▾ BPL_TEST2_Batch script with FMPy ver 0.3.15

The key library FMPy ver 0.3.15 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 22.04.2 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/')

    --2023-09-11 06:33:27--  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::6810:8203,
    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   145MB/s    in 0.5s

    2023-09-11 06:33:28 (145 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
```

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

```
    conda 23.7.3
    Python 3.9.17
```

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

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

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

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

      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()
      <Figure size 984.252x787.402 with 0 Axes>
```

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

```
import warnings
warnings.filterwarnings("ignore")
```
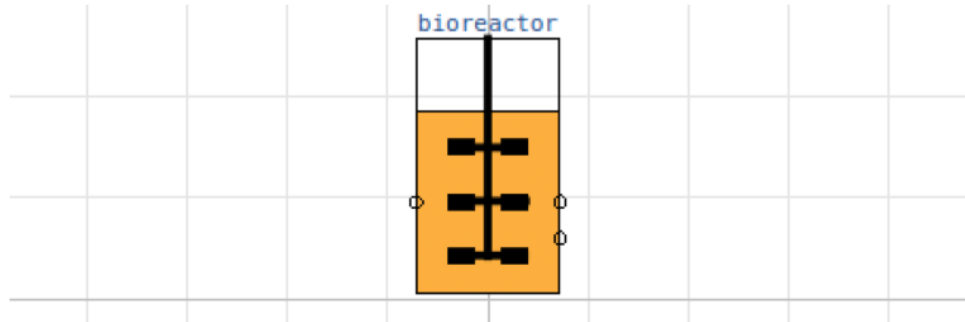
BPL_TEST2_Batch - demo

```
describe('culture'); print(); #describe('liquidphase')                              # Pump schedule pa
```
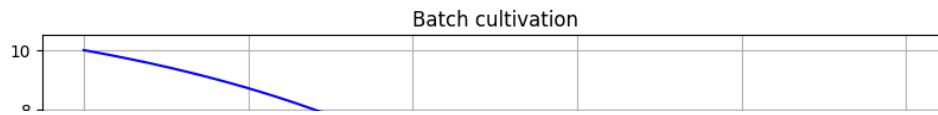
> Simplified text book model - only substrate S and cell concentration X

```
process_diagram()
```

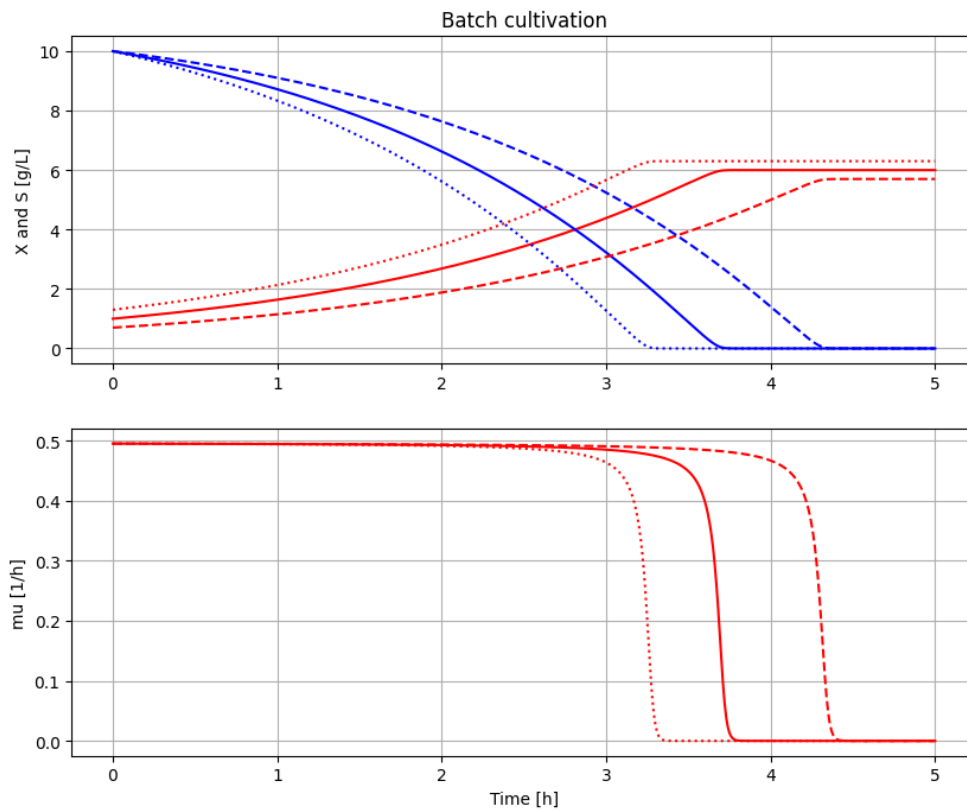> No processDiagram.png file in the FMU, but try the file on disk.


```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu()
```
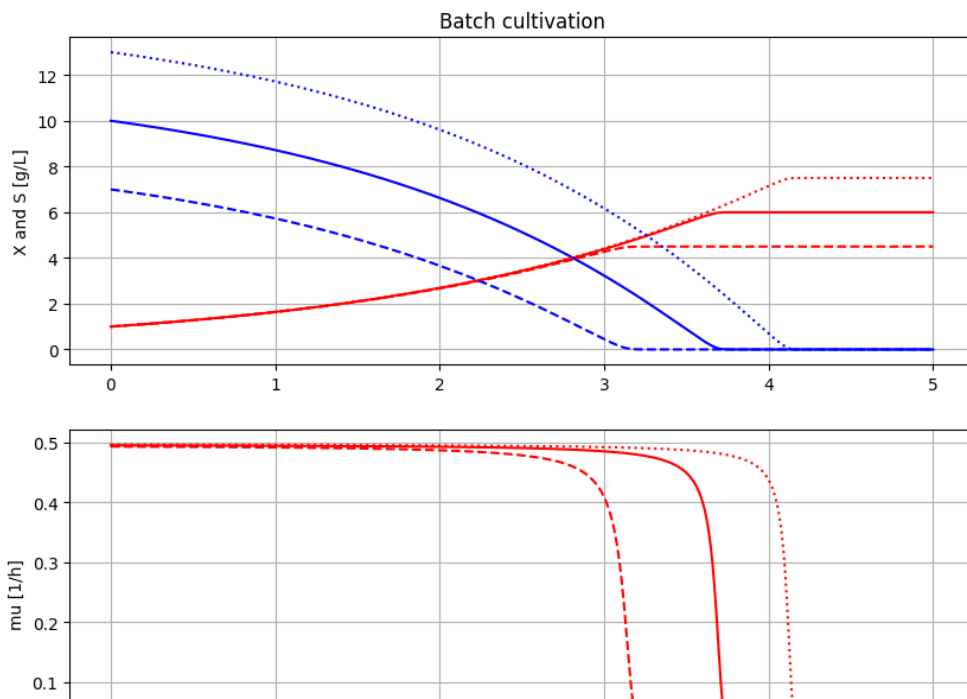
BPL_TEST2_Batch - demo

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

# Restore default value of VX_0
init(VX_0=1.0)
```



```
# 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)
```

```
# 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()

    System information
     -OS: Linux
     -Python: 3.10.12
     -Scipy: not installed in the notebook
     -FMPy: 0.3.15
     -FMU by: OpenModelica Compiler OpenModelica 1.21.0
     -FMI: 2.0
     -Type: ME
     -Name: BPL_TEST2.Batch
     -Generated: 2023-04-19T18:37:26Z
     -MSL: 3.2.3
     -Description: Bioprocess Library version 2.1.1
     -Interaction: FMU-explore for FMPy version 0.9.8
```

✓ 0s   completed at 09:00   ● ✕