⌄ BPL_TEST2_Batch script with PyFMI

The key library PyFMI 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 22.04.4 LTS
   Release:        22.04
   Codename:       jammy
```

```
%env PYTHONPATH=
```

```
⤓  env: PYTHONPATH=
```

```
!python --version
```

```
⤓  Python 3.11.11
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
!chmod +x Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
!bash ./Miniconda3-py311_24.11.1-0-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.11/site-packages/')
```

```
⤓  --2025-02-06 09:29:18--  https://repo.anaconda.com/miniconda/Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
   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 OK
   Length: 145900576 (139M) [application/octet-stream]
   Saving to: 'Miniconda3-py311_24.11.1-0-Linux-x86_64.sh'

   Miniconda3-py311_24 100%[===================>] 139.14M   121MB/s    in 1.1s

   2025-02-06 09:29:19 (121 MB/s) - 'Miniconda3-py311_24.11.1-0-Linux-x86_64.sh' saved [145900576/145900576]

   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
       ---------------------------|-----------------
       ca-certificates-2024.12.31 |       h06a4308_0         128 KB
       certifi-2025.1.31          | py311h06a4308_0         163 KB
       ------------------------------------------------------------
                                              Total:         291 KB

   The following packages will be UPDATED:

     ca-certificates                   2024.11.26-h06a4308_0 --> 2024.12.31-h06a4308_0
     certifi                 2024.8.30-py311h06a4308_0 --> 2025.1.31-py311h06a4308_0


   Downloading and Extracting Packages:
```

```
        certifi-2025.1.31    | 163 KB    | :    0% 0/1 [00:00<?, ?it/s]
        certifi-2025.1.31    | 163 KB    | : 100% 1.0/1 [00:00<00:00, 19.36it/s]
        certifi-2025.1.31    | 163 KB    | : 100% 1.0/1 [00:00<00:00, 11.39it/s]
        ca-certificates-2024 | 128 KB    | : 100% 1.0/1 [00:00<00:00,  9.53it/s]


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

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

```
⇥   conda 24.11.1
    Python 3.11.11
```

```
!conda config --set channel_priority strict
```

```
!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

```bash
%%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.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()
```
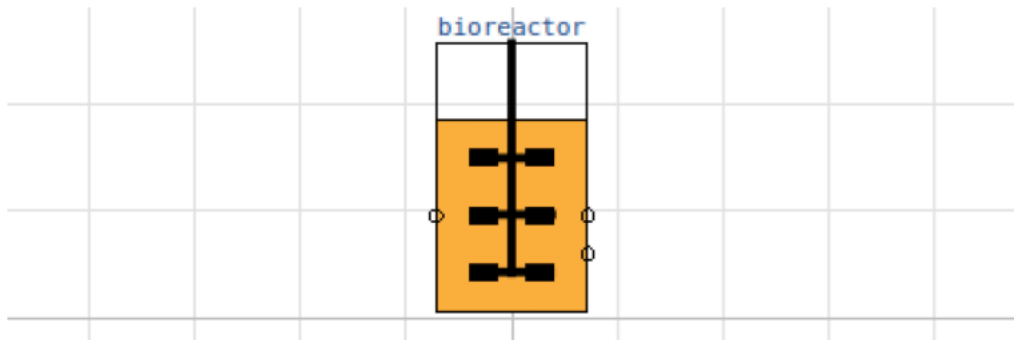
```python
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

˅ BPL_TEST2_Batch - demo

```
process_diagram()
```

```
No processDiagram.png file in the FMU, but try the file on disk.
```



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

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

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

```
Could not find cannot import name 'dopri5' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/__i
Could not find cannot import name 'rodas' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/__in
Could not find cannot import name 'odassl' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/__i
Could not find ODEPACK functions.
Could not find RADAR5
Could not find GLIMDA.
```
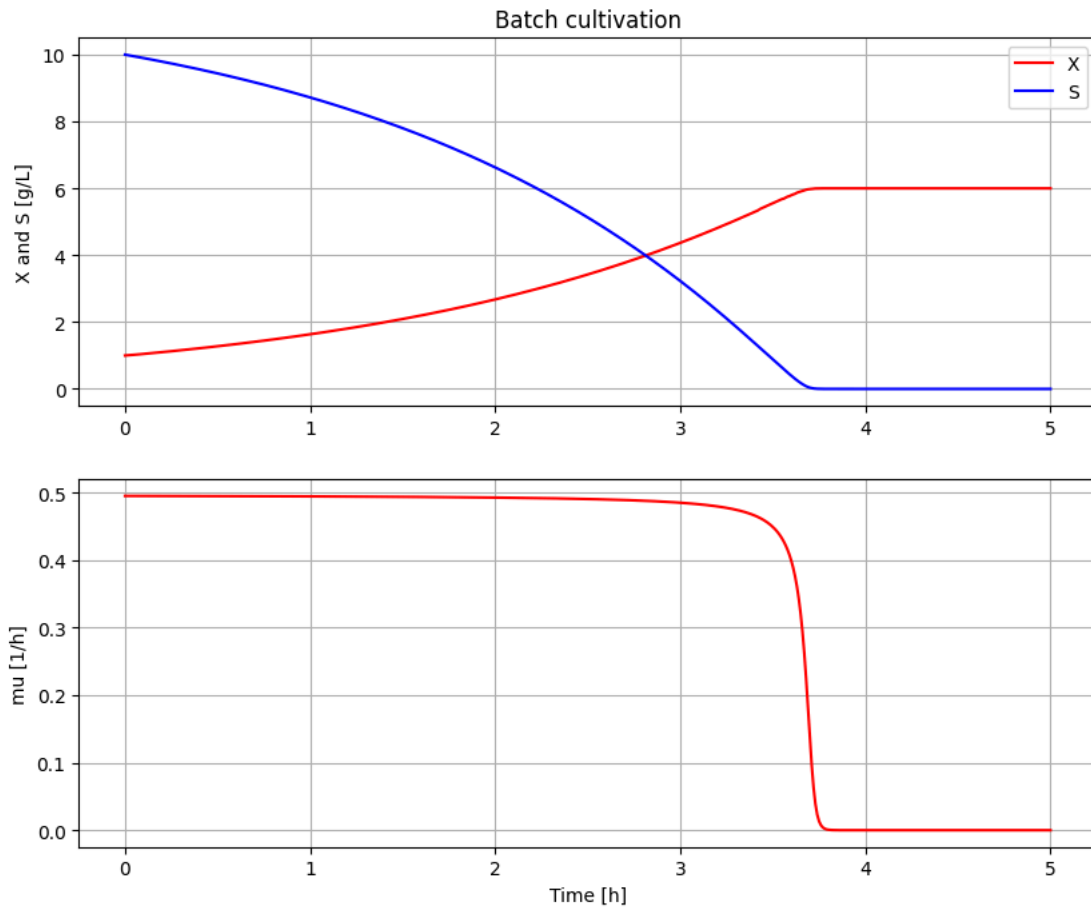


```
# Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

# Restore default value of VX_start
init(VX_start=1.0)
```

Batch cultivation
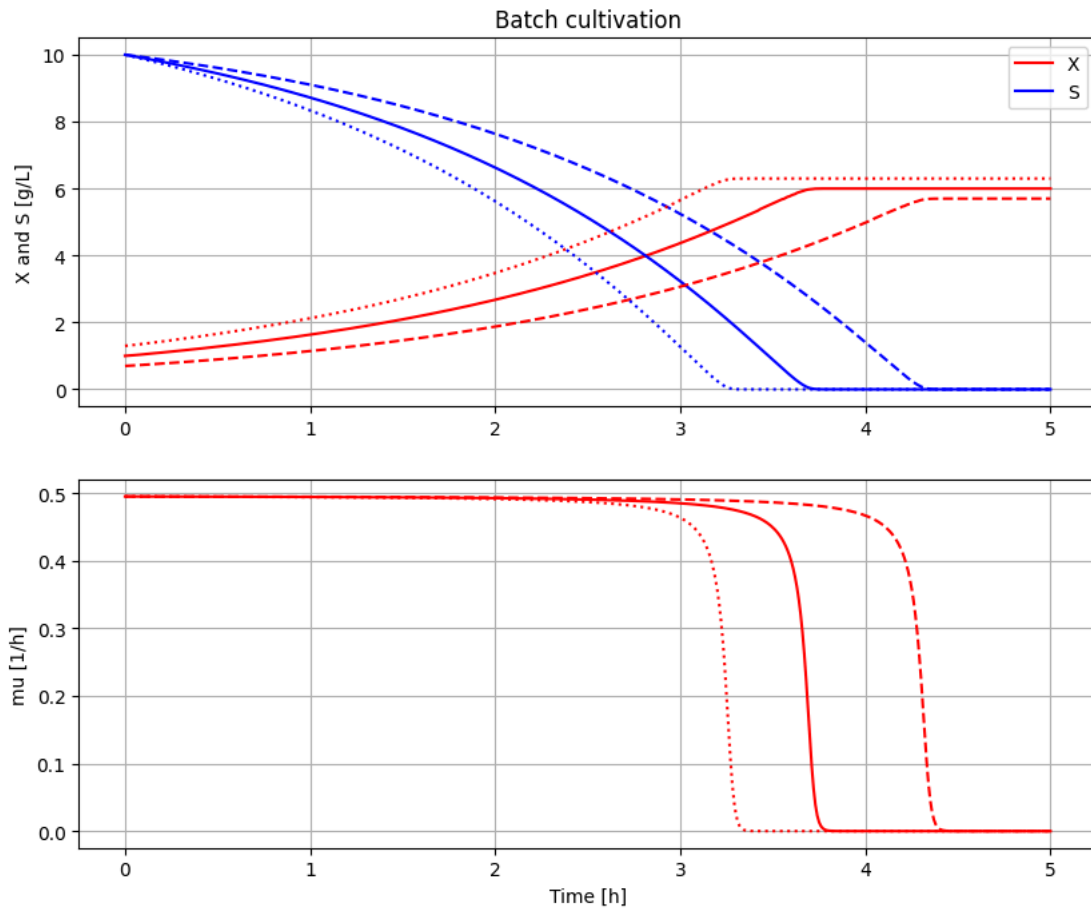
```
# Simulation were initial value of substrate VS_0 is varied
newplot(plotType='TimeSeries')
for value in [10, 7, 13]: init(VS_start=value); simu(5)

# Restore default value of VS_start
init(VS_start=10)
```
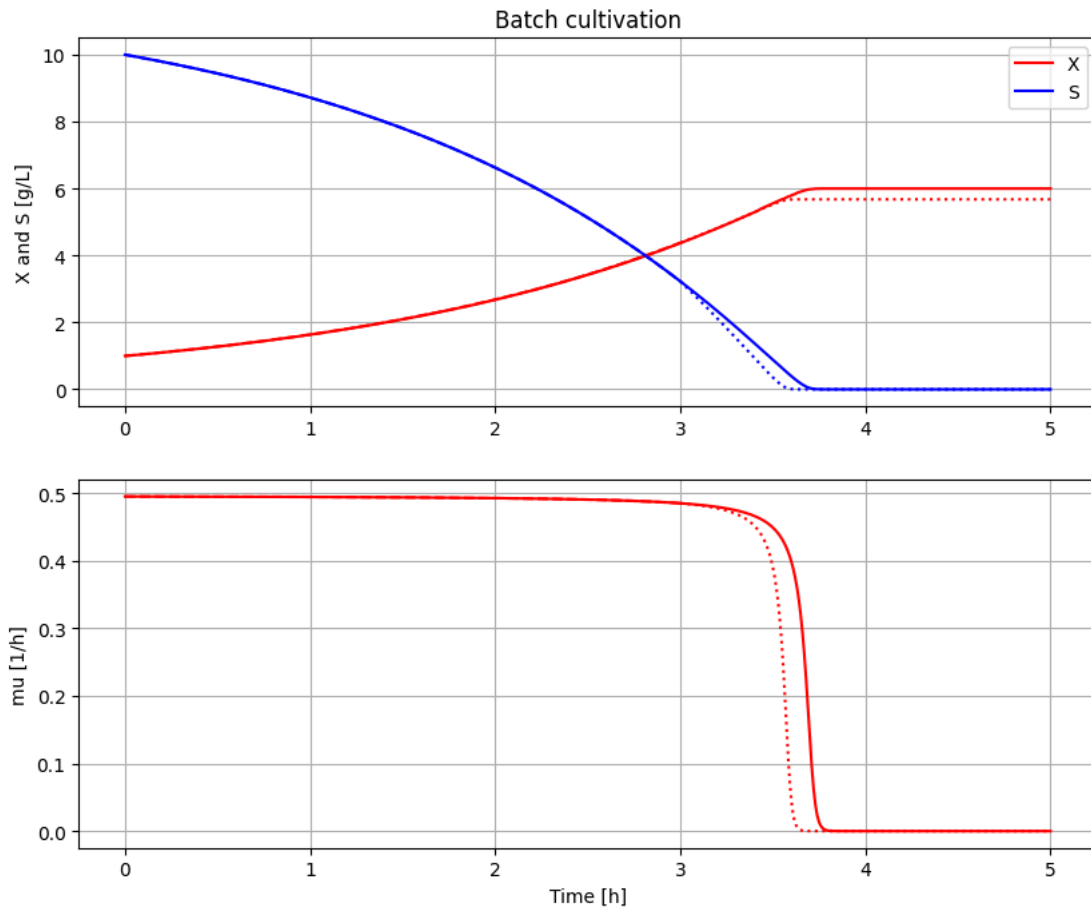

Batch cultivation
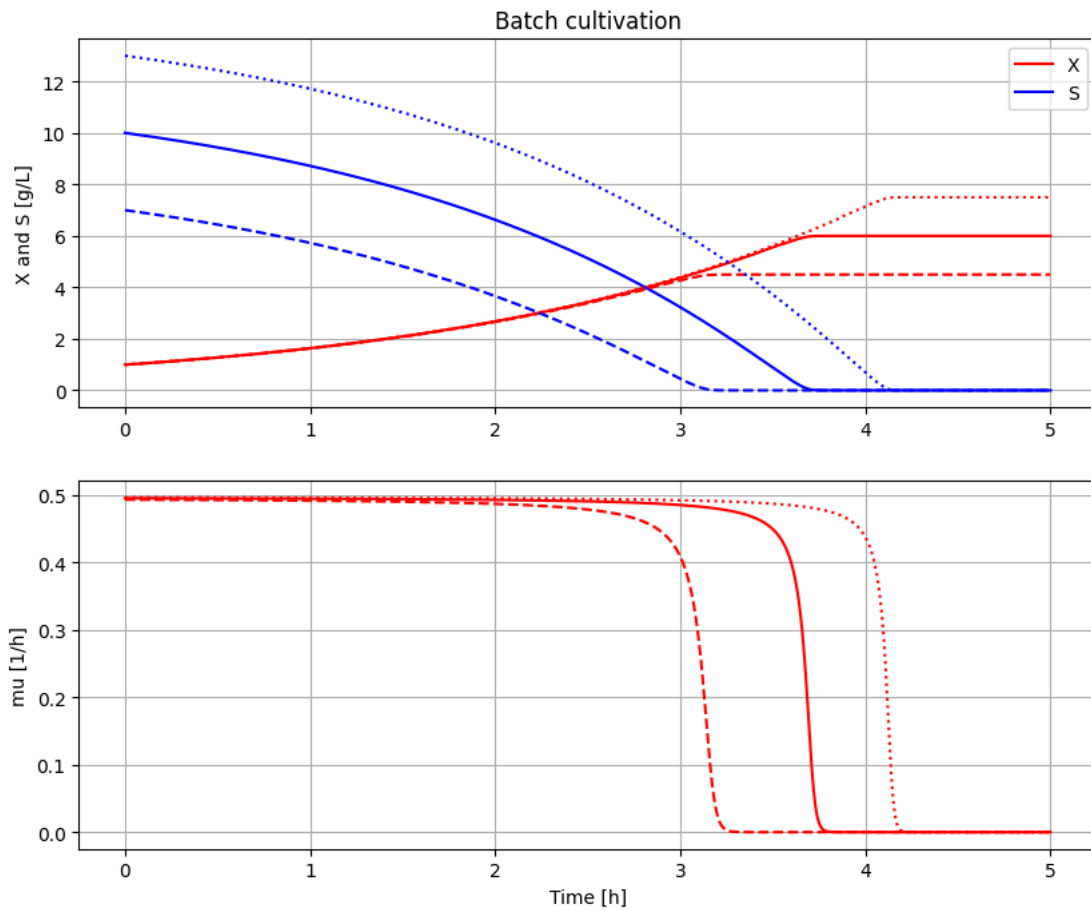
```
# Simulation where metabolism is changed after 3 hours
newplot(plotType='TimeSeries')
simu(5)

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)
```



```
disp('culture')
```

```
Y : 0.4
qSmax : 1.25
Ks : 0.1
```

```
describe('mu')
```

```
Cell specific growth rate variable : 0.0 [ 1/h ]
```

```
describe('parts')
```

```
['bioreactor', 'bioreactor.culture']
```