

▼ 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 22.04.2 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/')

--2023-08-19 10:49:21-- https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.130.3, 104.16.131.3, 2606:4700::6810:8303, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.130.3|: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 82.7MB/s in 0.9s

2023-08-19 10:49:22 (82.7 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 23.7.2  
Python 3.10.12
```

```
!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/BPL_TEST2_Fedbatch

Cloning into 'BPL_TEST2_Fedbatch'...

%cd BPL_TEST2_Fedbatch

/content/BPL_TEST2_Fedbatch

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

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]

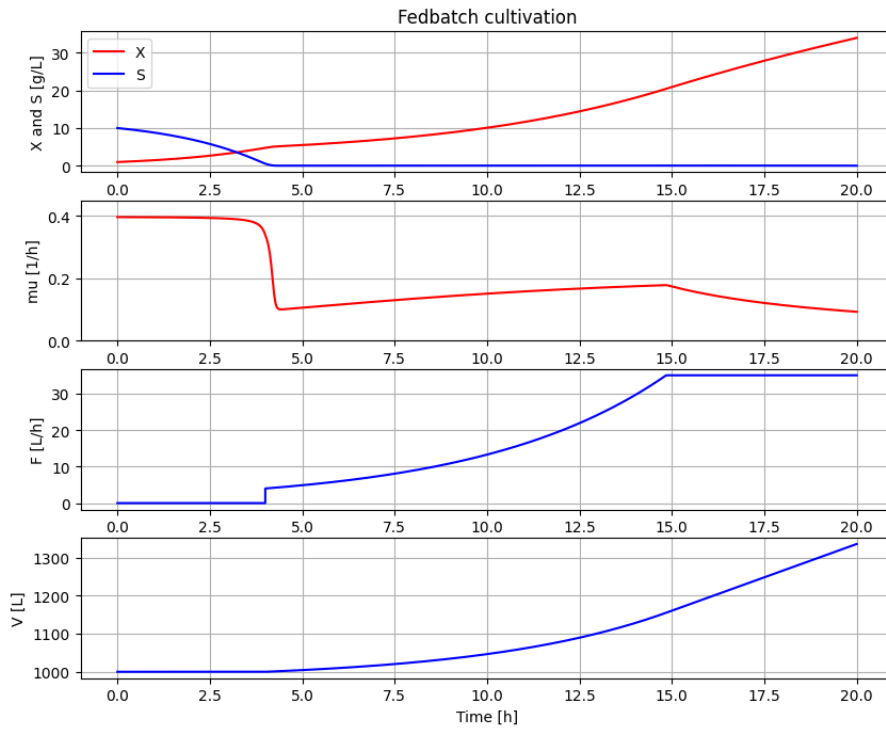
import warnings
warnings.filterwarnings("ignore")

describe('culture'); print(); #describe('liquidphase') # Pump schedule parameter

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)
```

Error: feedtank_S_in - seems not an accessible parameter - check the spelling



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

```
Y : 0.4
qSmax : 1.0
Ks : 0.1
```

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

```
Cell specific growth rate variable : 0.093 [ 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: 3.10.12
-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.Fedbatch
-Generated: 2023-04-20T12:24:29Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.1.1
-Interaction: FMU-explore version 0.9.7
```

✓ 0s completed at 12:52

● ×