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 22.04.3 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/')
```

```
--2025-01-15 07:31:54--  https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.158, 2606:4700::6810:bf9e,
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|: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   229MB/s    in 0.3s

2025-01-15 07:31:55 (229 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 23.1.0
Python 3.10.16
```

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

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

Notes: BPL_TEST2_PID_Fedbatch_reg

This notebook just produce the Figure 6 in the paper "Design ideas behind Bioprocess Library for Modelica", by J P Axelsson, to be presented in the 15th International Modelica Conference in Aachen, Germany, October 9-11, 2023.

Test run for in BPL_TEST2_PID test-case fedbatch_reg that demonstarate substrate control of the feed flow around fixed exponential dosage scheme. Note, that here is a small drift from mu_ref at the end.

Note For the JModelica compilation the derivative part and thus Td, and N cannot be used. Likely due to usage of MSL 3.2.2

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

- FMU - BPL_TEST2_PID_Fedbatch_reg6_linux_om_me.fmu
- Setup-file - BPL_TEST2_PID_Fedbatch_reg6_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_PID_Fedbatch_reg6_explore.py
```

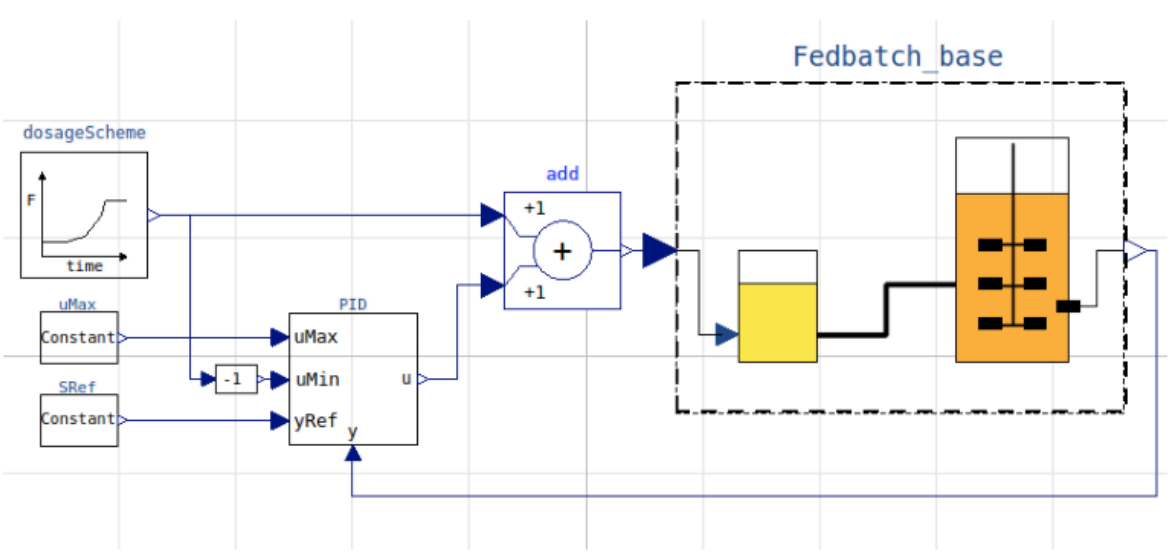
```
Linux - run FMU pre-comiled OpenModelica 1.21.0

    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]
```

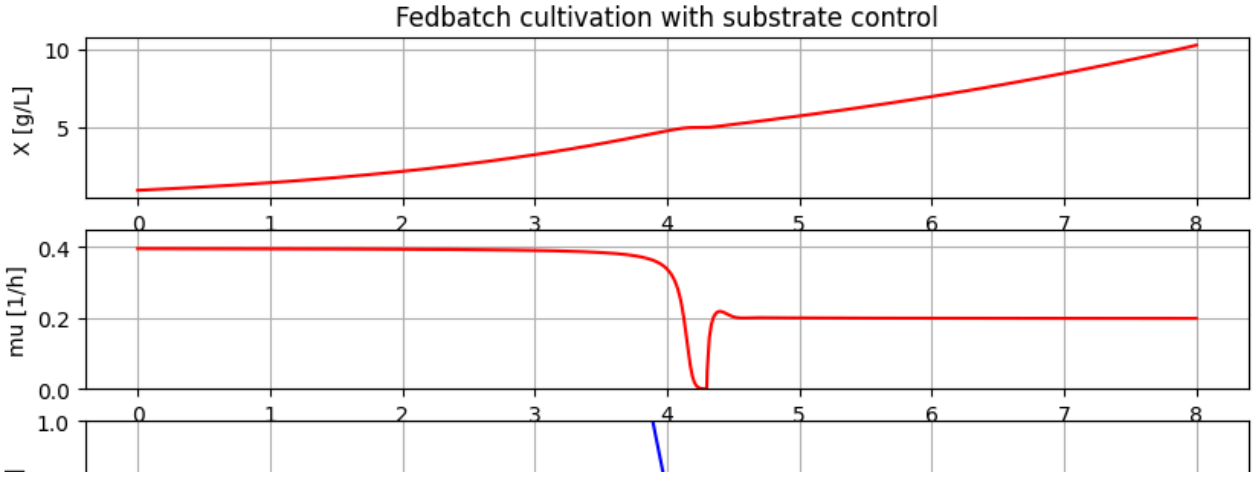
```
import warnings
warnings.filterwarnings("ignore")
```

```
process_diagram()
```




```
# Simulation of the process with controller
par(Y=0.40, qSmax=1.0, Ks=0.1)                  # Culture parameters
init(V_0=1e3, VX_0=1e3, VS_0=10*1e3)            # Process initialization

par(S_in=600)                                   # Feed profile
par(t_start=4.3, F_start=4, mu_feed=0.2, F_max=35)

par(S_ref=0.1)                                  # Substrate controller
par(t_regStart=4.3)
par(uMax=50)

newplot()
ax2.set_ylim([0, 0.45]); ax3.set_ylim([0, 1])
setLines(['-']);
par(K=30, Ti=0.5)
simu(8)
```

```
Could not find cannot import name 'dopri5' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/
Could not find cannot import name 'rodas' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/a
Could not find cannot import name 'odassl' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/
Could not find ODEPACK functions.
Could not find RADAR5
Could not find GLIMDA.
```




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

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

```
system_info()
```

```
System information
 -OS: Linux
 -Python: 3.10.12
 -Scipy: not installed in the notebook
 -PyFMI: 2.16.1
 -FMU by: OpenModelica Compiler OpenModelica 1.21.0
 -FMI: 2.0
 -Type: FMUModelME2
 -Name: BPL_TEST2_PID.Fedbatch_reg6
 -Generated: 2023-08-22T10:54:51Z
 -MSL: 3.2.3
 -Description: Bioprocess Library version 2.1.1-beta
 -Interaction: FMU-explore version 0.9.8
```

Start coding or generate with AI.