

▼ 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 20.04.5 LTS
Release:        20.04
Codename:       focal
```

```
%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/')
```

```
--2023-04-21 06:22:14-- 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,
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.130.3|:443... conne
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 182MB/s in 0.4s
```

```
2023-04-21 06:22:15 (182 MB/s) - 'Miniconda3-py39_23.1.0-1-Linux-x86_64.sh' sa
```

```
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
```

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

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

```
conda 23.3.1  
Python 3.9.16
```

```
!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
```

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

```
Note that both disp() and describe() takes values from the last simulation
```

```
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]
```

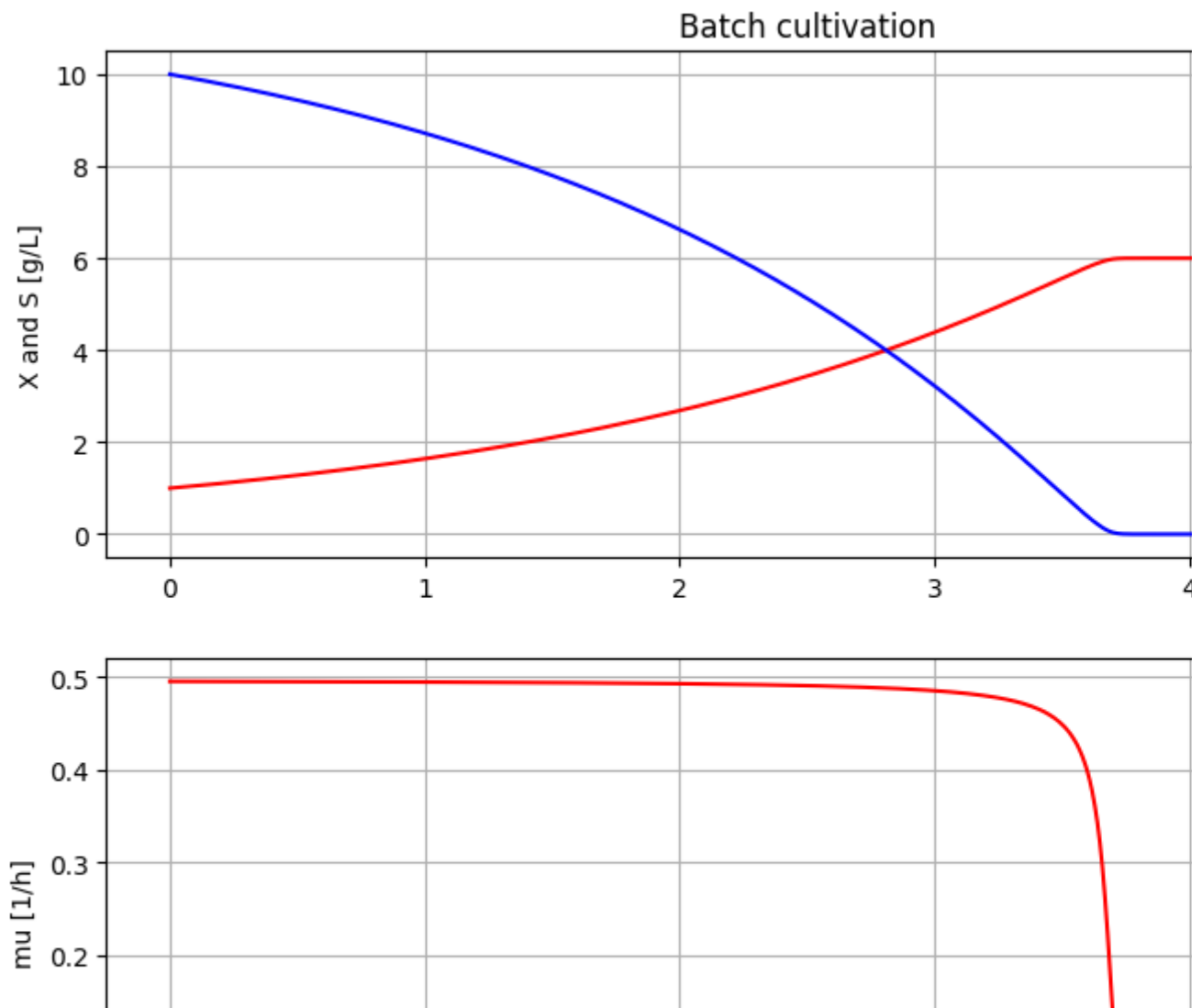
```
import warnings
warnings.filterwarnings("ignore")
```

▼ BPL_TEST2_Batch - demo

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

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

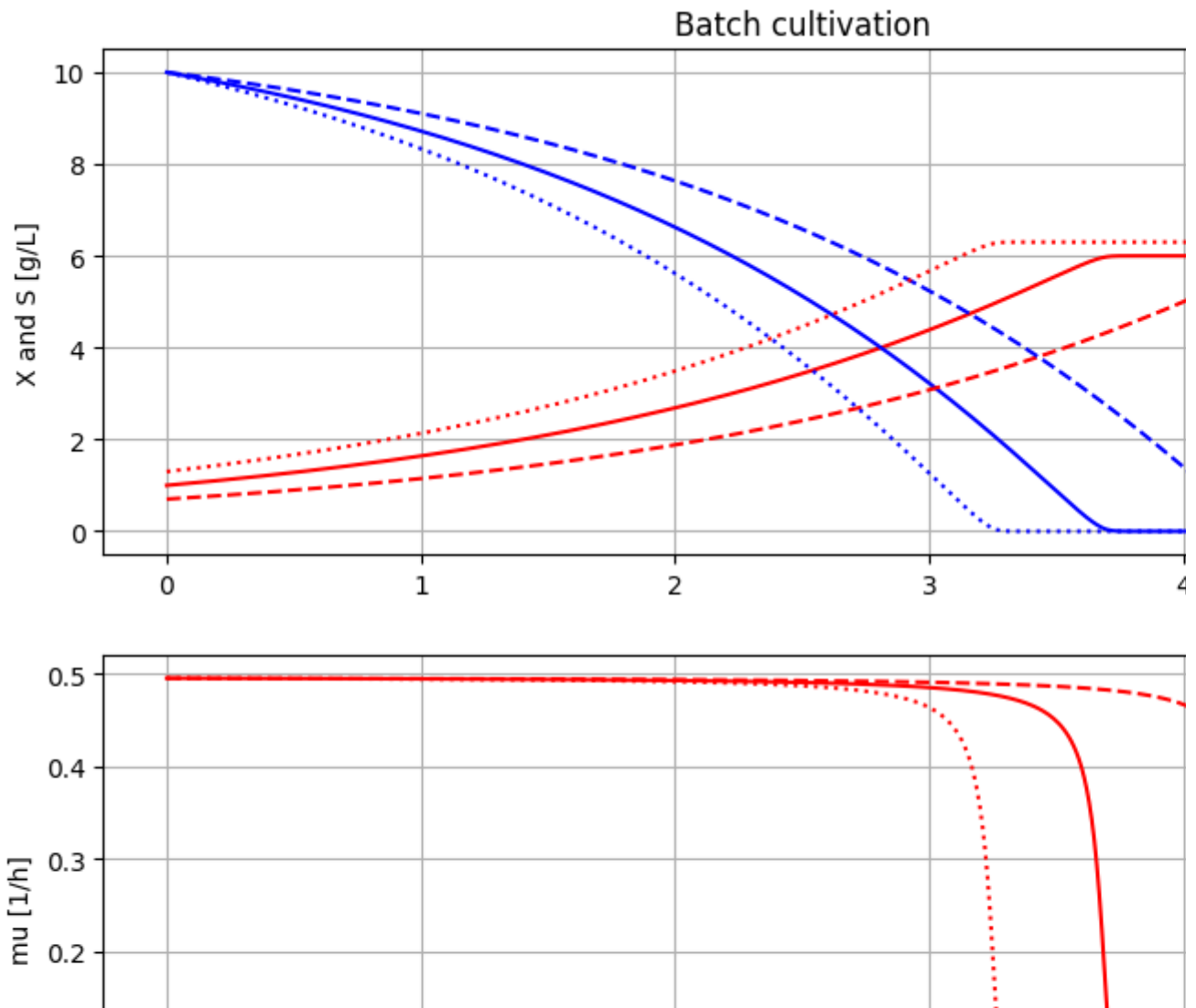
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu()
```



```
# Simulation were initial value of biomass VX_0 is varied
```

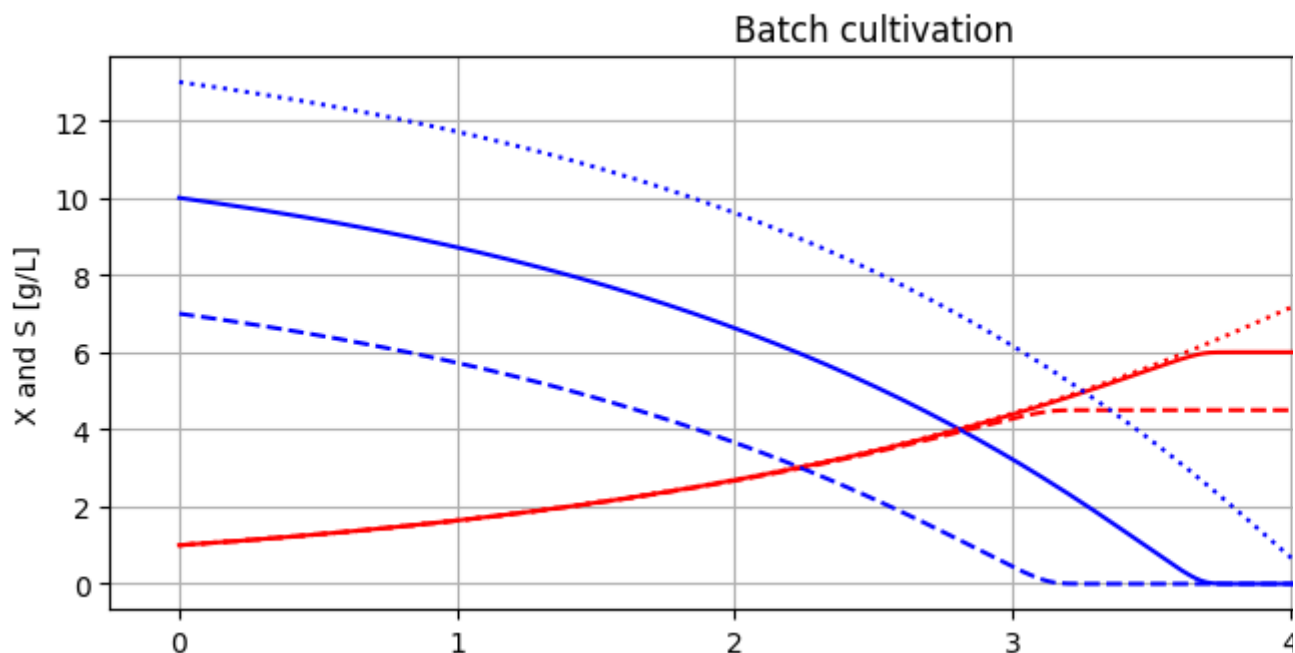
```
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_0=value); simu(5)
```

```
# 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: 3.9.16
-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 0.9.7

```

✓ 0s completed at 08:25

● ×