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 20.04.5 LTS
Release:        20.04
Codename:       focal
```

```
%env PYTHONPATH=
```

```
env: PYTHONPATH=
```

```
!wget·https://repo.anaconda.com/miniconda/Miniconda3-py39_23.1.0-1-Linux-x86_64.sh·
!chmod·+x·Miniconda3-py39_23.1.0-1-Linux-x86_64.sh
!bash·./Miniconda3-py39_23.1.0-1-Linux-x86_64.sh·-b·-f·-p·/usr/local·
import·sys·
sys.path.append('/usr/local/lib/python3.9/site-packages/')
```

```
--2023-04-21 06:39:36--  https://repo.anaconda.com/miniconda/Miniconda3-py39_23.1.0-1-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.131.3, 104.16.130.3, 2606:4700::6810:8203, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.131.3|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 69888122 (67M) [application/x-sh]
Saving to: ‘Miniconda3-py39_23.1.0-1-Linux-x86_64.sh’

Miniconda3-py39_23. 100%[===================>]  66.65M   183MB/s    in 0.4s

2023-04-21 06:39:36 (183 MB/s) - ‘Miniconda3-py39_23.1.0-1-Linux-x86_64.sh’ saved [69888122/69888122]

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 23.3.1
     Python 3.9.16
```

```
!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
```

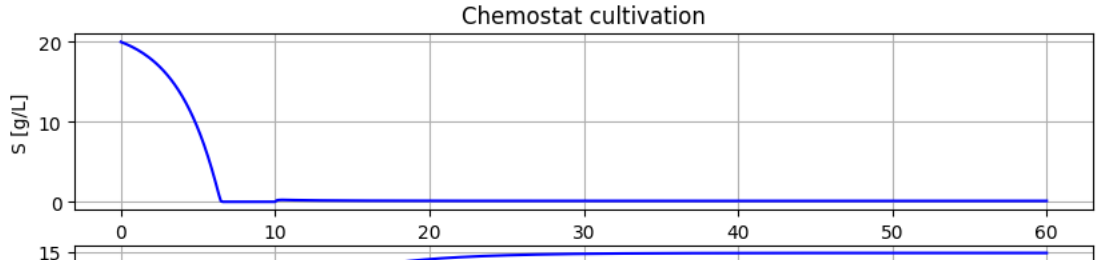
```
/content/BPL_TEST2_Chemostat
```

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

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

```
newplot()
par(Y=0.50, qSmax=0.75,  Ks=0.1)         # Culture parameters
init(V_0=1.0, VX_0=1.0, VS_0=20)         # Bioreactor startup
par(S_in=30, t0=0, F0=0, t1=10, F1=0.2)  # Substrate feeding
simu(60)
```




```
# 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', 'dosagescheme', 'feedtank', 'harvesttank']
```



```
system_info()
```

```
    System information
     -OS: Linux
     -Python: 3.9.16
     -Scipy: not installed in the notebook
     -PyFMI: 2.10.2
     -FMU by: OpenModelica Compiler OpenModelica 1.21.0
     -FMI: 2.0
     -Type: FMUModelME2
     -Name: BPL_TEST2.Chemostat
     -Generated: 2023-04-20T12:24:50Z
     -MSL: 3.2.3
     -Description: Bioprocess Library version 2.1.1
     -Interaction: FMU-explore version 0.9.7
```