

✓ 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.sh
!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/')
```

```
➔ --2024-05-15 09:54:49-- https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linux-
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.158, 2606:4700::
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... connected.
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 87.1MB/s in 1.6s
```

```
2024-05-15 09:54:51 (87.1 MB/s) - 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh' saved [143351488]
```

```
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	
conda-24.5.0	py312h06a4308_0	1.2 MB
frozendict-2.4.2	py312h06a4308_0	36 KB
openssl-3.0.13	h7f8727e_1	5.2 MB
Total:		6.5 MB

The following NEW packages will be INSTALLED:

frozendict pkgs/main/linux-64::frozendict-2.4.2-py312h06a4308_0

The following packages will be UPDATED:

conda 24.3.0-py312h06a4308_0 --> 24.5.0-py312h06a4308_0
openssl 3.0.13-h7f8727e_0 --> 3.0.13-h7f8727e_1

Downloading and Extracting Packages:

openssl-3.0.13	5.2 MB	:	0% 0/1 [00:00<?, ?it/s]
conda-24.5.0	1.2 MB	:	0% 0/1 [00:00<?, ?it/s]
frozendict-2.4.2	36 KB	:	0% 0/1 [00:00<?, ?it/s]
openssl-3.0.13	5.2 MB	:	0% 0.002997347135570501/1 [00:00<00:58, 58.78s/it]
frozendict-2.4.2	36 KB	:	44% 0.43853215920344746/1 [00:00<00:00, 2.46it/s]
openssl-3.0.13	5.2 MB	:	87% 0.8662333221798748/1 [00:00<00:00, 3.87it/s]
conda-24.5.0	1.2 MB	:	100% 1.0/1 [00:00<00:00, 1.78it/s]

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

!conda --version
!python --version

conda 24.5.0
Python 3.12.2

!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 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 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")
```

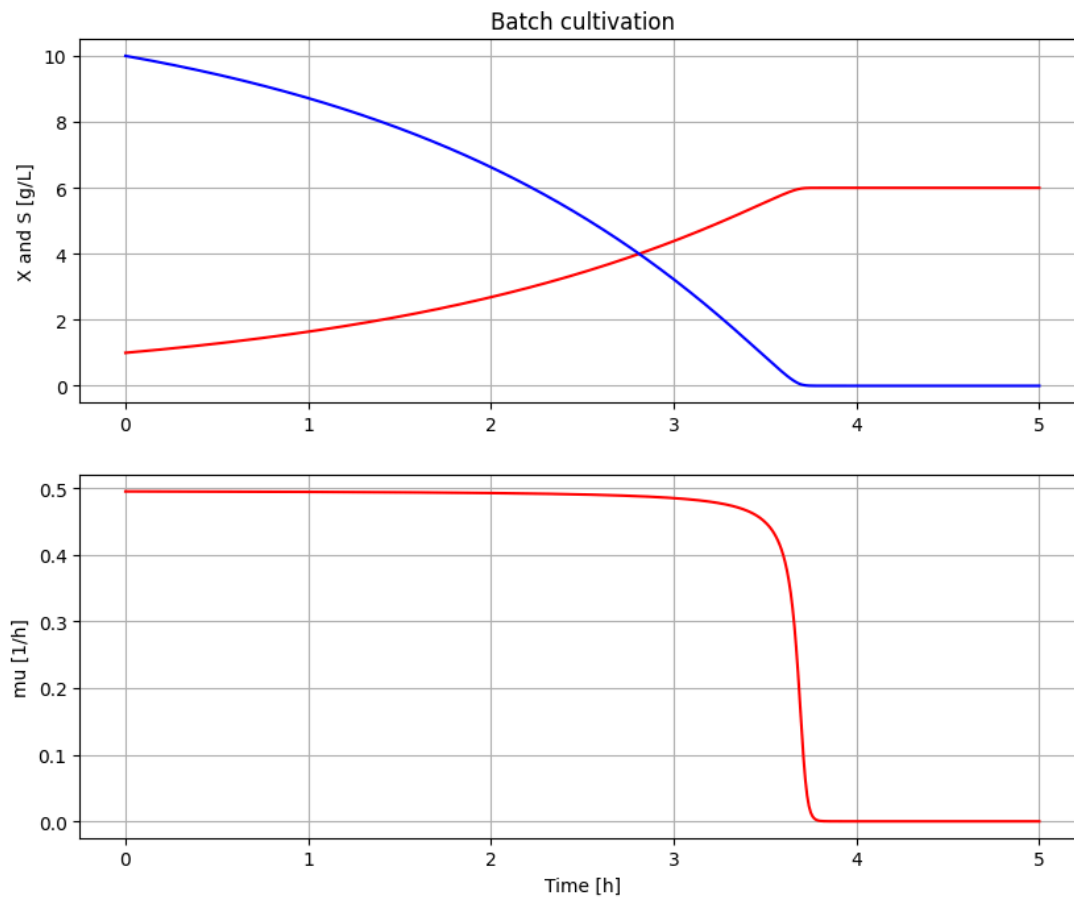
✓ BPL_TEST2_Batch - demo

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

Pump sc

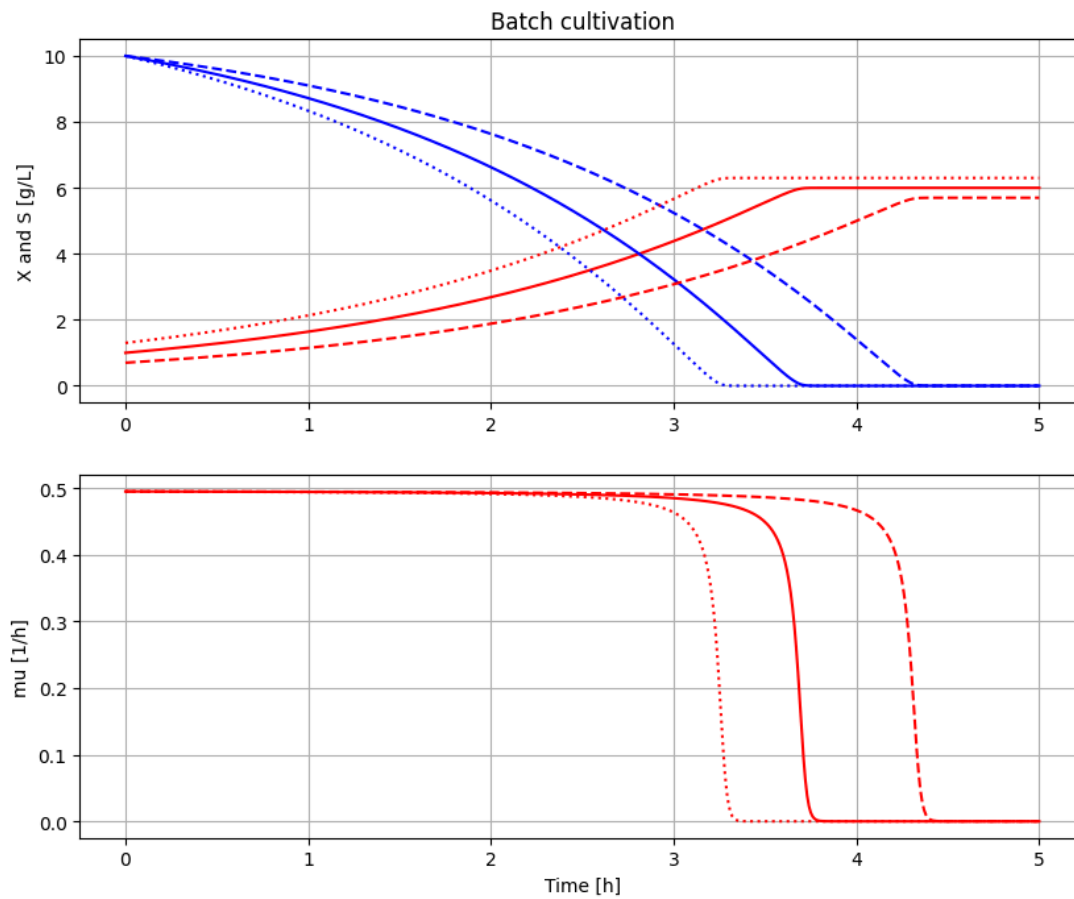
Simplified text book model – only substrate S and cell concentration X

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



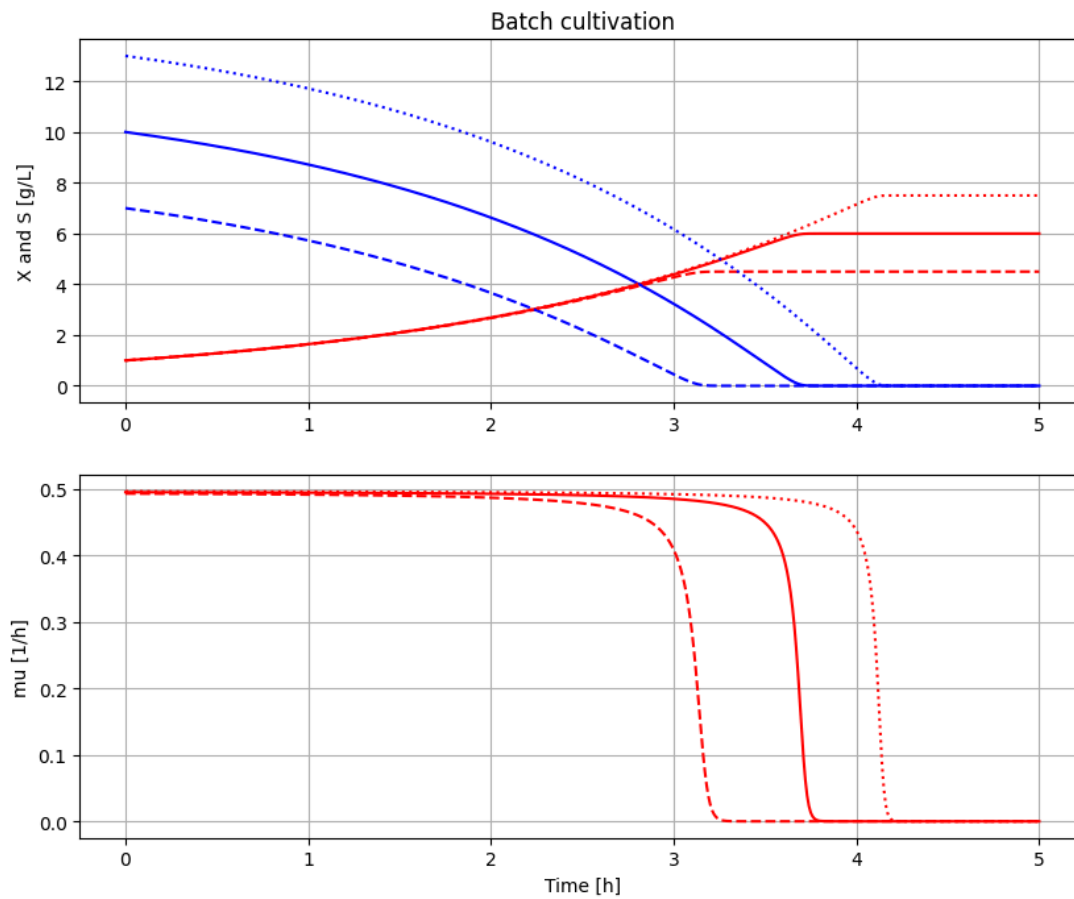
```
# Simulation were initial value of biomass VX_start is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_start=value); simu(5)

# 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)
```

