▾ BPL_TEST2_Chemostat script with FMPy ver 0.3.15

The key library FMPy v0.3.15 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-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/')
```

```
--2023-03-23 14:05:36--  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::6810:8203, ...
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   144MB/s    in 0.4s

2023-03-23 14:05:37 (144 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 23.1.0
Python 3.8.15
```

```
!conda install -c conda-forge fmpy --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_fmpy_explore.py

```
%%bash
git clone https://github.com/janpeter19/BPL_TEST2_Chemostat
```

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

```
%cd BPL_TEST2_Chemostat
```

```
/content/BPL_TEST2_Chemostat
```

▾ BPL_TEST2_Chemostat - demo

```
run -i BPL_TEST2_Chemostat_fmpy_explore.py
```

```
Linux - run FMU pre-compiled 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()
```
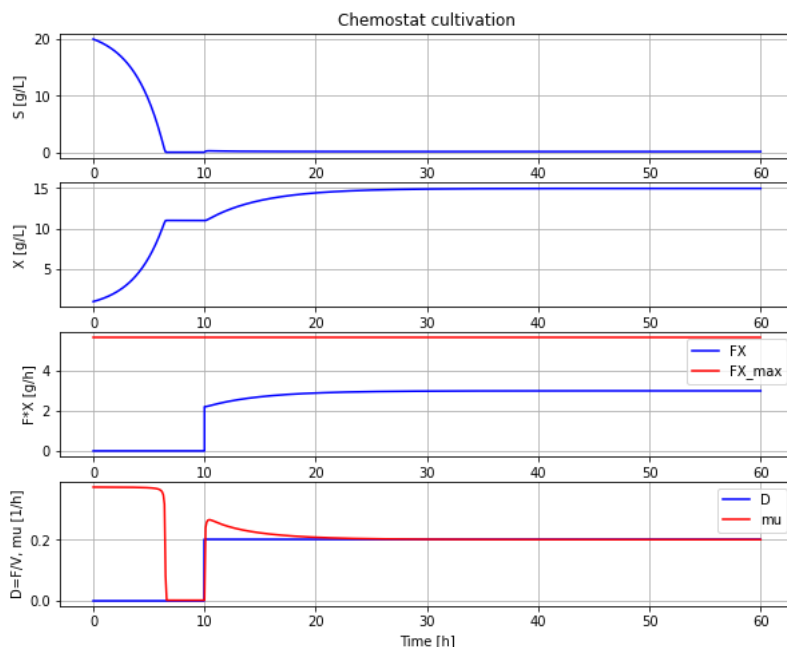
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

```
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)
```

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

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

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

```
    MSL: 3.2.3 - used components: RealInput, RealOutput, CombiTimeTable, Types
```

```
system_info()
```

```
    System information
     -OS: Linux
     -Python: 3.9.16
     -Scipy: not installed in the notebook
     -FMPy: 0.3.15
     -FMU by: OpenModelica Compiler OpenModelica 1.21.0~dev-185-g9d983b8
     -FMI: 2.0
     -Type: ME
     -Name: BPL_TEST2.Chemostat
     -Generated: 2023-02-13T10:27:14Z
     -MSL: 3.2.3
     -Description: Bioprocess Library version 2.1.1-beta
     -Interaction: FMU-explore for FMPy version 0.9.7c
```

✓ 0 s   kördes kl. 15:09   ● ✕