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.
!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/')
```

```
--2024-10-03 05:52:36--  https://repo.anaconda.com/miniconda/Miniconda3-py312
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.1
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... conn
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   142MB/s    in 1.0s

2024-10-03 05:52:37 (142 MB/s) - ‘Miniconda3-py312_24.3.0-0-Linux-x86_64.sh’ s

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
```

```
    openssl                                  3.0.13-h7f8727e_0 --> 3.0.15-h5eee18


    Downloading and Extracting Packages:
    openssl-3.0.15       | 5.2 MB    | :   0% 0/1 [00:00<?, ?it/s]
    conda-24.9.1         | 1.1 MB    | :   0% 0/1 [00:00<?, ?it/s]

    certifi-2024.8.30    | 163 KB    | :   0% 0/1 [00:00<?, ?it/s]


    ca-certificates-2024 | 130 KB    | :   0% 0/1 [00:00<?, ?it/s]



    openssl-3.0.15       | 5.2 MB    | :   0% 0.003007460830410892/1 [00:00<01:01


    frozendict-2.4.2     | 36 KB     | :  44% 0.43853215920344746/1 [00:00<00:00,


    ca-certificates-2024 | 130 KB    | :  12% 0.12323429860849944/1 [00:00<00:01,
    conda-24.9.1         | 1.1 MB    | :   1% 0.013746684778550339/1 [00:00<00:18


    ca-certificates-2024 | 130 KB    | : 100% 1.0/1 [00:00<00:00,  1.96s/it]

    certifi-2024.8.30    | 163 KB    | :  10% 0.09811307196196202/1 [00:00<00:02,


    frozendict-2.4.2     | 36 KB     | : 100% 1.0/1 [00:00<00:00,  3.04it/s]



    frozendict-2.4.2     | 36 KB     | : 100% 1.0/1 [00:00<00:00,  3.04it/s]

    openssl-3.0.15       | 5.2 MB    | : 100% 1.0/1 [00:00<00:00,  1.27it/s]
    conda-24.9.1         | 1.1 MB    | : 100% 1.0/1 [00:00<00:00,  1.21it/s]









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

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

```
conda 24.9.1
Python 3.12.2
```

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

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

    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()
```

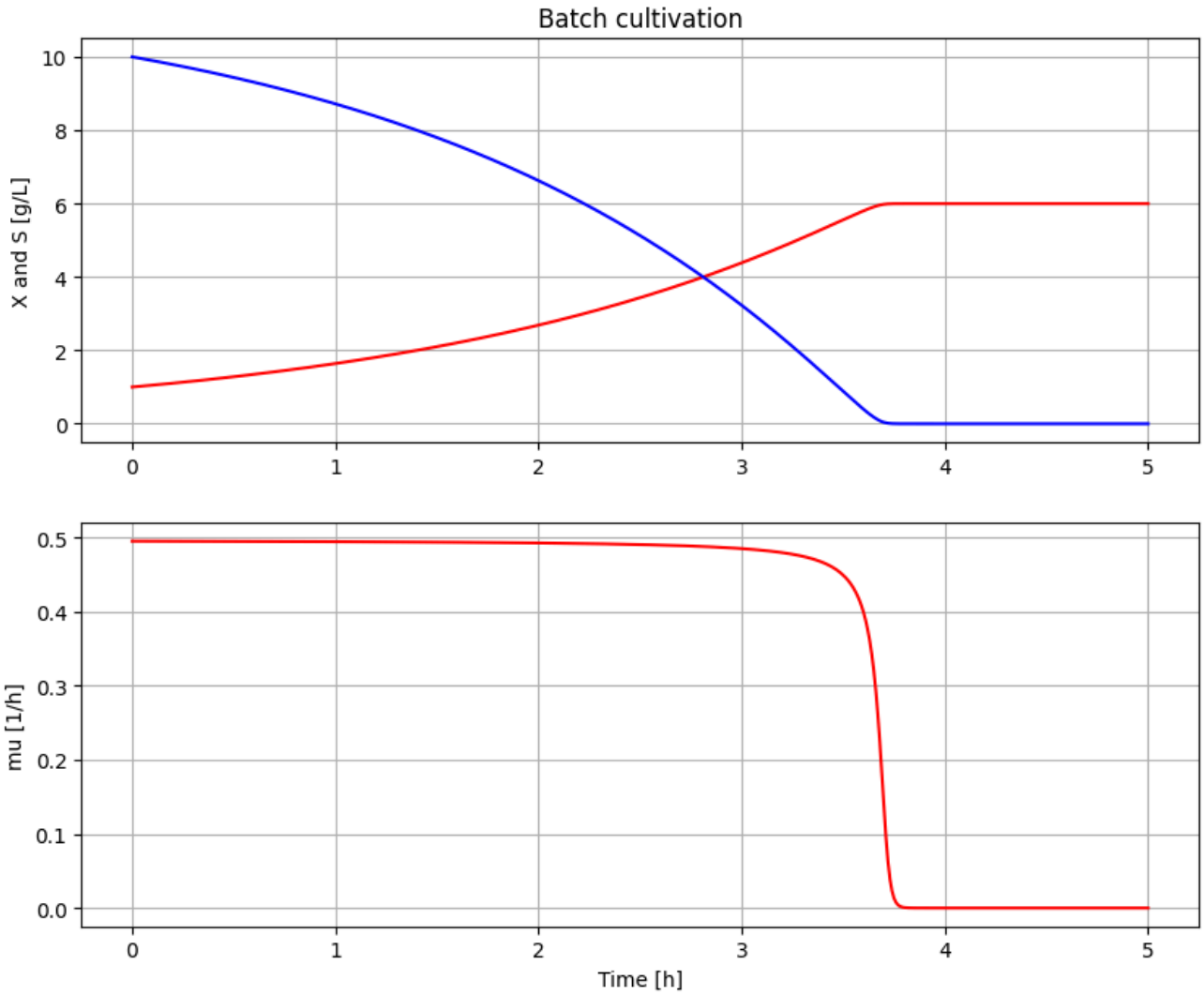
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]


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

BPL_TEST2_Batch - demo

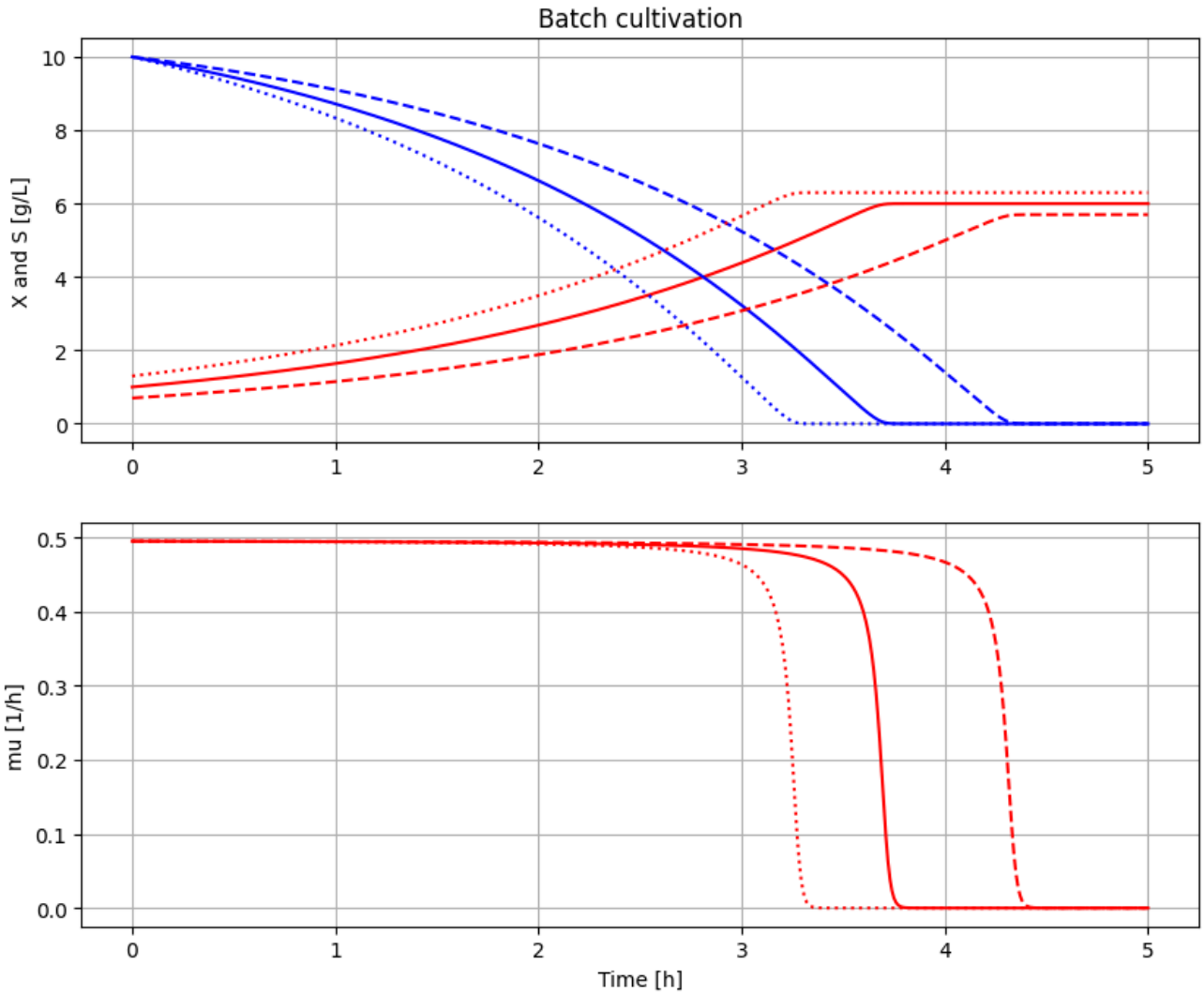
```
describe('culture'); print(); #describe('liquidphase')
```

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

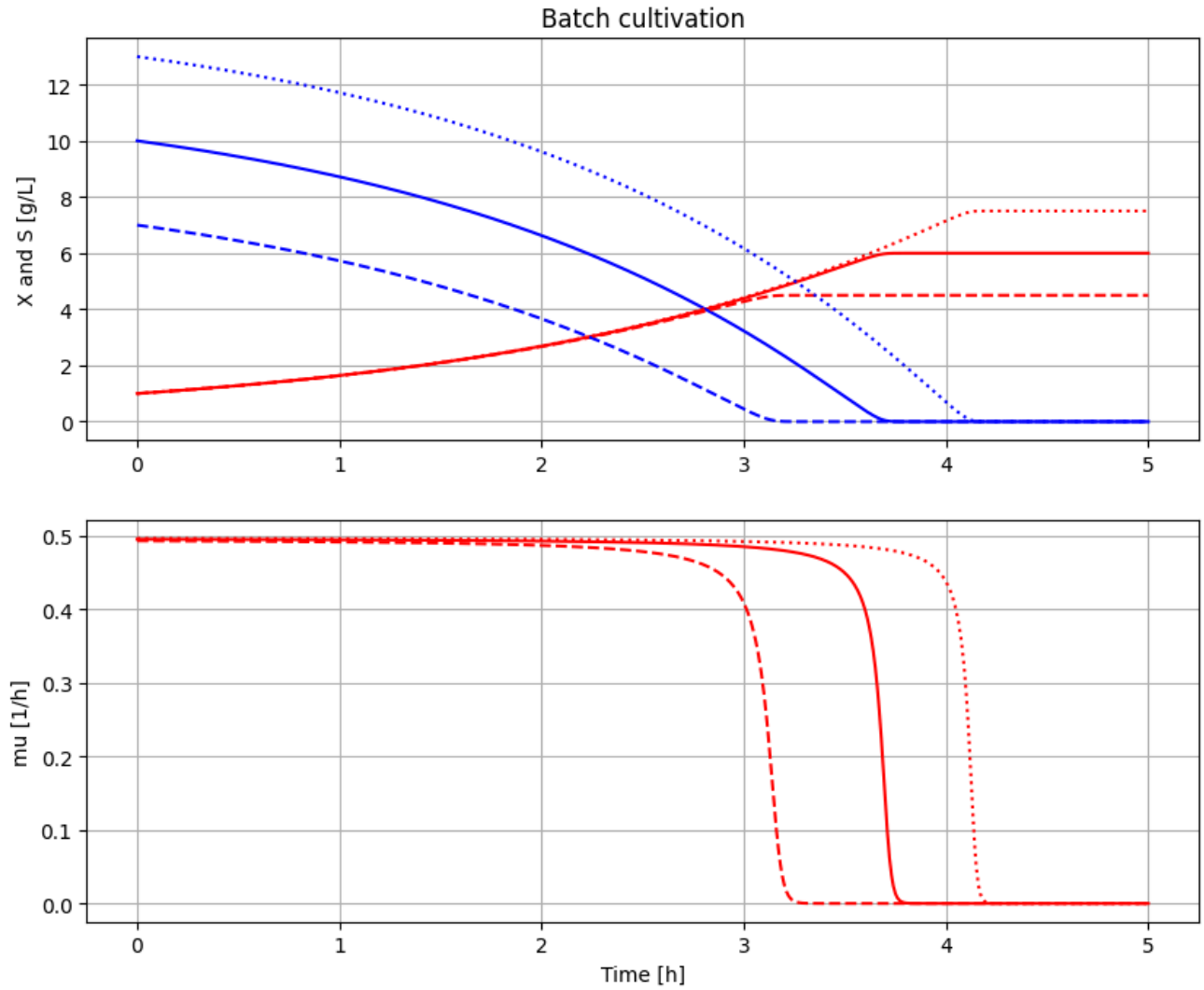
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu()
```



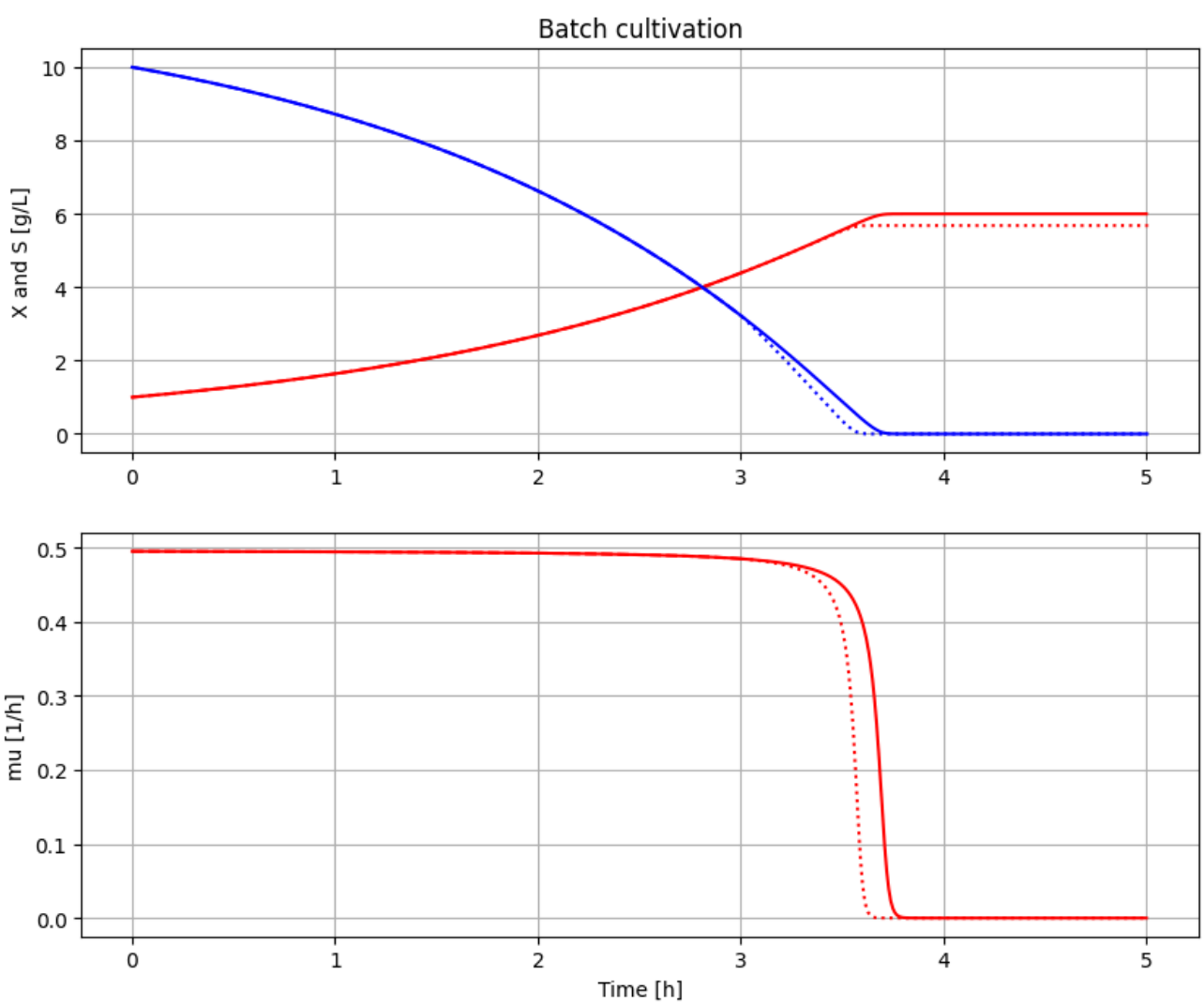

```
# Simulation were initial value of biomass VX_start is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

# 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)
```




```
# 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 : 0.5
qSmax : 1.0
Ks : 0.1
```