

✓ 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 22.04.3 LTS
   Release:        22.04
   Codename:       jammy
```

```
%env PYTHONPATH=
```

```
⇒ env: PYTHONPATH=
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-Linux-x86_64.
!chmod +x Miniconda3-py310_23.1.0-1-Linux-x86_64.sh
!bash ./Miniconda3-py310_23.1.0-1-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.10/site-packages/')
```

```
⇒ --2024-05-23 11:11:01-- https://repo.anaconda.com/miniconda/Miniconda3-py310
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: 74403966 (71M) [application/x-sh]
Saving to: 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh'
```

```
Miniconda3-py310_23 100%[=====>] 70.96M 143MB/s in 0.5s
```

```
2024-05-23 11:11:01 (143 MB/s) - 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh' :
```

```
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 23.1.0  
   Python 3.10.14
```

```
!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
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 1.23.0-dev
```

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()

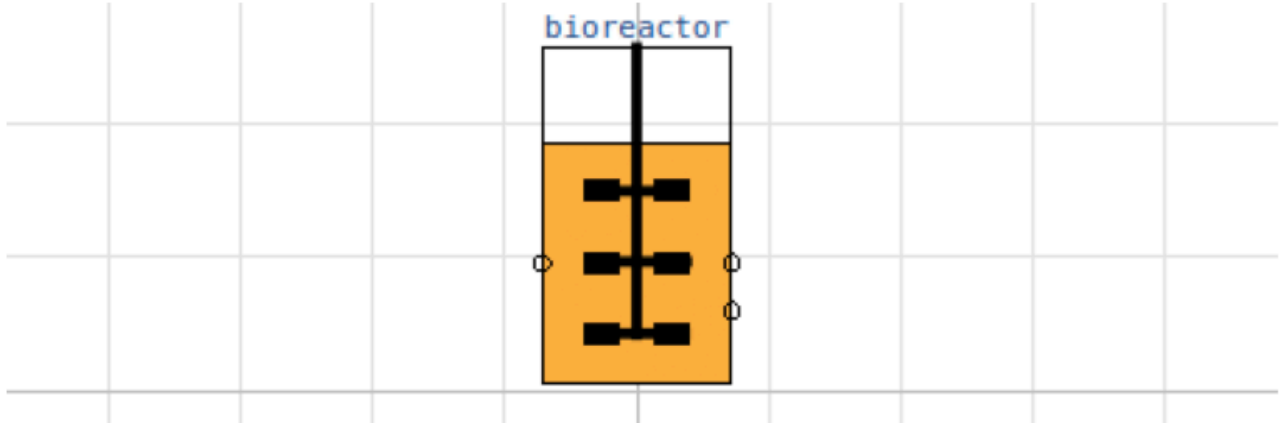
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

✓ BPL_TEST2_Batch - demo

```
process_diagram()
```

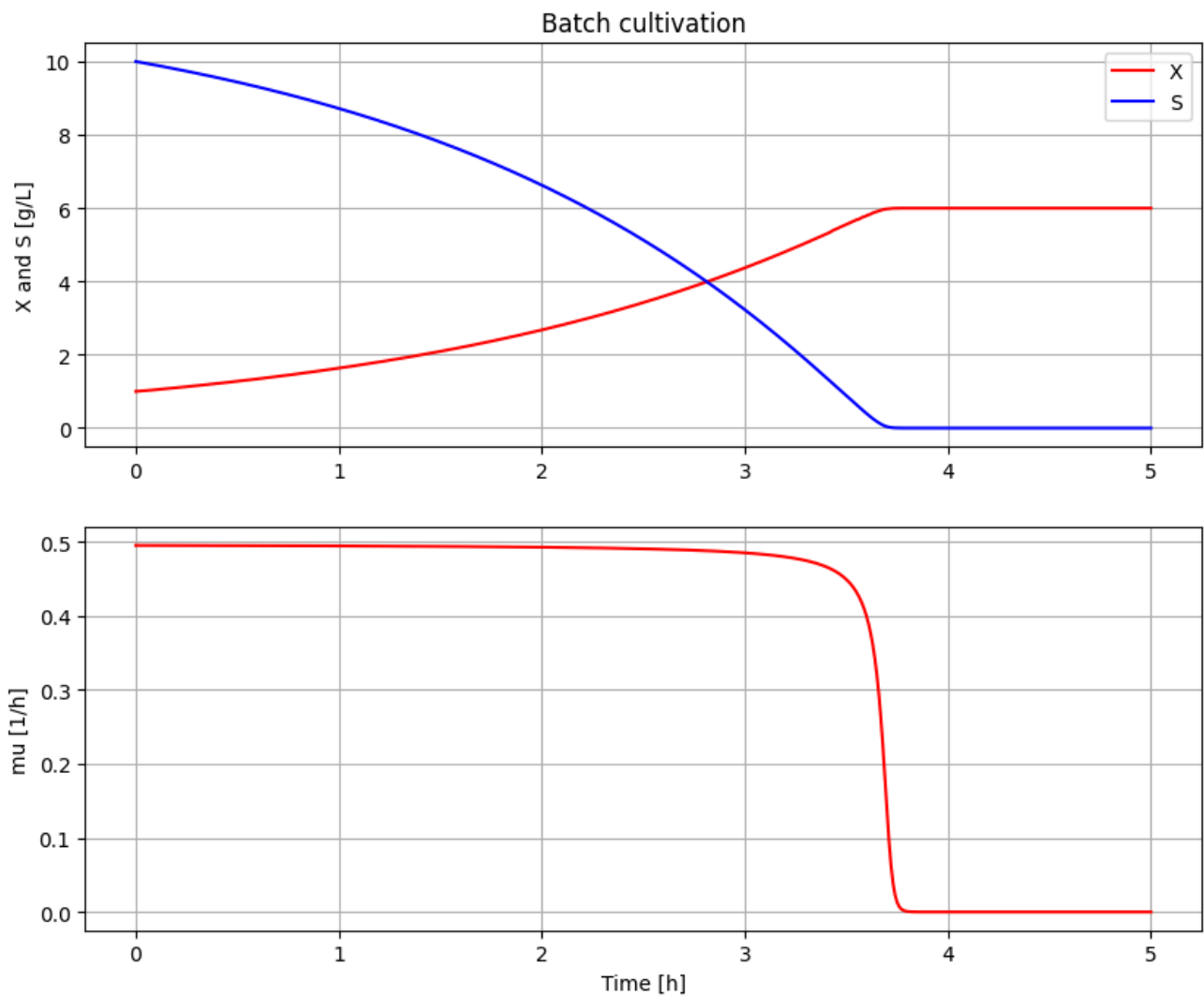
➞ No processDiagram.png file in the FMU, but try the file on disk.



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

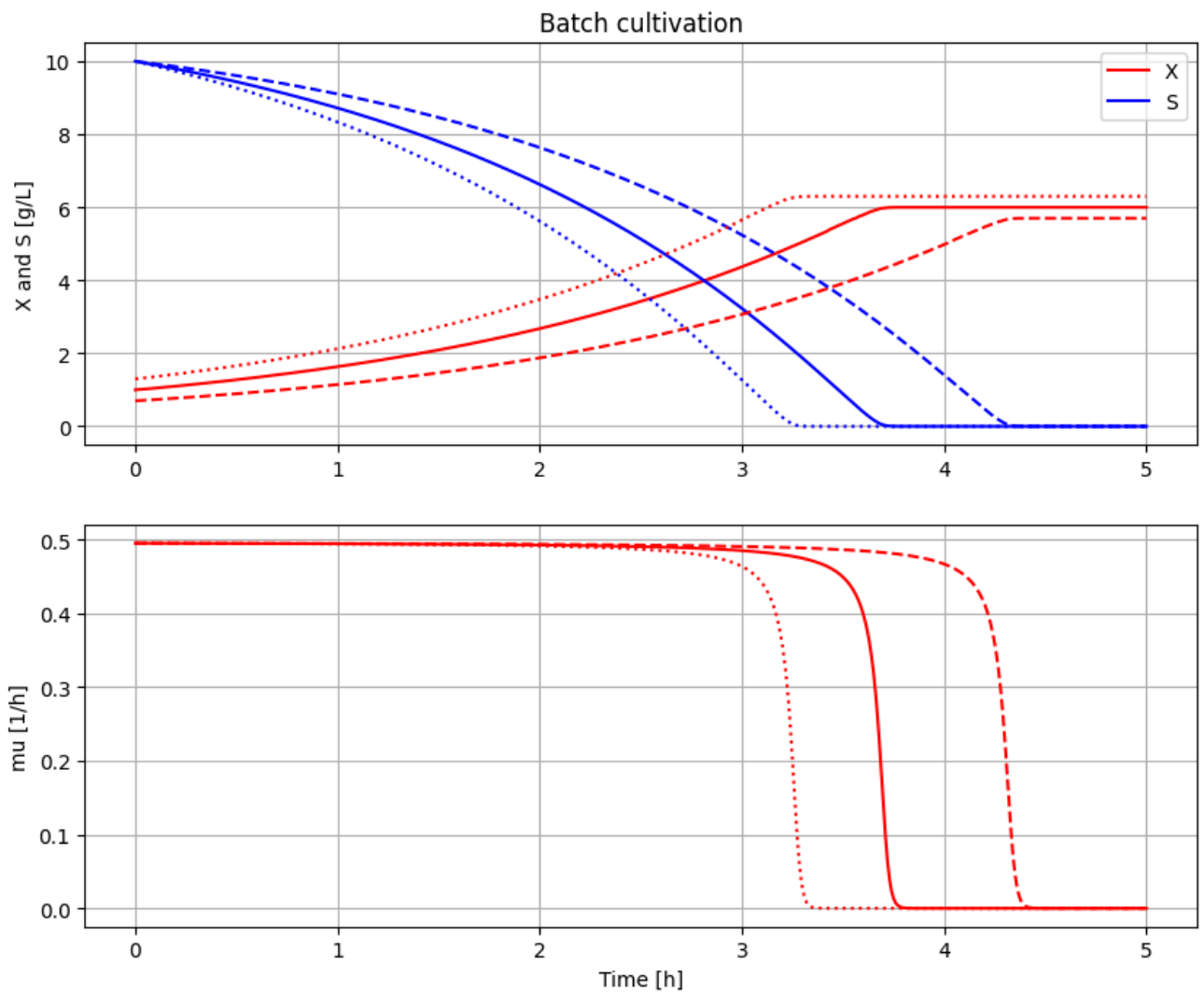
➞ Simplified text book model – only substrate S and cell concentration X

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



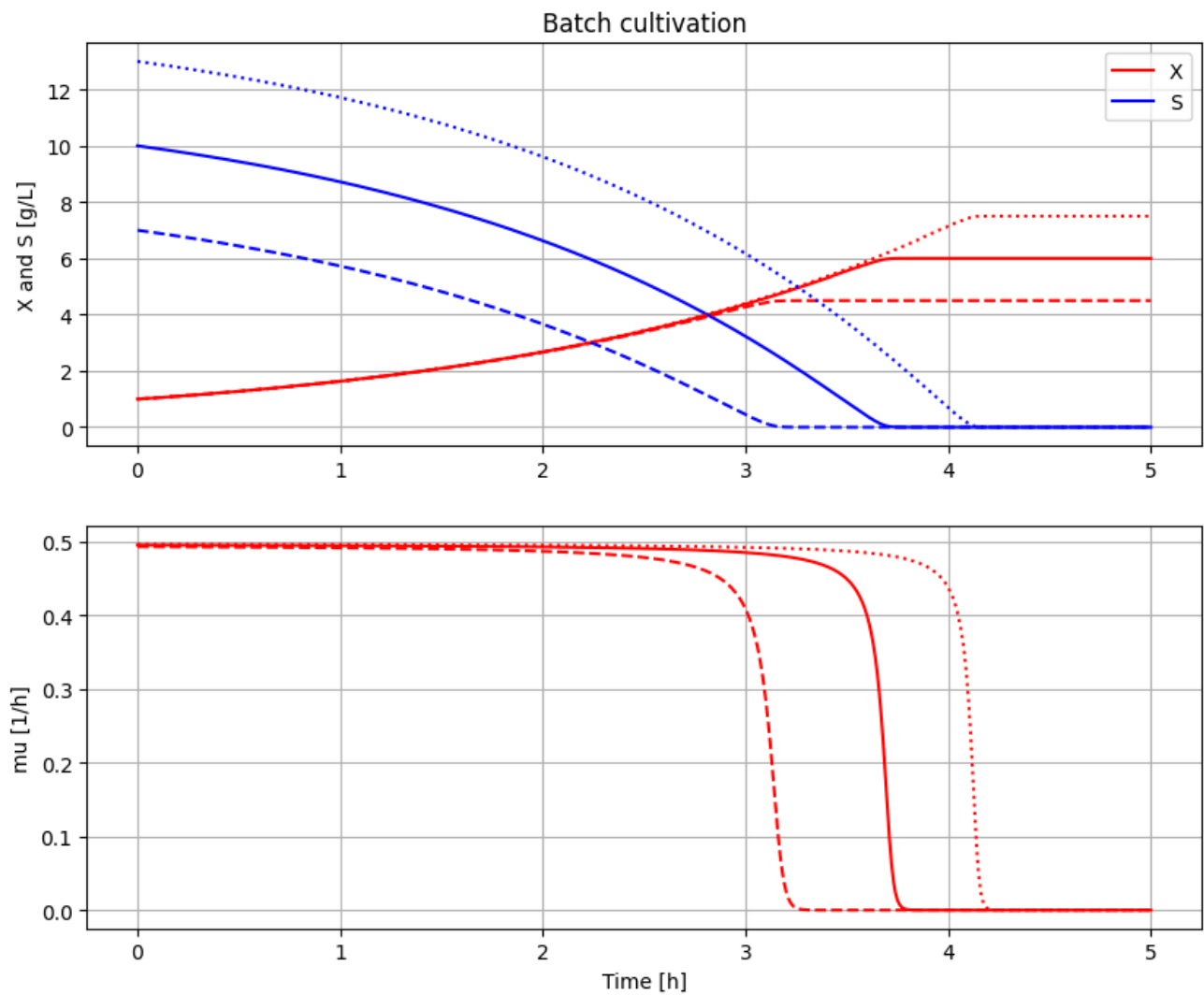
```
# Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

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



```
# 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)

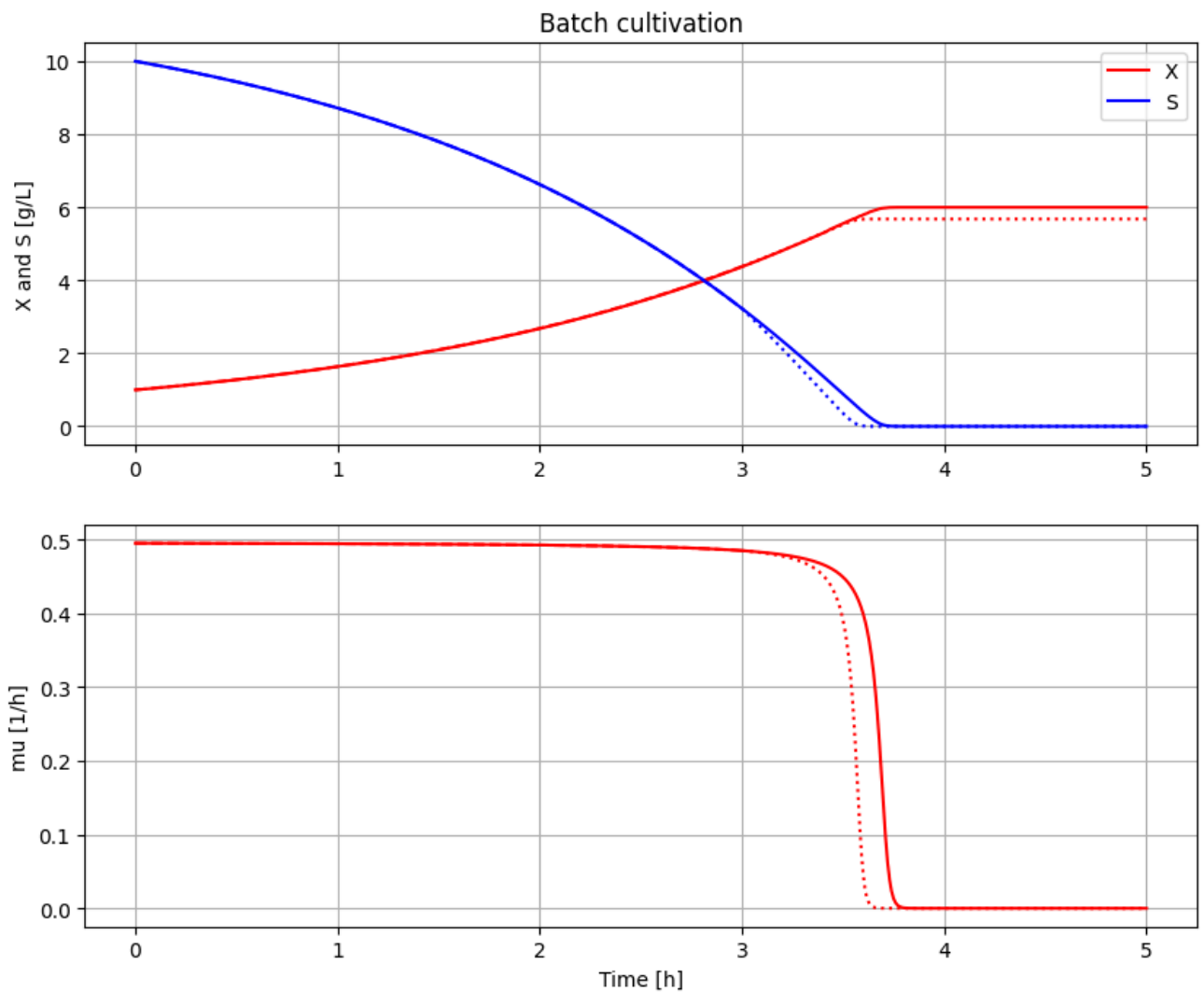
# Restore default value of VS_start
init(VS_start=10)
```



```
# 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']
```

```
describe('MSL')
```

```
—
```