

✓ 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 22.04.4 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.sh
```

```
!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/')
```

```
➦ --2025-02-06 12:22:35-- 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, 104.16.191.158, 2606:4700::6810:20f1, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... connected.
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 107MB/s in 1.3s
```

```
2025-02-06 12:22:36 (107 MB/s) - 'Miniconda3-py311_24.11.1-0-Linux-x86_64.sh' saved [145900576/145900576]
```

```
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-2024.12.31	h06a4308_0	128 KB
certifi-2025.1.31	py311h06a4308_0	163 KB
Total:		291 KB

The following packages will be UPDATED:

```
ca-certificates      2024.11.26-h06a4308_0 --> 2024.12.31-h06a4308_0
certifi              2024.8.30-py311h06a4308_0 --> 2025.1.31-py311h06a4308_0
```

Downloading and Extracting Packages:

certifi-2025.1.31	163 KB	: 0% 0/1 [00:00<?, ?it/s]
ca-certificates-2024	128 KB	: 0% 0/1 [00:00<?, ?it/s]
certifi-2025.1.31	163 KB	: 100% 1.0/1 [00:00<00:00, 10.11it/s]
ca-certificates-2024	128 KB	: 100% 1.0/1 [00:00<00:00, 9.26it/s]

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

!conda --version
!python --version

🔄 conda 24.11.1
Python 3.11.11

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

🔄

Preparing transaction: done
Verifying transaction: done
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')
```

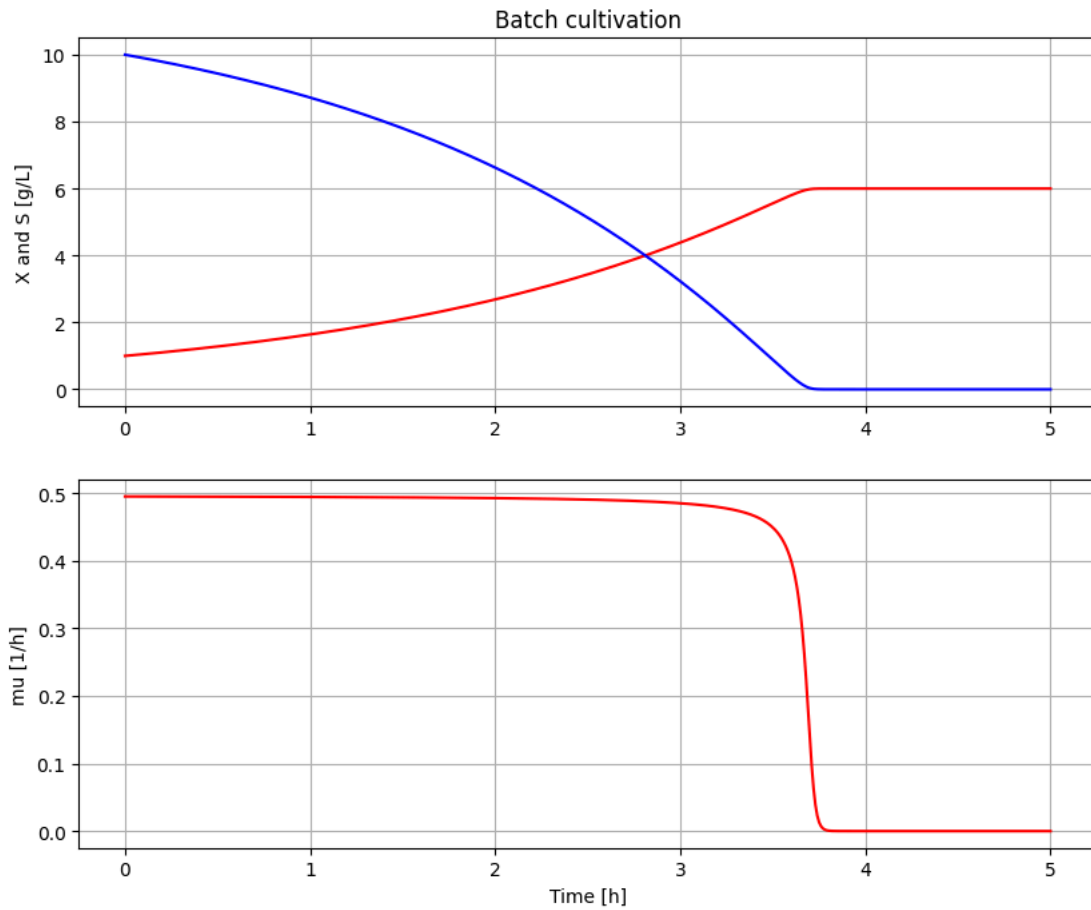
```
# Pump schedule parameter
```

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

```
# Simulation with default values of the process
```

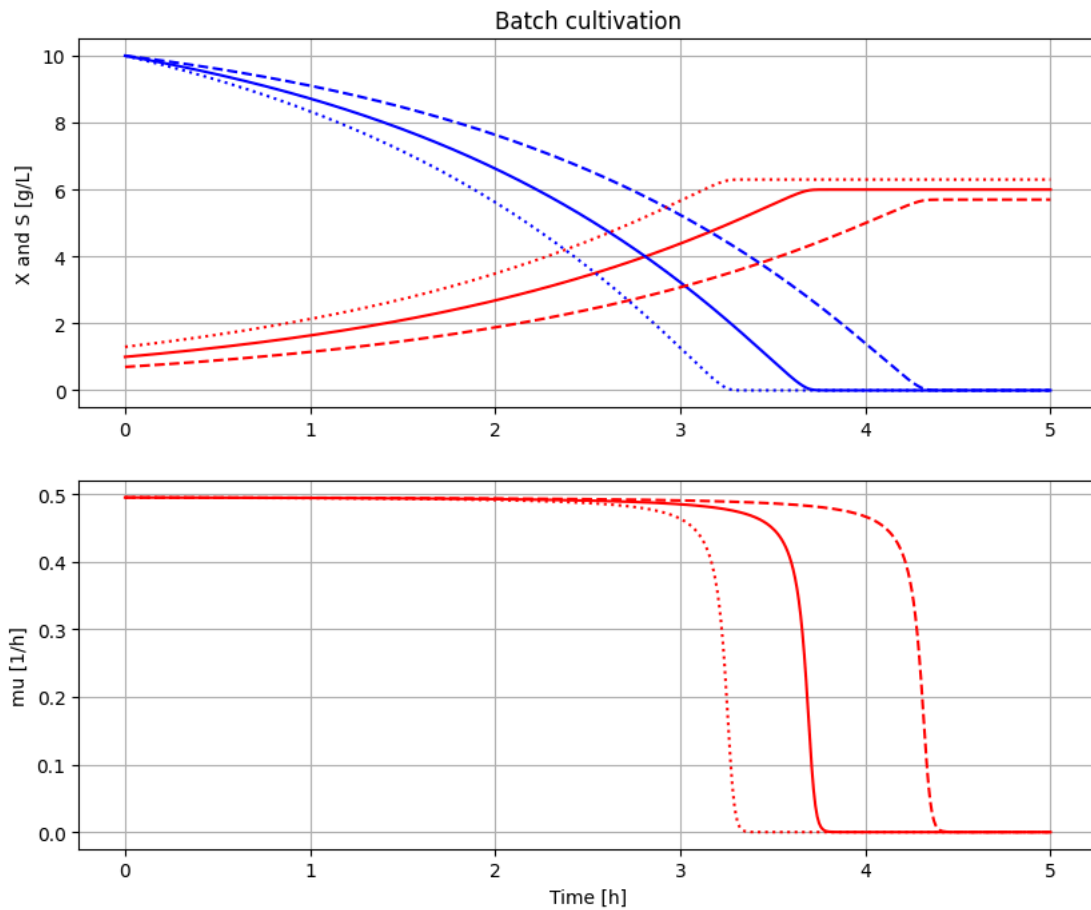
```
newplot(plotType='TimeSeries')
```

```
simu()
```



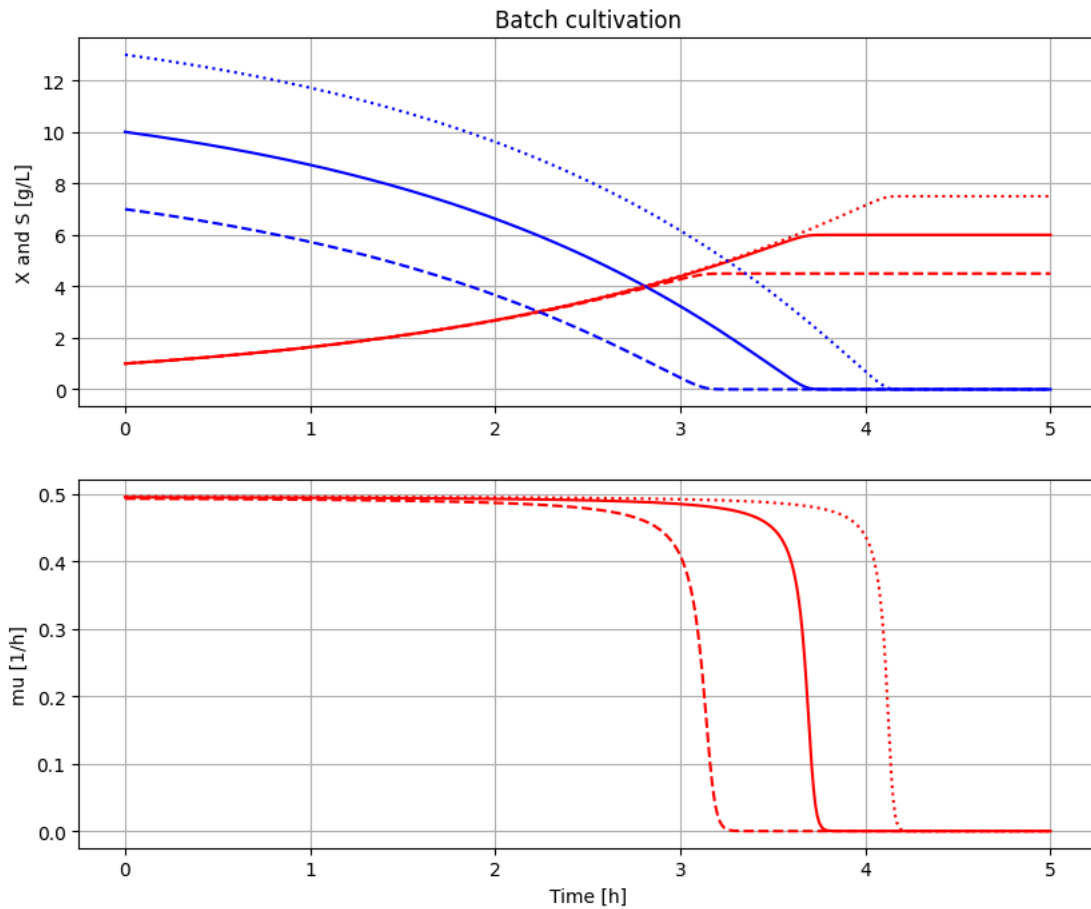
```
# Simulation were initial value of biomass VX_start is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

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



```
# Simulation where 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)
```



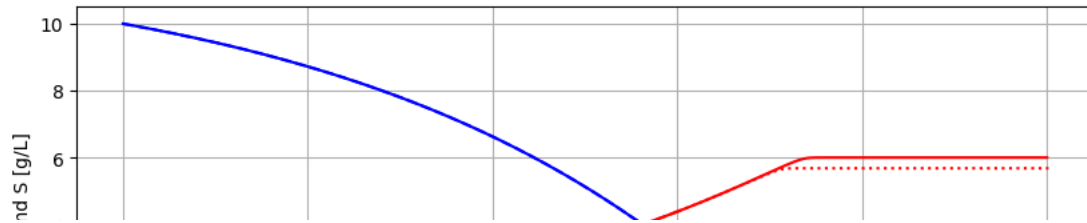
```
# Simulation where metabolism is changed after 3 hours
newplot(plotType='TimeSeries')
simu(5)
```

```
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)
```



Batch cultivation



```
disp('culture')
```



```
Y : 0.5
qSmax : 1.0
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: 3.11.11
-Scipy: not installed in the notebook
-FMPy: 0.3.19
-FMU by: OpenModelica Compiler OpenModelica 1.25.0~dev-133-ga5470be
-FMI: 2.0
-Type: ME
-Name: BPL.Examples_TEST2.Batch
-Generated: 2024-11-06T21:35:34Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.3.0
-Interaction: FMU-explore for FMPy version 1.0.1
```

Start coding or generate with ΔT