

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

```
%env PYTHONPATH=
```

```
⇒ env: PYTHONPATH=
```

```
!python --version
```

```
⇒ Python 3.11.11
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py311_24.11.1-0-Linux-x86_64
!chmod +x Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
!bash ./Miniconda3-py311_24.11.1-0-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.11/site-packages/')
```

```
⇒ --2025-03-25 09:22:21-- https://repo.anaconda.com/miniconda/Miniconda3-py311\_24.11.1-0-Linux-x86\_64.sh
   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: 145900576 (139M) [application/octet-stream]
   Saving to: 'Miniconda3-py311_24.11.1-0-Linux-x86_64.sh'
```

```
Miniconda3-py311_24 100%[=====>] 139.14M 67.7MB/s in 2.1s
```

```
2025-03-25 09:22:23 (67.7 MB/s) - 'Miniconda3-py311_24.11.1-0-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
```



Channels:

- defaults

Platform: linux-64

Collecting package metadata (repodata.json): done

Solving environment: done

Package Plan

environment location: /usr/local

added / updated specs:

- conda

The following packages will be downloaded:

package	build	
ca-certificates-2025.2.25	h06a4308_0	129 KB
certifi-2025.1.31	py311h06a4308_0	163 KB
openssl-3.0.16	h5eee18b_0	5.2 MB
Total:		5.5 MB

The following packages will be UPDATED:

```

ca-certificates          2024.11.26-h06a4308_0 --> 2025.2.25-h06a4308_0
certifi                  2024.8.30-py311h06a4308_0 --> 2025.1.31-py311h06a4308_0
openssl                  3.0.15-h5eee18b_0 --> 3.0.16-h5eee18b_0

```

Downloading and Extracting Packages:

```

openssl-3.0.16          | 5.2 MB | : 0% 0/1 [00:00<?, ?it/s]
certifi-2025.1.31      | 163 KB | : 0% 0/1 [00:00<?, ?it/s]

openssl-3.0.16          | 5.2 MB | : 3% 0.026843345551458574/1 [00:00<00:03
certifi-2025.1.31      | 163 KB | : 100% 1.0/1 [00:00<00:00, 9.99it/s]
certifi-2025.1.31      | 163 KB | : 100% 1.0/1 [00:00<00:00, 9.99it/s]

ca-certificates-2025   | 129 KB | : 99% 0.9905458612637259/1 [00:00<00:00,
ca-certificates-2025   | 129 KB | : 100% 1.0/1 [00:00<00:00, 9.85it/s]
ca-certificates-2025   | 129 KB | : 100% 1.0/1 [00:00<00:00, 9.85it/s]

```

Preparing transaction: done

Verifying transaction: done

Executing transaction: done

!conda --version

!python --version



conda 24.11.1

Python 3.11.11

```
!conda config --set channel_priority strict
```

```
!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

Model for the process 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]

```

```

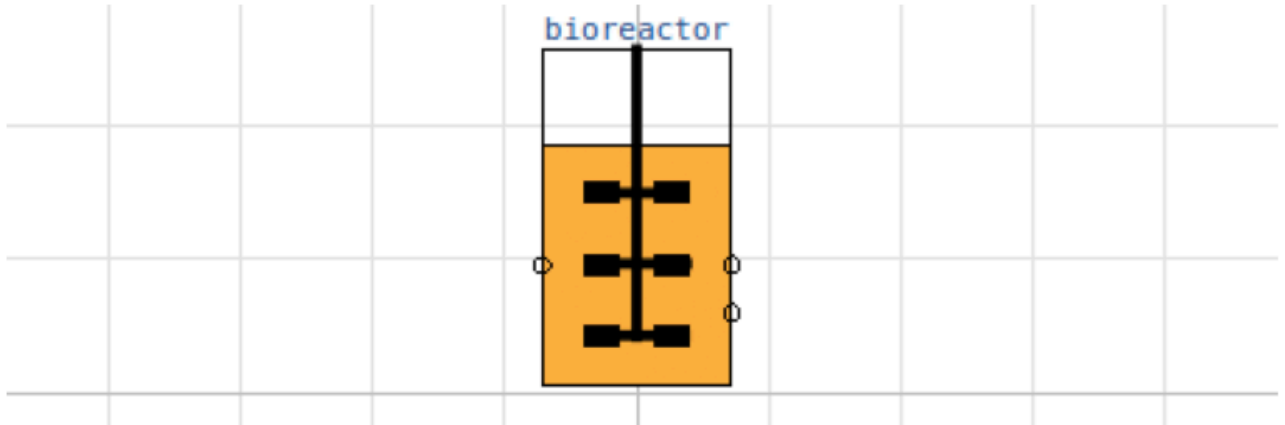
import warnings
warnings.filterwarnings("ignore")

```

✓ BPL_TEST2_Batch - demo

```
process_diagram()
```

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

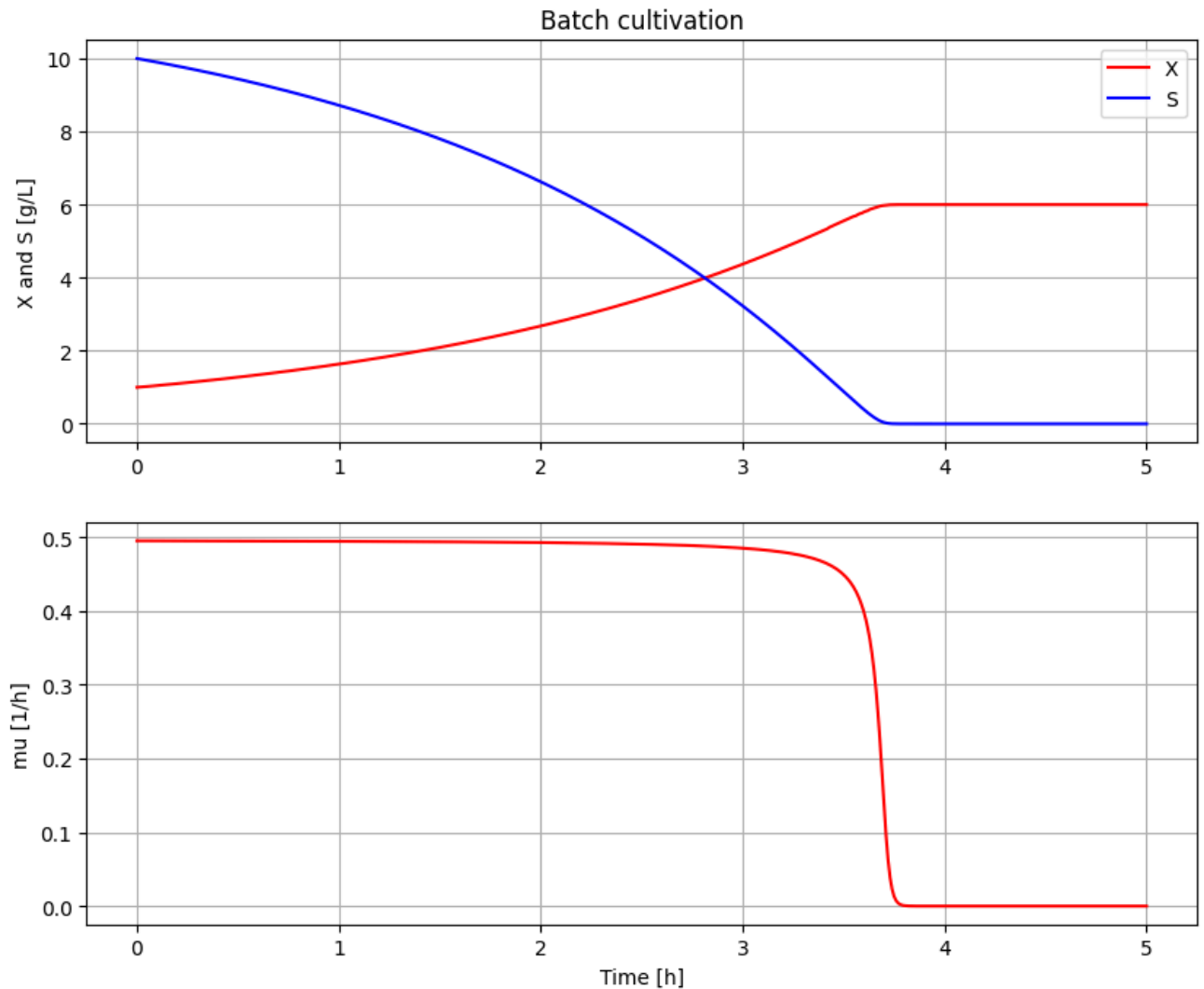


```
describe('culture'); print(); #describe('liquidphase')
```

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

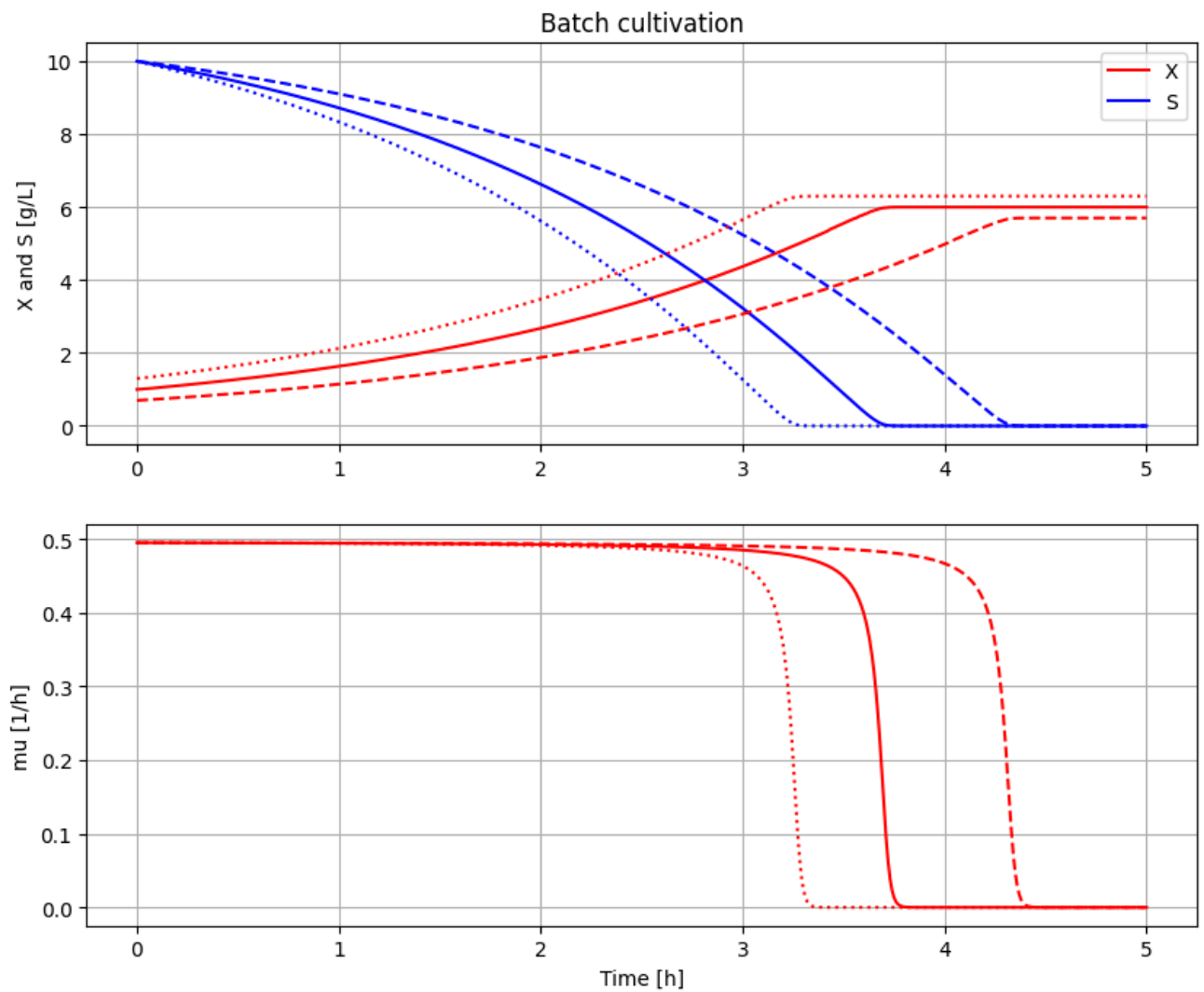
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu()
```

⚠ Could not find cannot import name 'dopri5' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/assimulo/lib)
 Could not find cannot import name 'rodas' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/assimulo/lib)
 Could not find cannot import name 'odassl' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/assimulo/lib)
 Could not find ODEPACK functions.
 Could not find RADAR5
 Could not find GLIMDA.



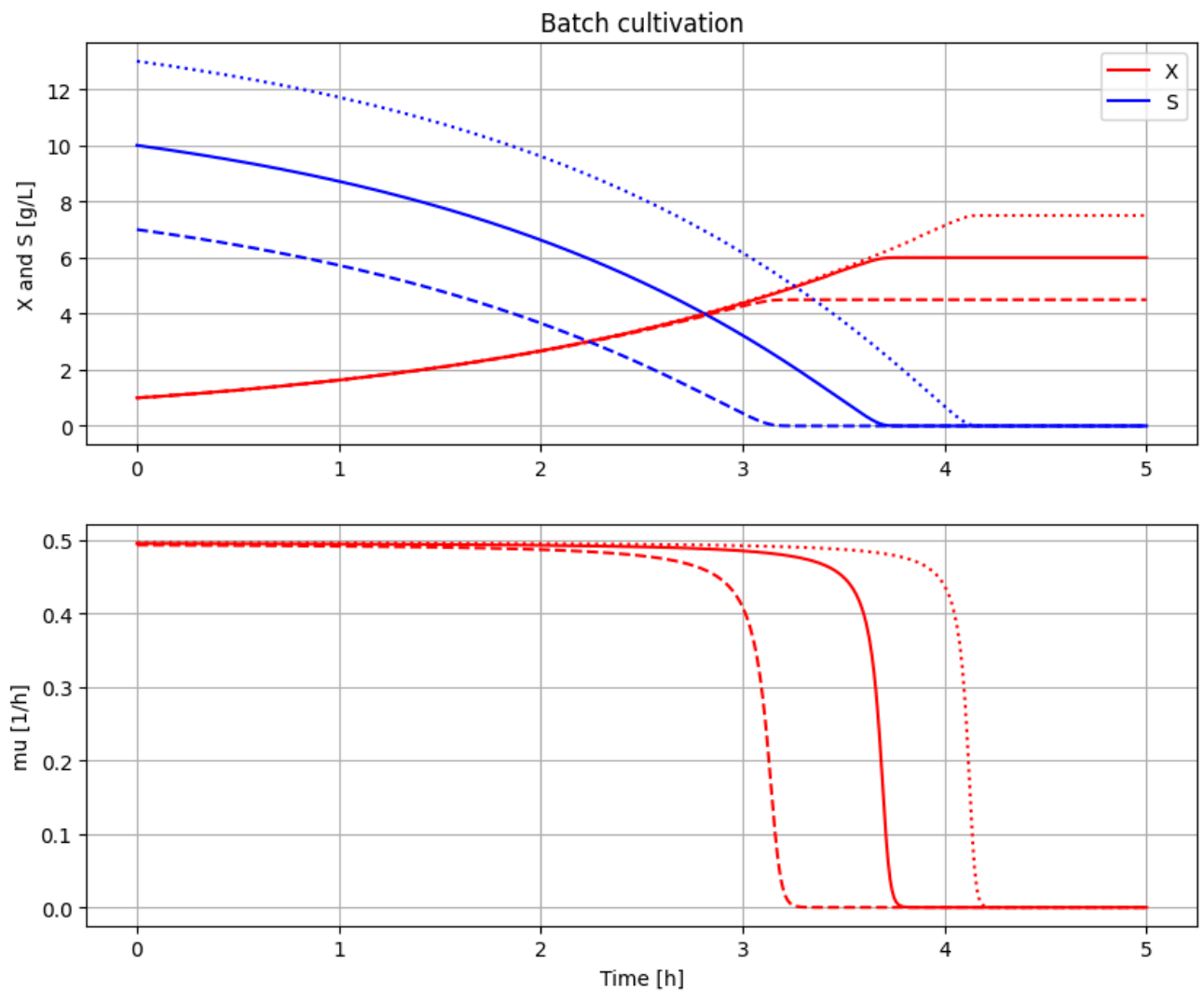
```
# Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

# 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)

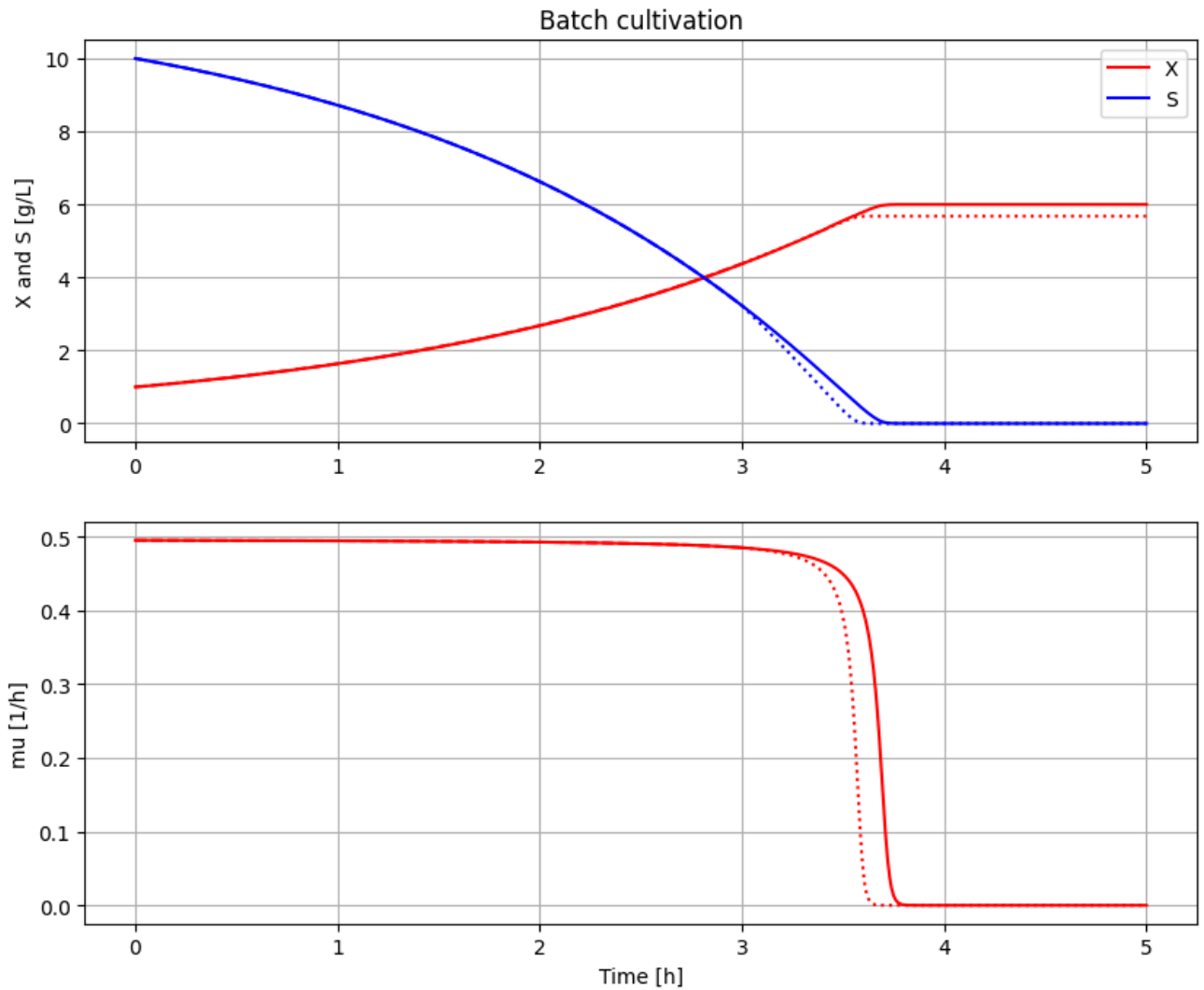
# Restore default value of VS_start
init(VS_start=10)
```



```
# 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')
```



```
MSL: 3.2.3 - used components: none
```