BPL_TEST2_Chemostat script with PyFMI

The key library PyFMI is installed.

After the installation a small application BPL_TEST2_Chemostat 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=
```

```
!python --version
```

```
Python 3.10.12
```

```
!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/')
```

```
--2024-10-24 09:09:04--  https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-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: 74403966 (71M) [application/x-sh]
Saving to: ‘Miniconda3-py310_23.1.0-1-Linux-x86_64.sh’

Miniconda3-py310_23 100%[===================>]  70.96M   178MB/s    in 0.4s

2024-10-24 09:09:04 (178 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 3.10.15
```

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

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

Now specific installation run a simulation and notebook for that

Start with connecting to Github. Then upload the two files:

- FMU - BPL_TEST2_Chemostat_linux_om_me.fmu
- Setup-file - BPL_TEST2_Chemostat_explore.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_Chemostat
```

```
Cloning into 'BPL_TEST2_Chemostat'...
```

```
%cd BPL_TEST2_Chemostat
```

```
/content/BPL_TEST2_Chemostat
```

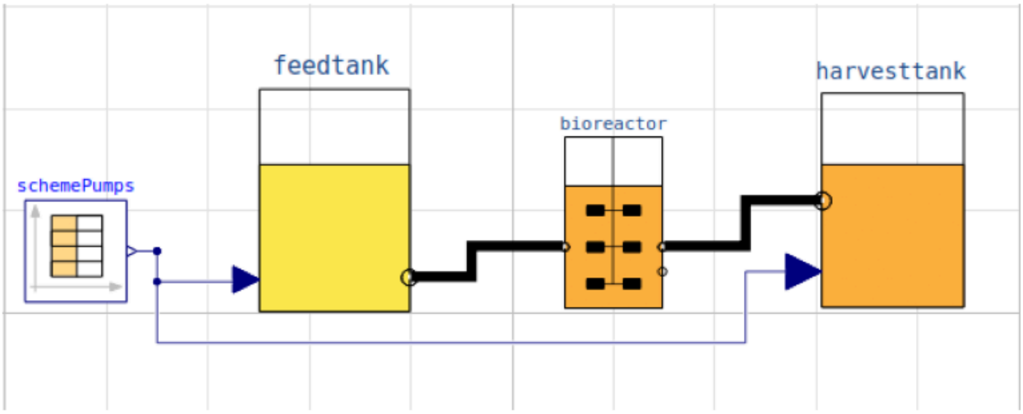
```
run -i BPL_TEST2_Chemostat_explore.py
```

```
Linux - run FMU pre-comiled OpenModelica

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]
```

```
process_diagram()
```

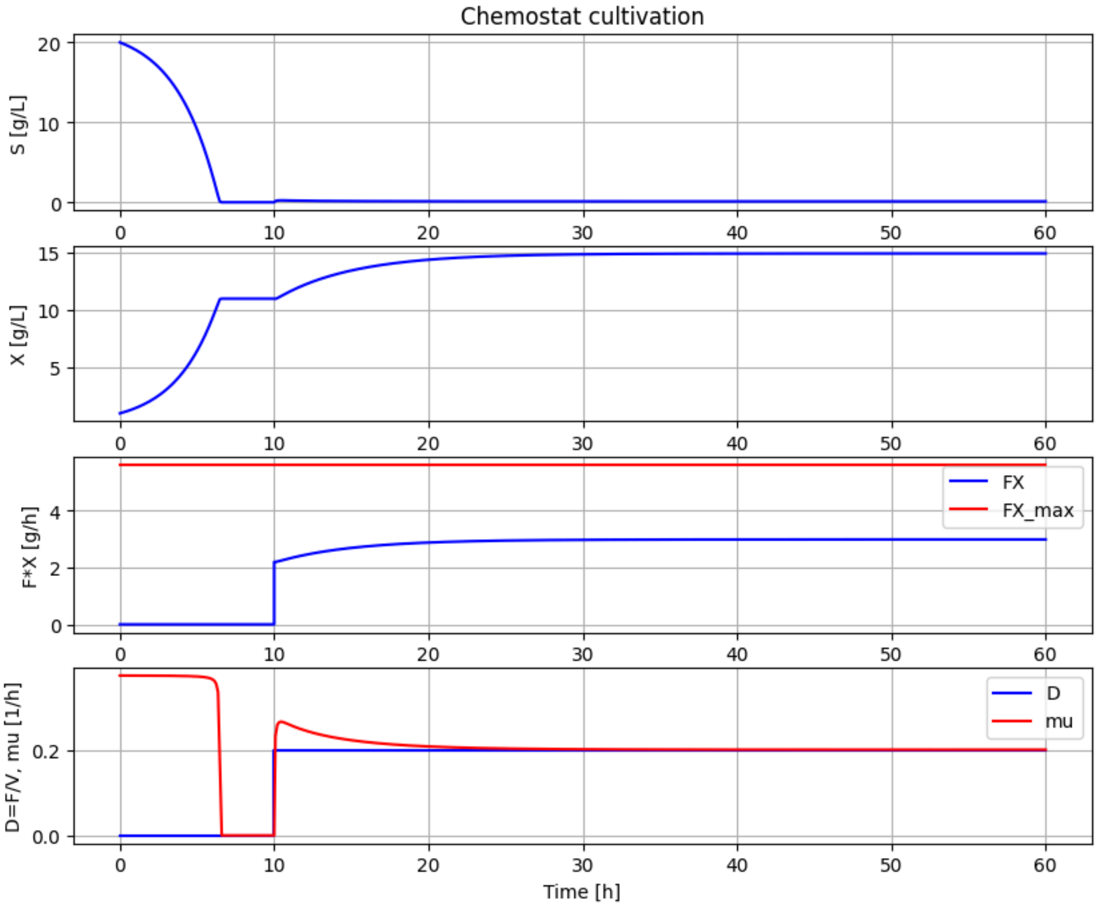
```
No processDiagram.png file in the FMU, but try the file on disk.
```



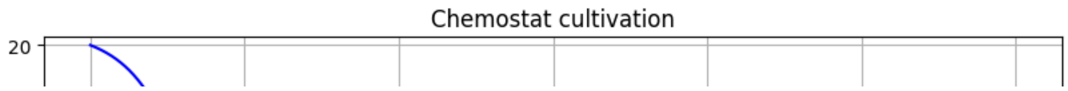
```
describe('culture')
```

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

```
newplot()
par(Y=0.50, qSmax=0.75,  Ks=0.1)            # Culture parameters
init(V_start=1.0, VX_start=1.0, VS_start=20)  # Bioreactor startup
par(S_in=30, t0=0, F0=0, t1=10, F1=0.2)      # Substrate feeding
simu(60)
```



```
# Check simu('cont')
newplot()
simu(20)
simu(40,'cont')
```



```
# The maximal biomass productivity FX_max [g/h] marked red in the diagram above
# can be calculated for CSTR from the FMU and is
cstrProdMax(model)
```

```
5.625
```

```
describe('cstrProdMax')
```

```
Calculate from the model maximal chemostat productivity FX_max : 5.625 [ g/h ]
```

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

```
['bioreactor', 'bioreactor.culture', 'D', 'feedtank', 'harvesttank', 'schemePumps']
```

```
system_info()
```

```
System information
 -OS: Linux
 -Python: 3.10.12
 -Scipy: not installed in the notebook
 -PyFMI: 2.14.0
 -FMU by: OpenModelica Compiler OpenModelica 1.25.0~dev-51-ge672d09
 -FMI: 2.0
 -Type: FMUModelME2
 -Name: BPL.Examples_TEST2.Chemostat
 -Generated: 2024-10-12T15:10:56Z
 -MSL: 3.2.3
 -Description: Bioprocess Library version 2.2.2 - GUI
 -Interaction: FMU-explore version 1.0.0
```

Start coding or generate with AI.