

## ✓ BPL\_TEST2\_Fedbatch script with PyFMI

The key library PyFMI is installed.

After the installation a small application BPL\_TEST2\_Fedbatch 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/')
```

```

--2025-02-10 08:15:45--  https://repo.anaconda.com/miniconda/Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.191.158, 104.16.32.241, 2606:4700::6810:20f1, ..
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.191.158|: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 118MB/s in 1.2s
```

```
2025-02-10 08:15:46 (118 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, 10.24it/s]
ca-certificates-2024	128 KB	: 100% 1.0/1 [00:00<00:00, 9.48it/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\_Fedbatch setup

This notebook just produce the Figure 2 in the paper "Design ideas behind Bioprocess Library for Modelica", by J P Axelsson, to be presented at the 15th International Modelica Conference in Aachen, Germany, October 9-11, 2023.


Now specific installation and the run simulations. Start with connecting to Github. Then upload the two files:

- FMU - BPL\_TEST2\_Fedbatch\_linux\_om\_me.fmu
- Setup-file - BPL\_TEST2\_Fedbatch\_explore.me.py

```

%%bash
git clone https://github.com/janpeter19/CONF_2023_10_MODELICA15


```

 Cloning into 'CONF\_2023\_10\_MODELICA15'...

```

%cd CONF_2023_10_MODELICA15

```

 /content/CONF\_2023\_10\_MODELICA15

```

run -i BPL_TEST2_Fedbatch_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]

```

```

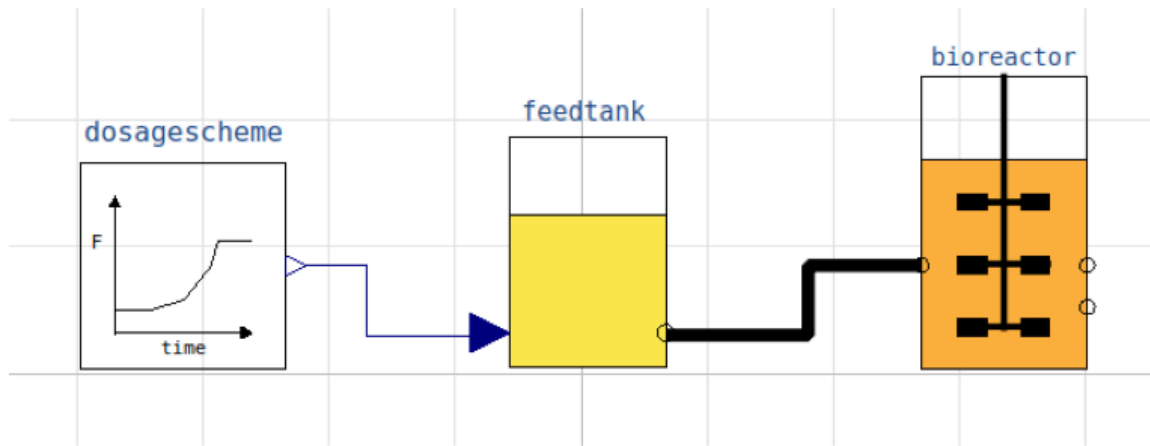
import warnings
warnings.filterwarnings("ignore")

```

```

process_diagram()

```



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

```
# Pump schedule param
```



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

```
# Simulation of the process
newplot(plotType='TimeSeries')
ax2.set_ylim([0, 0.45])
init(V_0=1000, VX_0=1*1e3, VS_0=10*1e3)
par(feedtank_S_in=600, Ks=0.1, Y=0.40)
par(t_start=4, F_start=4.0, mu_feed=0.2, F_max=35)
simu(20)
```

```

↳ Could not find cannot import name 'dopri5' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/a
↳ Could not find cannot import name 'rodas' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/as
↳ Could not find cannot import name 'odassl' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/a
↳ Could not find ODEPACK functions

```

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

```

↳ Y : 0.4
  qSmax : 1.0
  Ks : 0.1

```



Start coding or [generate](#) with AI.



```
describe('mu')
```

```
↳ Cell specific growth rate variable : 0.098 [ 1/h ]
```



```
describe('parts')
```

```
↳ ['bioreactor', 'bioreactor.culture', 'dosagescheme', 'feedtank']
```



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

```
↳ MSL: 3.2.3 - used components: RealInput, RealOutput
```



```
system_info()
```

```

↳
System information
-OS: Linux
-Python: 3.11.11
-Scipy: not installed in the notebook
-PyFMI: 2.16.3
-FMU by: OpenModelica Compiler OpenModelica 1.21.0
-FMI: 2.0
-Type: FMUModelME2
-Name: BPL_TEST2.Fedbatch
-Generated: 2023-04-20T12:24:29Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.1.1
-Interaction: FMU-explore version 0.9.8

```

Start coding or [generate](#) with AI.