

## ▼ 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 22.04.2 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.sh
```

```
!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/')
```

```
--2023-09-25 13:17:45-- https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.131.3, 104.16.130.3, 2606:4700::6810:82
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.131.3|:443... connected.
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 199MB/s in 0.4s
```

```
2023-09-25 13:17:46 (199 MB/s) - 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh' saved [74403966/74403966]
```

```
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 23.7.4  
Python 3.10.13
```

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



## ▼ 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-comiled 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 schedul
```

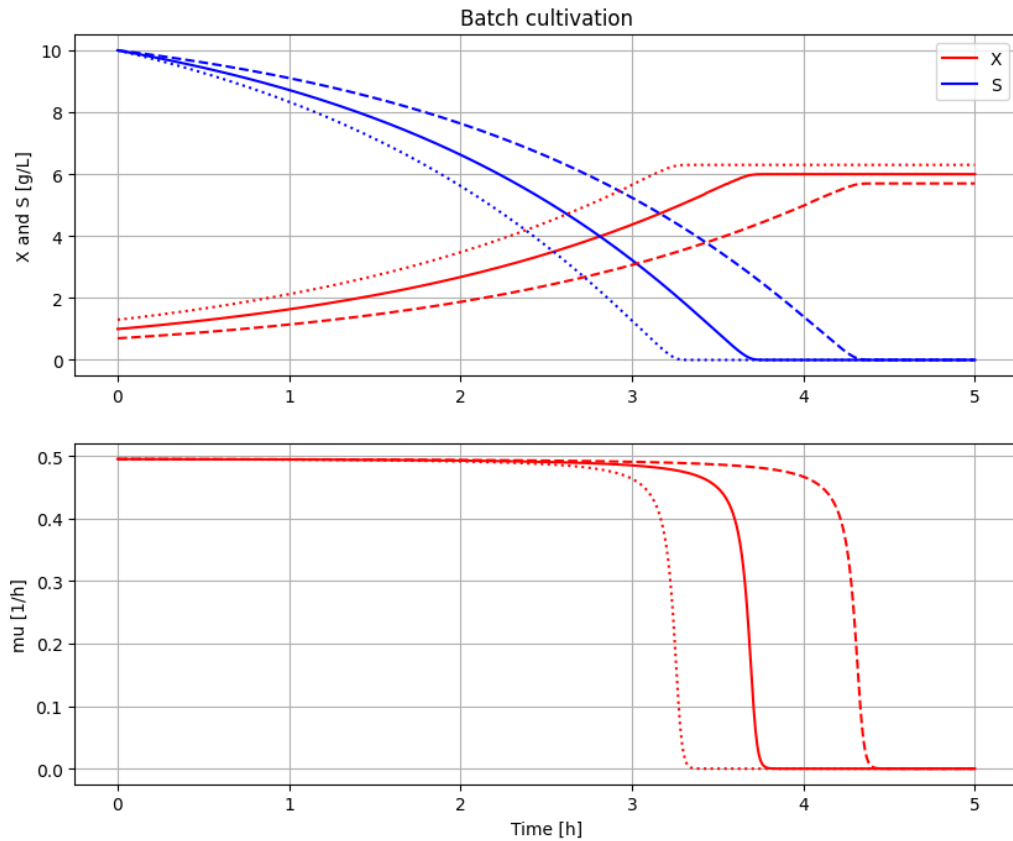
Simplified text book model - only substrate S and cell concentration X

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

## Batch cultivation

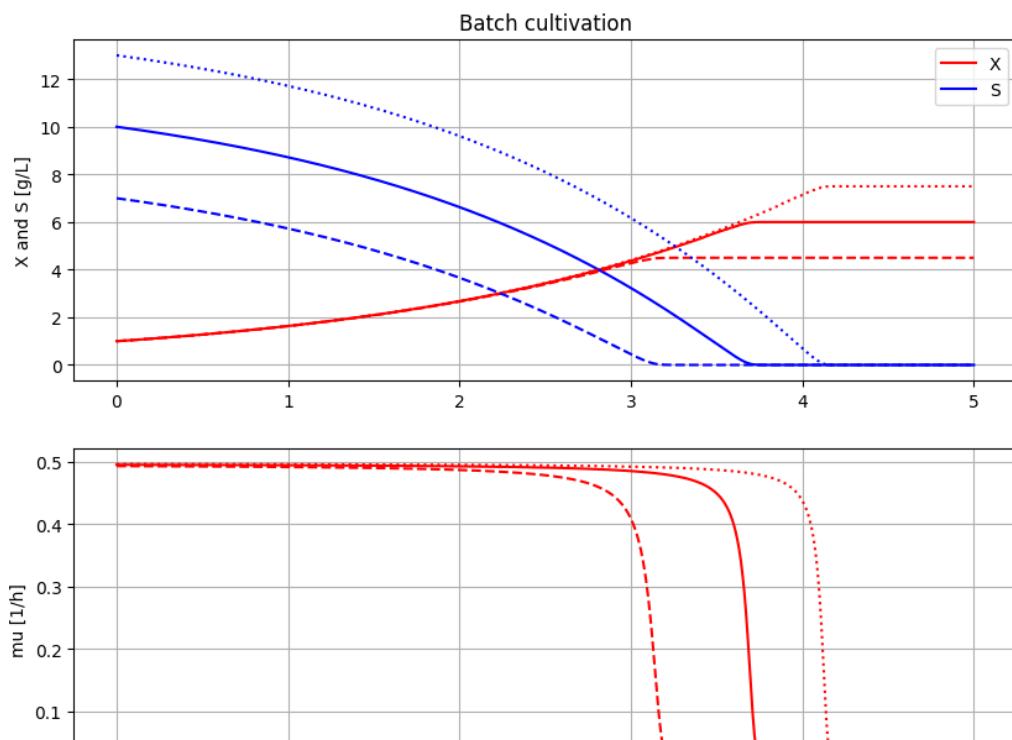
```
# Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_0=value); simu(5)

# Restore default value of VX_0
init(VX_0=1.0)
```



```
# Simulation were initial value of substrate VS_0 is varied
newplot(plotType='TimeSeries')
for value in [10, 7, 13]: init(VS_0=value); simu(5)

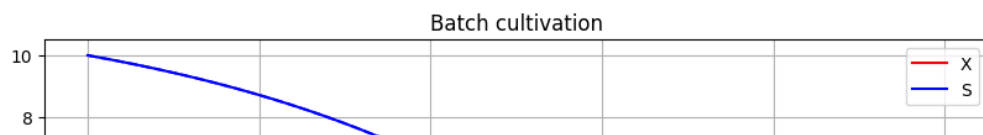
# Restore default value of VS_0
init(VS_0=10)
```



```
# 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
```



```
system_info()
```

```
System information
```

```
-OS: Linux
-Python: 3.10.12
-Scipy: not installed in the notebook
-PyFMI: 2.11.0
-FMU by: OpenModelica Compiler OpenModelica 1.21.0
-FMI: 2.0
-Type: FMUModelME2
-Name: BPL_TEST2.Batch
-Generated: 2023-04-19T18:37:26Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.1.1
-Interaction: FMU-explore version 0.9.8
```