BPL_TEST2_Fedbatch script with FMPy

The key library FMPy 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-py312_24.3.0-0-Linux-x86_64.sh
!chmod +x Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
!bash ./Miniconda3-py312_24.3.0-0-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.12/site-packages/')
```

```
--2024-08-13 08:15:18--  https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.191.158, 104.16.32.241, 2606:4700::6810:bf9e, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.191.158|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 143351488 (137M) [application/octet-stream]
Saving to: ‘Miniconda3-py312_24.3.0-0-Linux-x86_64.sh’

Miniconda3-py312_24 100%[===================>] 136.71M  83.3MB/s    in 1.6s

2024-08-13 08:15:20 (83.3 MB/s) - ‘Miniconda3-py312_24.3.0-0-Linux-x86_64.sh’ saved [143351488/143351488]

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
```

```
  ca-certificates                    2024.3.11-h06a4308_0 --> 2024.7.2-h06a4308_0
  certifi                        2024.2.2-py312h06a4308_0 --> 2024.7.4-py312h06a4308_0
  conda                            24.3.0-py312h06a4308_0 --> 24.7.1-py312h06a4308_0
  openssl                               3.0.13-h7f8727e_0 --> 3.0.14-h5eee18b_0
```

```
conda-24.7.1          | 1.2 MB    | : 100% 1.0/1 [00:00<00:00,  1.76it/s]


frozendict-2.4.2      | 36 KB     | : 100% 1.0/1 [00:00<00:00,  1.69it/s]









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

```
!conda --version
!python --version
```

```
conda 24.7.1
Python 3.12.2
```

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

```


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

```
#!conda install matplotlib --yes
```

```
#!conda install scipy --yes
```

```
#!conda install xlrd --yes
```

```
#!conda install openpyxl --yes
```

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_fmpy_explore.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_fmpy_explore.py
```

```
Linux - run FMU pre-comiled OpenModelica 1.23.0-dev

    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")
```

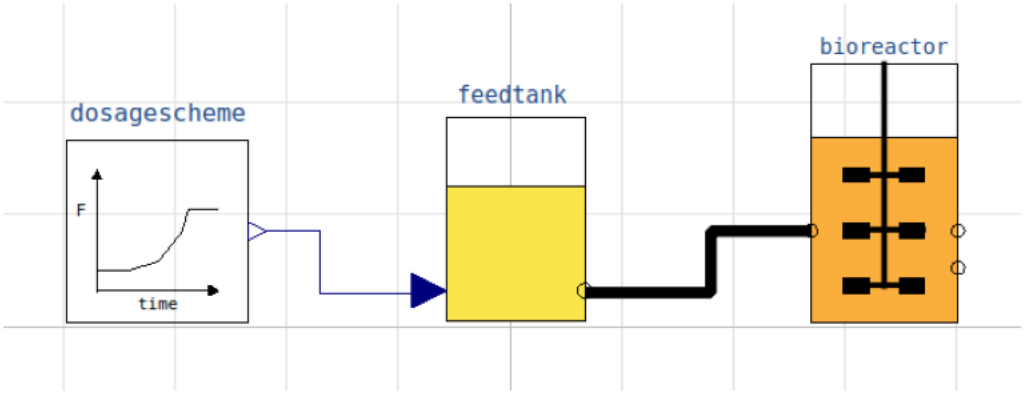
BPL_TEST2_Fedbatch - demo

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

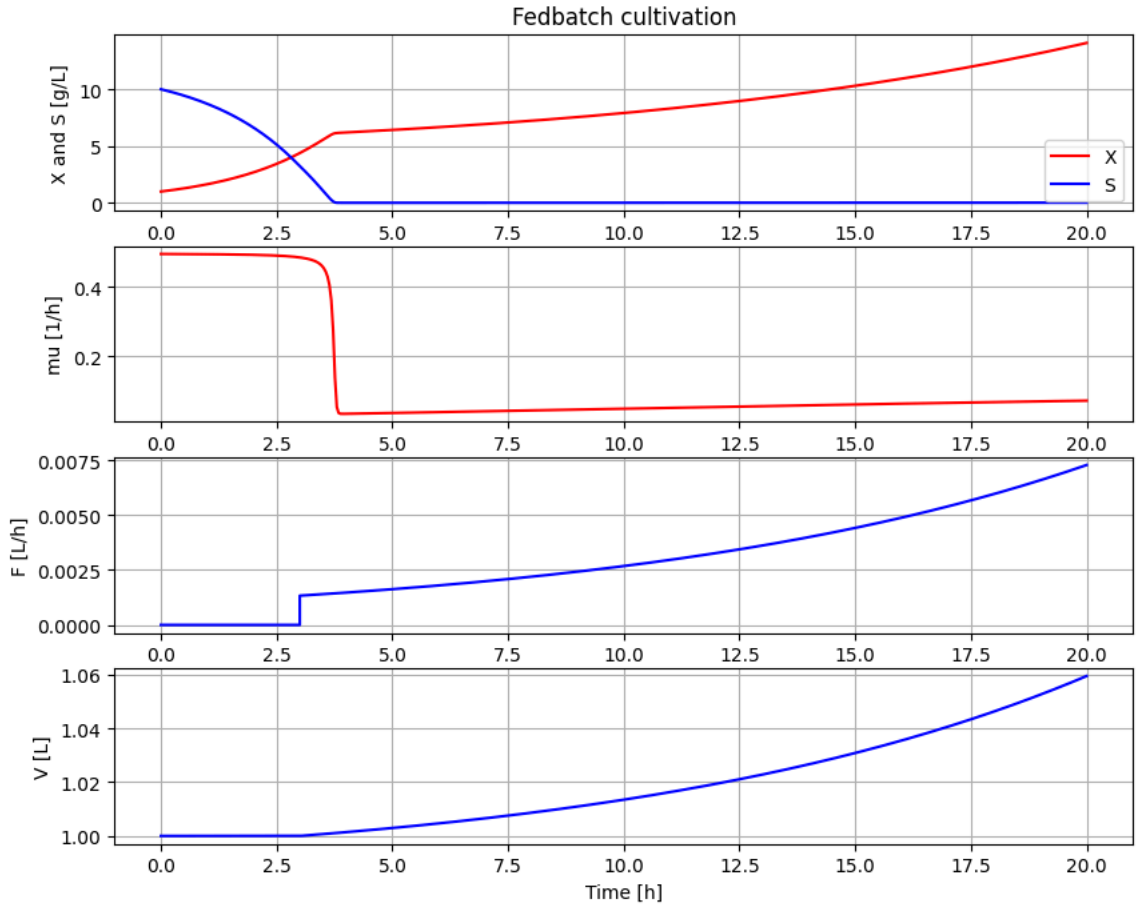
```
Simplified text book model - only substrate S and cell concentration X
```

```
process_diagram()
```

```
No processDiagram.png file in the FMU, but try the file on disk.
```



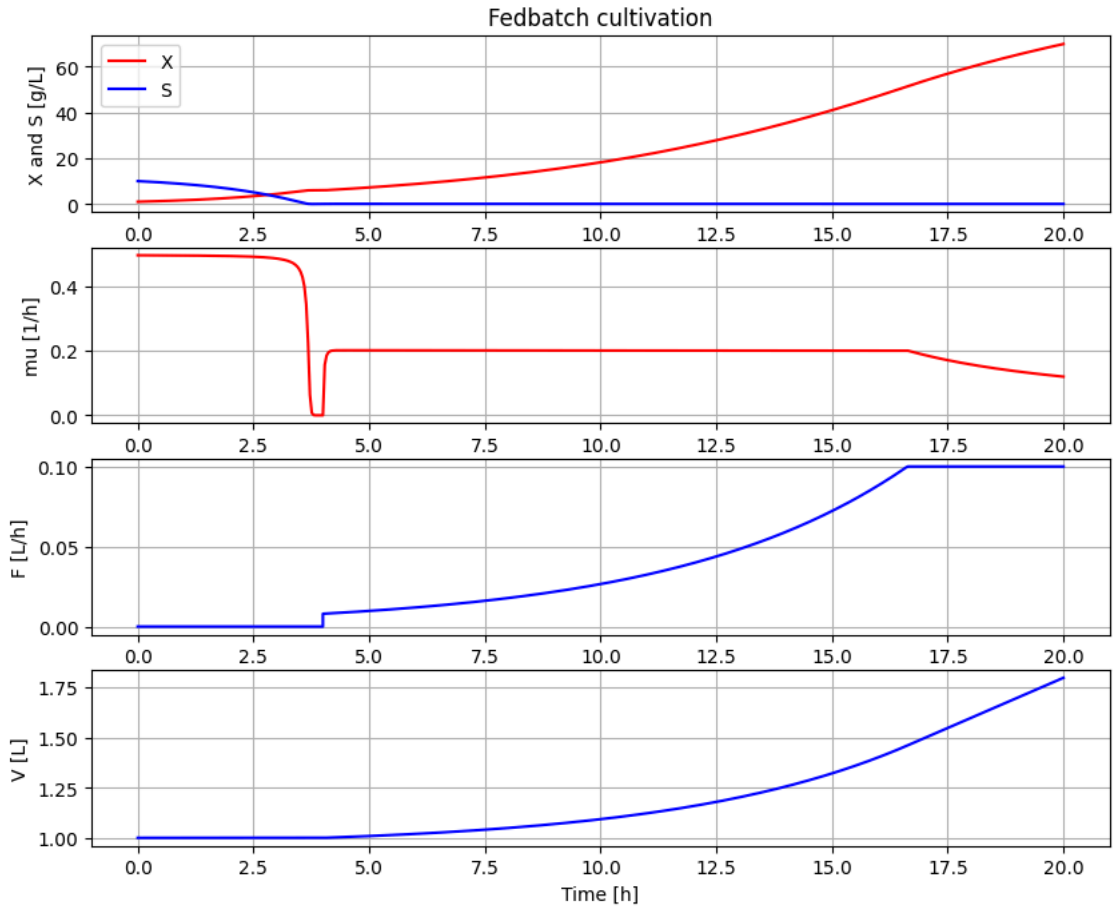

```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)
```




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

```
bioreactor.V_start : V_start : 1.0
bioreactor.m_start[1] : VX_start : 0.0
bioreactor.m_start[2] : VS_start : 0.0
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 : 0.0
feedtank.V_start : feedtank.V_start : 100.0
dosagescheme.mu_feed : mu_feed : 0.2
dosagescheme.t_startExp : t_startExp : 2.0
dosagescheme.F_startExp : F_startExp : 0.12
dosagescheme.F_max : F_max : 3.0
```

```
# A more typical feed scheme for the culture at hand
newplot(plotType='TimeSeries')
par(t_startExp=4, F_startExp=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
 -FMPy: 0.3.20
 -FMU by: OpenModelica Compiler OpenModelica 1.23.0~dev.beta.1-1-g379f714
 -FMI: 2.0
 -Type: ME
 -Name: BPL_TEST2.Fedbatch
 -Generated: 2024-05-20T13:38:03Z
 -MSL: 3.2.3
 -Description: Bioprocess Library version 2.2.0
 -Interaction: FMU-explore for FMPy version 1.0.1
```

Start coding or generate with AI.