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/')
```

```
--2024-01-18 09:46:49--  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::6810:8203, ...
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   135MB/s    in 0.5s

2024-01-18 09:46:49 (135 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 23.11.0
    Python 3.10.13
```

```
!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

```
%%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
```

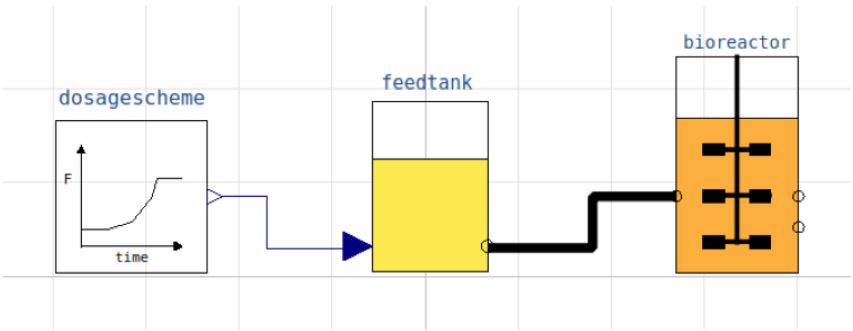
```
Linux - run FMU pre-comiled OpenModelica 1.21.0

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
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_Fedbatch - demo

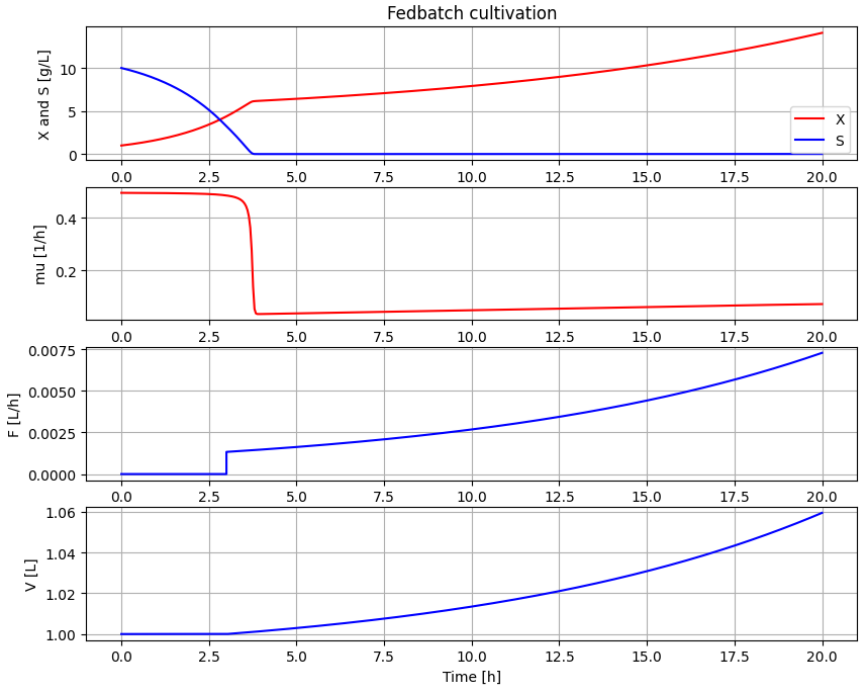
```
process_diagram()
```




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

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

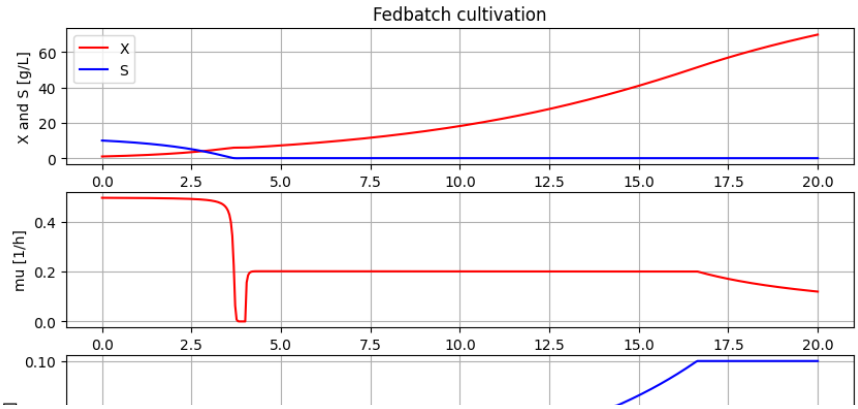
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)
```




```
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: 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 0.9.8
```