

✓ 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/')
```

```
⇒ --2024-10-24 08:25:23-- 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... con
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 74.8MB/s in 1.8s
```

```
2024-10-24 08:25:25 (74.8 MB/s) - 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh'
```

```
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
```

```
⇒
```

```

ca-certificates                2024.3.11-h06a4308_0 --> 2024.9.24-h06a
certifi                        2024.2.2-py312h06a4308_0 --> 2024.8.30-py31
conda                          24.3.0-py312h06a4308_0 --> 24.9.2-py312h
openssl                        3.0.13-h7f8727e_0 --> 3.0.15-h5eee1f

```

Downloading and Extracting Packages:

```

openssl-3.0.15                | 5.2 MB      | :    0% 0/1 [00:00<?, ?it/s]
conda-24.9.2                  | 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]

frozendict-2.4.2             | 36 KB       | :    0% 0/1 [00:00<?, ?it/s]

ca-certificates-2024         | 130 KB      | :   12% 0.12323429860849944/1 [00:00<00:01,

ca-certificates-2024         | 130 KB      | :  100% 1.0/1 [00:00<00:00, 1.47s/it]
openssl-3.0.15               | 5.2 MB      | :    0% 0.003007460830410892/1 [00:00<01:23

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

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

openssl-3.0.15               | 5.2 MB      | :   88% 0.8751711016495695/1 [00:00<00:00,

frozendict-2.4.2             | 36 KB       | :  100% 1.0/1 [00:00<00:00, 1.71it/s]
conda-24.9.2                 | 1.1 MB      | :  100% 1.0/1 [00:00<00:00, 1.58it/s]

```

```

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

```

```

!conda --version
!python --version

```

```

➞ conda 24.9.2
   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 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]
```

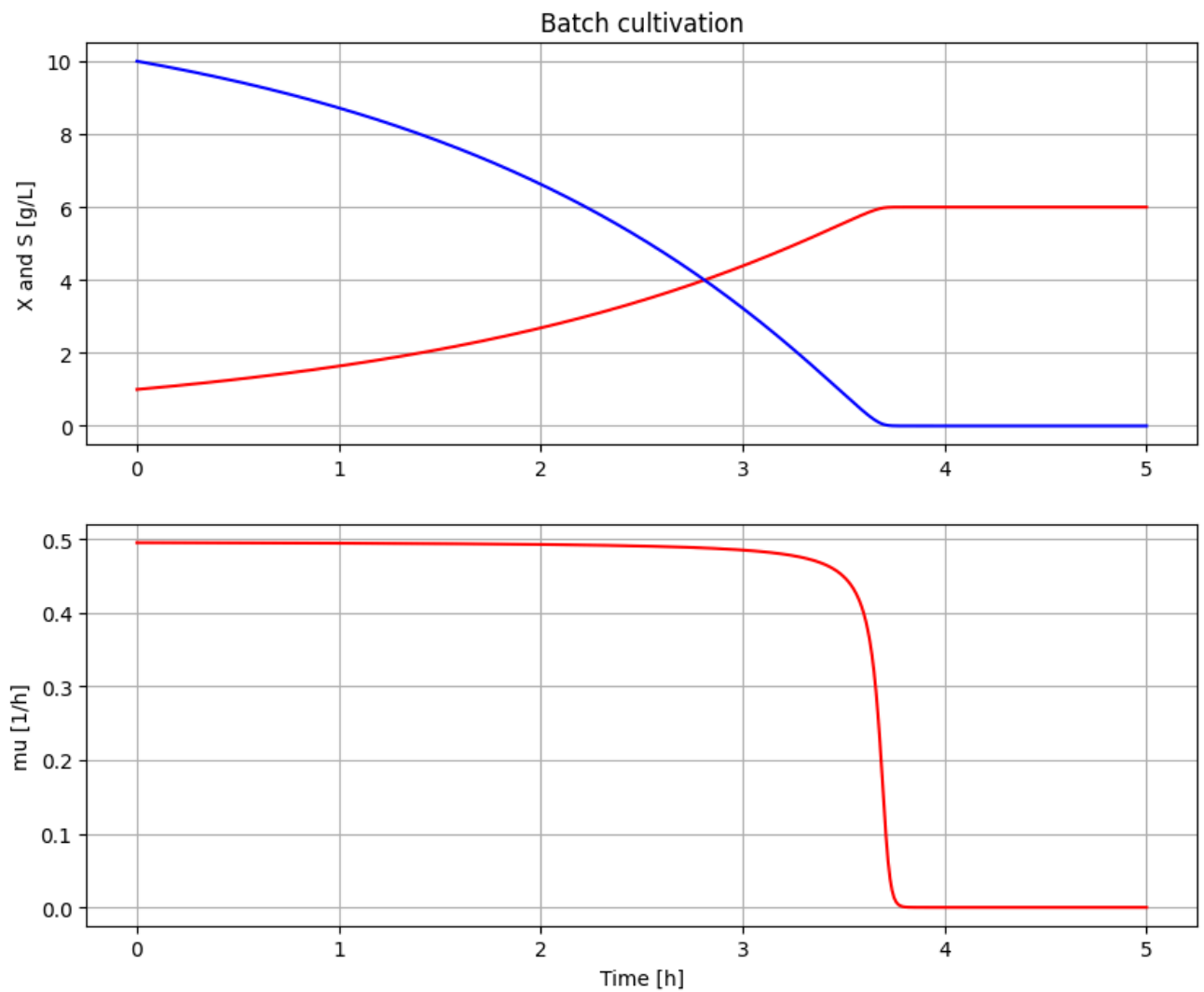
```
import warnings  
warnings.filterwarnings("ignore")
```

✓ BPL_TEST2_Batch - demo

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

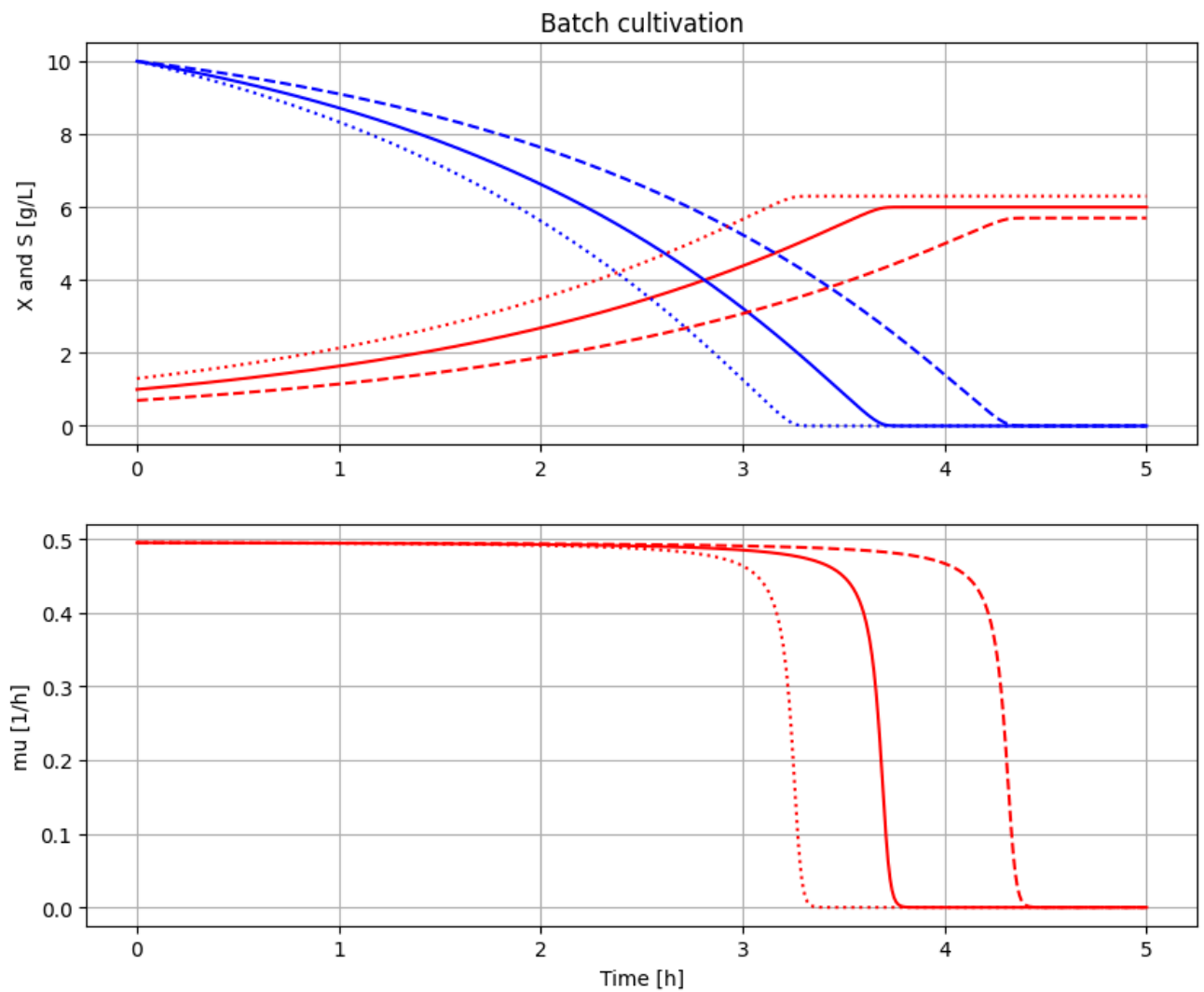
⇒ Simplified text book model – only substrate S and cell concentration X

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



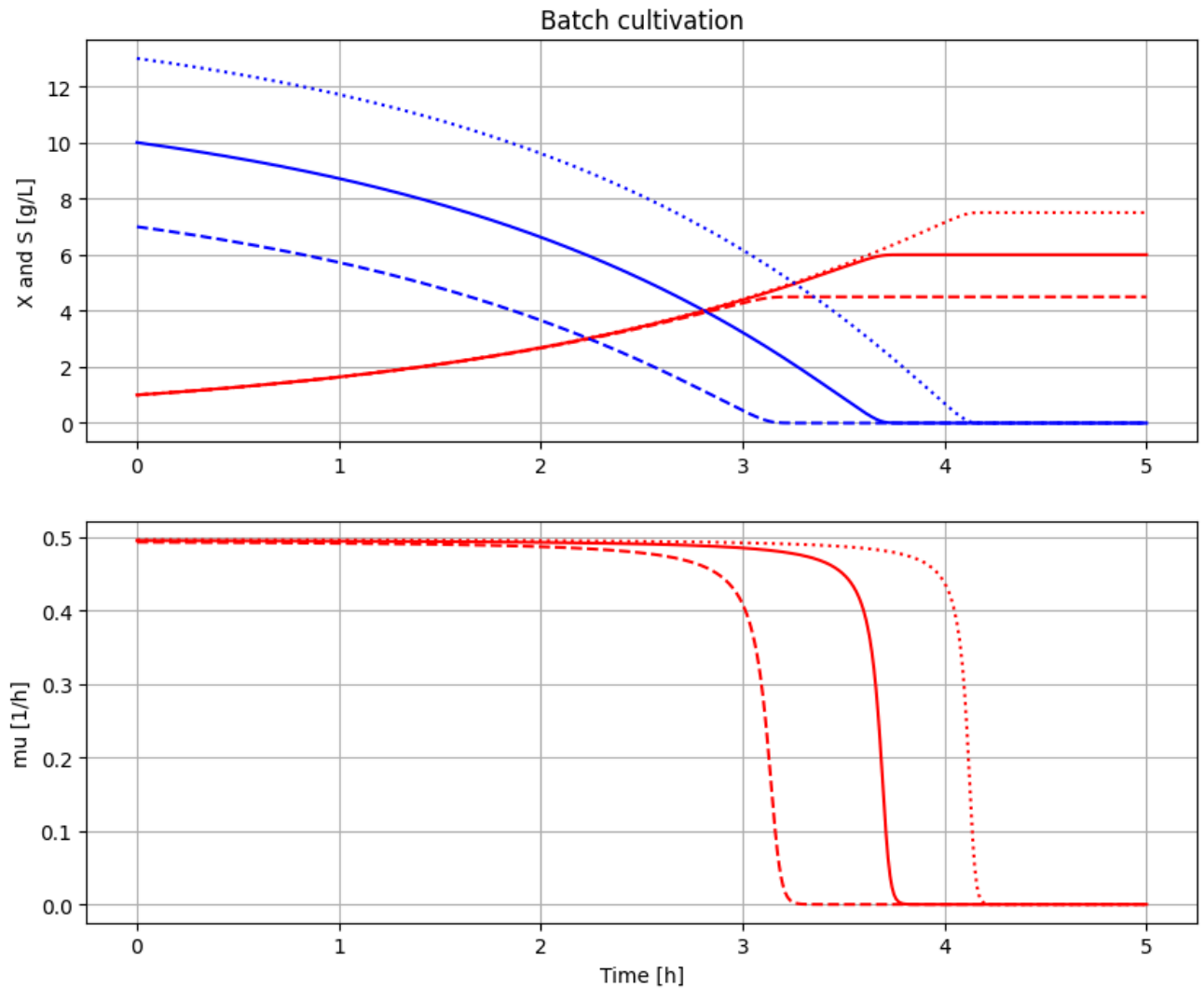
```
# Simulation were initial value of biomass VX_start is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

# 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)

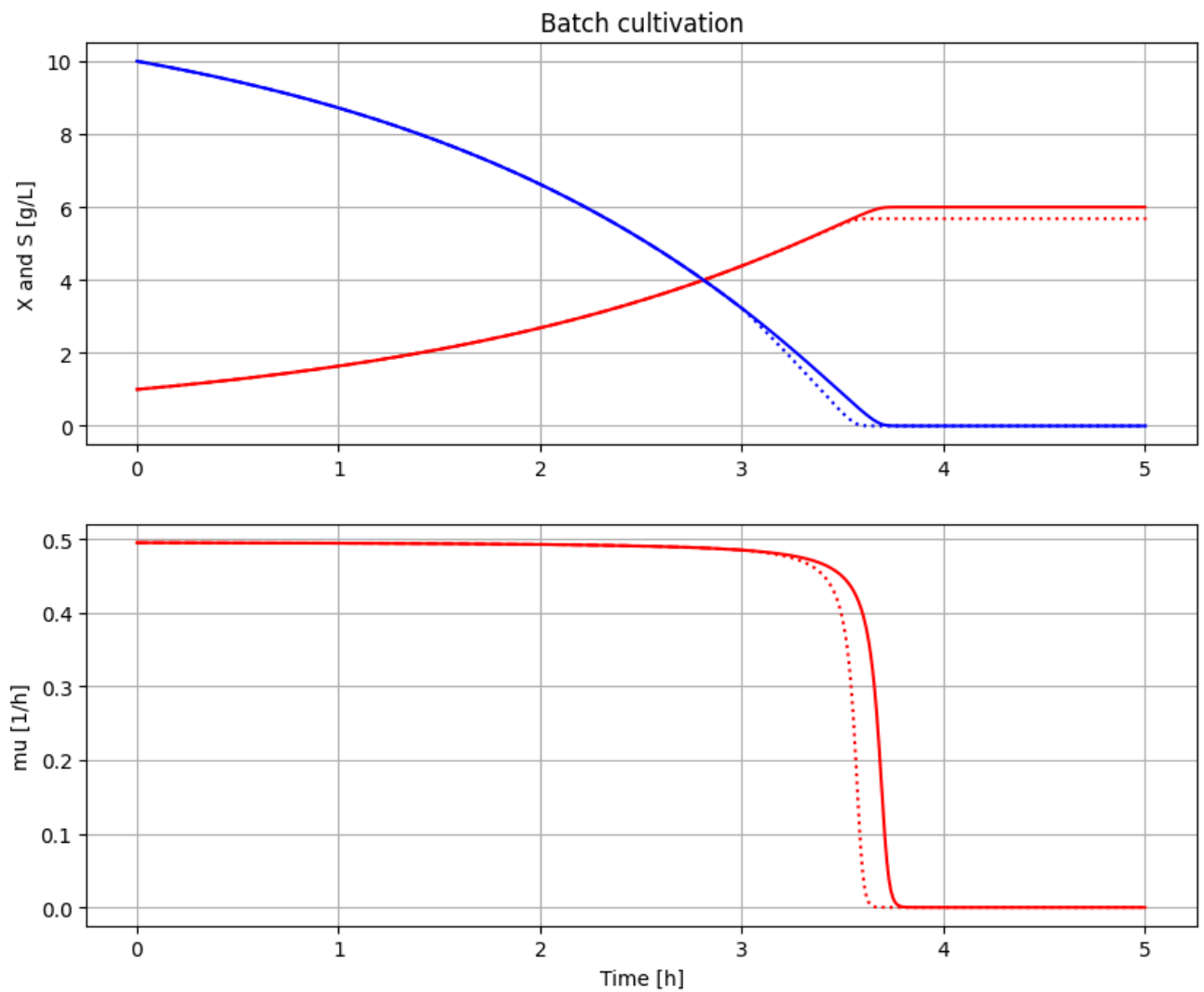
# Restore default value of VS_start
init(VS_start=10)
```



```
# 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
```