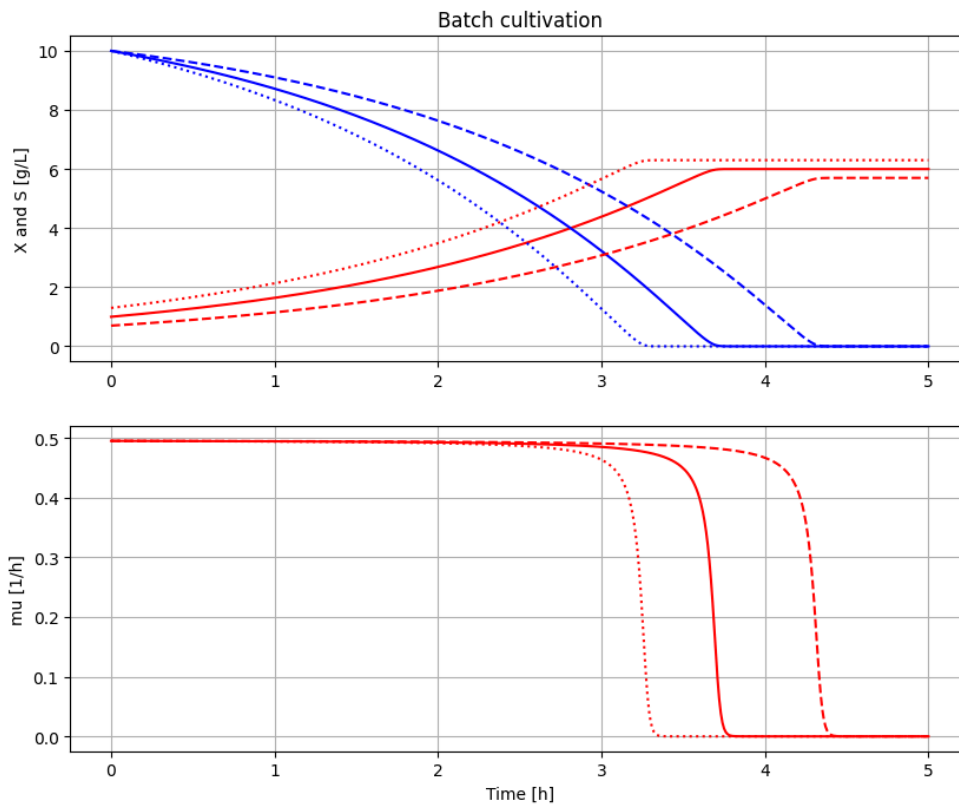
⇥ Simplified text book model – only substrate S and cell concentration X

```
# 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)
```

Batch cultivation

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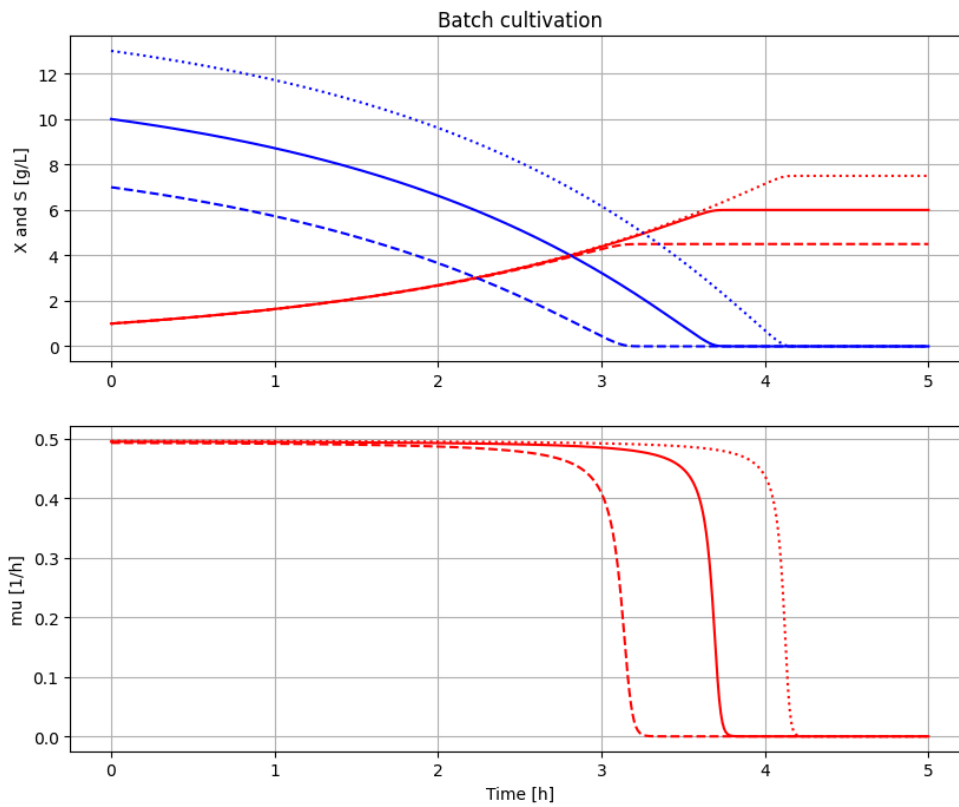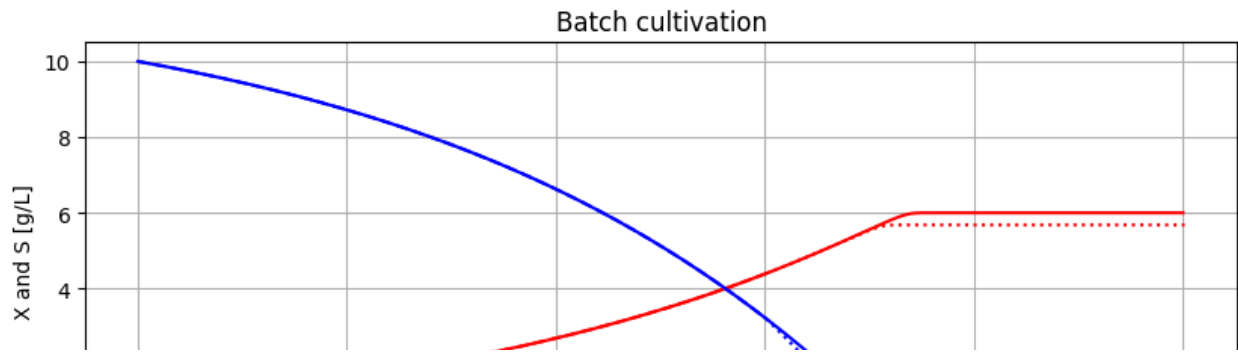
```
# Simulation where metabolism is changed after 3 hours
newplot(plotType='TimeSeries')
simu(5)

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)
```

Batch cultivation


```
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()
```