BPL_TEST2_Fedbatch script with PyFMI ver 2.9.8

The key library PyFMI ver 2.9.8 is installed.

After the installation a small application BPL_CHO_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 20.04.5 LTS
Release:        20.04
Codename:       focal
```

```
%env PYTHONPATH=
```

```
env: PYTHONPATH=
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py38_22.11.1-1-Linux-x86_64.sh
!chmod +x Miniconda3-py38_22.11.1-1-Linux-x86_64.sh
!bash ./Miniconda3-py38_22.11.1-1-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.8/site-packages/')
```

```
--2023-01-19 09:56:24--  https://repo.anaconda.com/miniconda/Miniconda3-py38_22.11.1-1-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: 64630241 (62M) [application/x-sh]
Saving to: 'Miniconda3-py38_22.11.1-1-Linux-x86_64.sh'

Miniconda3-py38_22. 100%[===================>]  61.64M  80.1MB/s    in 0.8s

2023-01-19 09:56:25 (80.1 MB/s) - 'Miniconda3-py38_22.11.1-1-Linux-x86_64.sh' saved [64630241/64630241]

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 22.11.1
     Python 3.8.15
```

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

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

BPL_TEST2_Fedbatch setup

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

```
# Filter out DepracationWarnings for 'np.float as alias' is needed - wish I could make filter more narrow
#import warnings
#warnings.filterwarnings("ignore")
```

```
%%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_me.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]
```
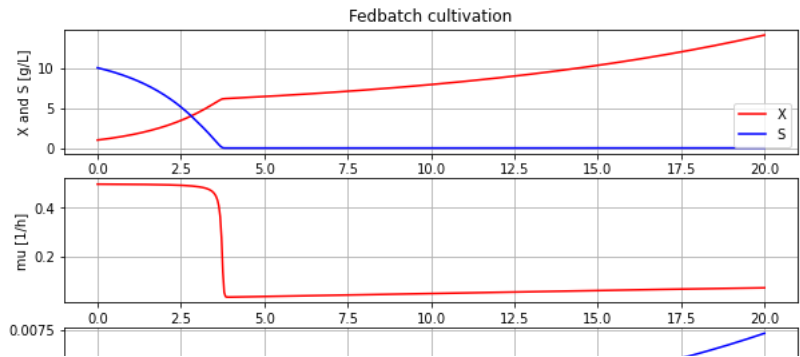
```
import warnings
warnings.filterwarnings("ignore")
```

BPL_TEST2_Fedbatch - demo

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

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

```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)
```

```
disp(mode='long')
```

```
    bioreactor.V_0 : V_0 : 1.0
    bioreactor.m_0[1] : VX_0 : 1.0
    bioreactor.m_0[2] : VS_0 : 10.0
    bioreactor.culture.Y : Y : 0.5
    bioreactor.culture.qSmax : qSmax : 1.0
    bioreactor.culture.Ks : Ks : 0.1
    feedtank.c_in[2] : feedtank.S_in : 300.0
    feedtank.V_0 : feedtank.V_0 : 10.0
    dosagescheme.mu_feed : mu_feed : 0.1
    dosagescheme.t_start : t_start : 3.0
    dosagescheme.F_start : F_start : 0.001
    dosagescheme.F_max : F_max : 0.3
```

```
# A more typical feed scheme for the culture at hand
newplot(plotType='TimeSeries')
par(t_start=4, F_start=0.008, mu_feed=0.2, F_max=0.1)
simu(20)
```
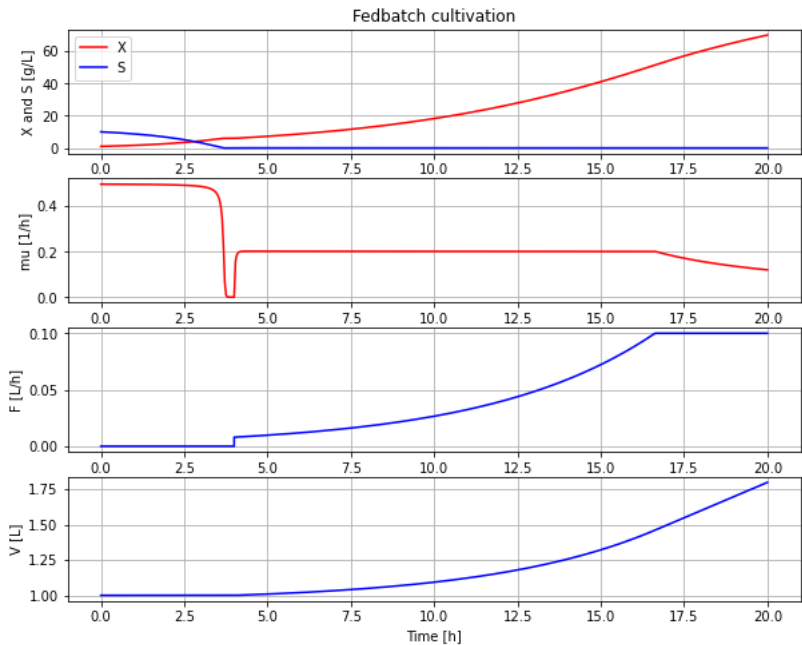


```
disp('culture')
```

```
    Y : 0.5
    qSmax : 1.0
    Ks : 0.1
```

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

```
    Cell specific growth rate variable : 0.12 [ 1/h ]
```

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

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

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

```
    MSL: information not accessible from this FMU
```

```
system info()
```

```
System information
 -OS: Linux
 -Python: 3.8.10
 -Scipy: not installed in the notebook
 -PyFMI: 2.9.8
 -FMU by: OpenModelica Compiler OpenModelica 1.21.0~dev-185-g9d983b8
 -FMI: 2.0
 -Type: FMUModelME2
 -Name: BPL_TEST2.Fedbatch
 -Generated: 2023-01-19T09:29:14Z
 -MSL: MSL.version information not accessible
 -Description: BPL.version information not accessible
 -Interaction: FMU-explore version 0.9.6d
```

✓ 0s   completed at 10:57