⌄ 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/')
```

```
--2025-01-14 09:19:32--  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::6810:20f1,
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   123MB/s    in 0.6s

2025-01-14 09:19:33 (123 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 3.10.16
```

```
!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

```python
# Filter out DepracationWarnings for 'np.float as alias' is needed – wish I could make filter more narrow
import warnings
warnings.filterwarnings("ignore")
```

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

⇥ Cloning into 'BPL_TEST2_Chemostat'...

```python
%cd BPL_TEST2_Chemostat
```

⇥ /content/BPL_TEST2_Chemostat

```python
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
```
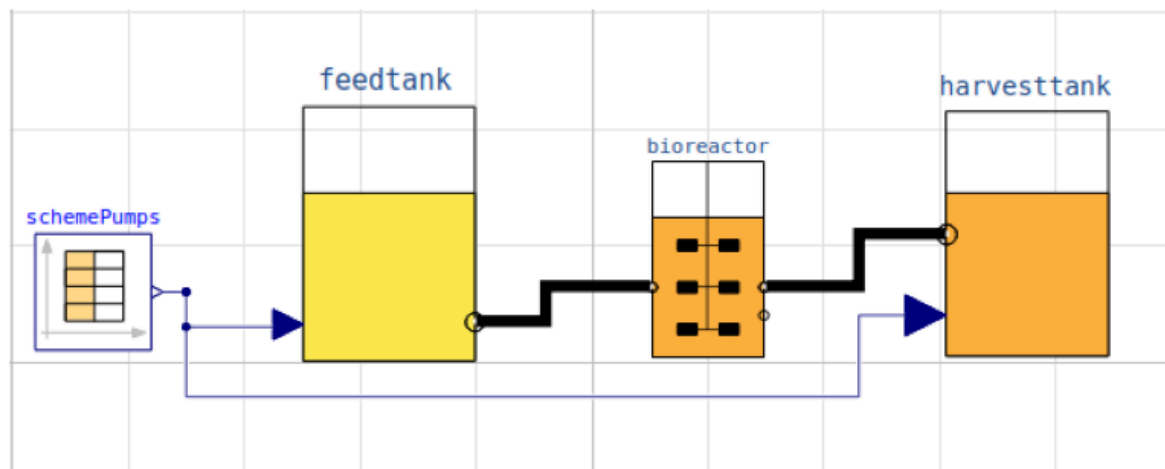
```
    Brief information about a command by help(), eg help(simu)
    Key system information is listed with the command system_info()
```

```
%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.
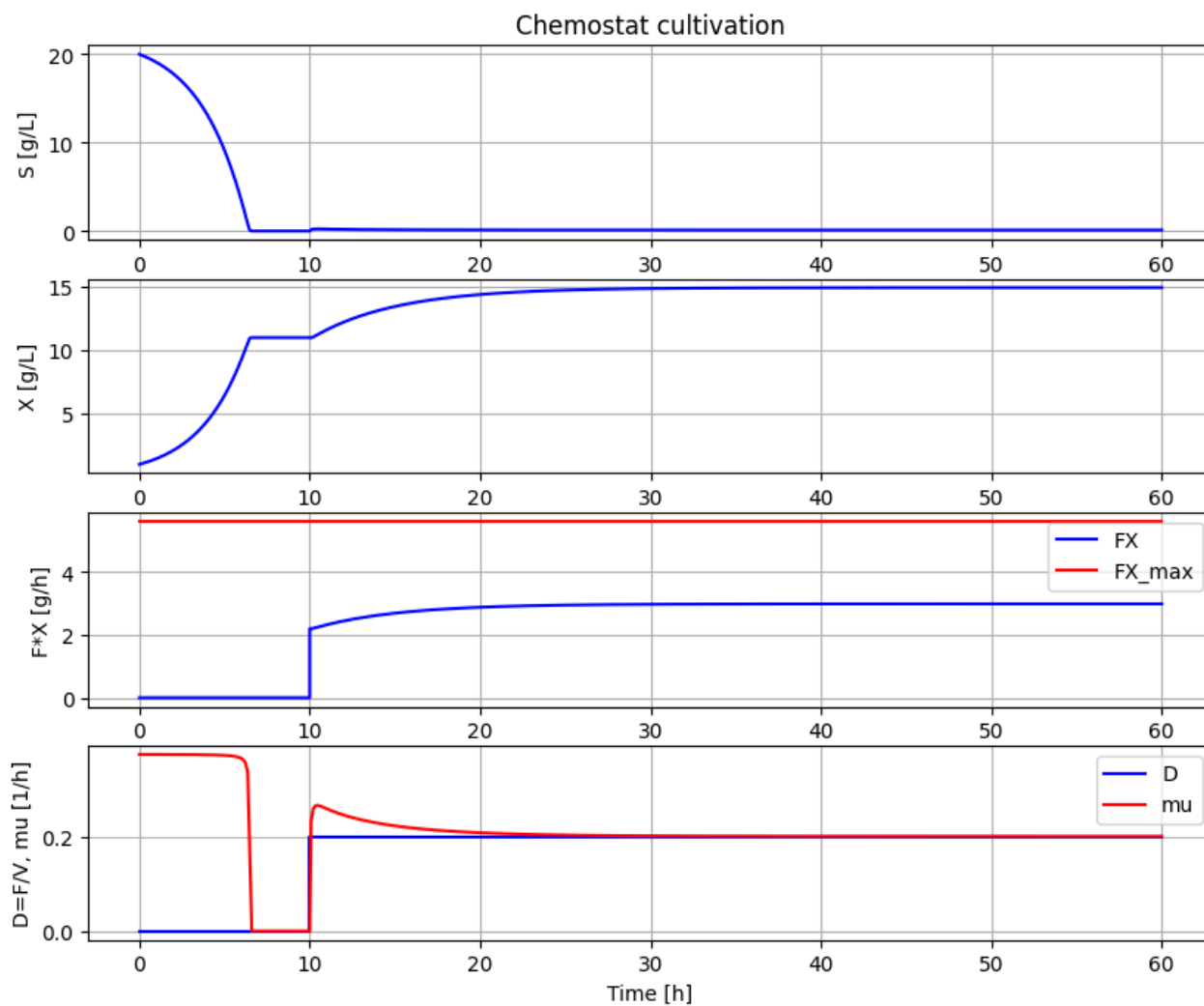


```
describe('culture')
```
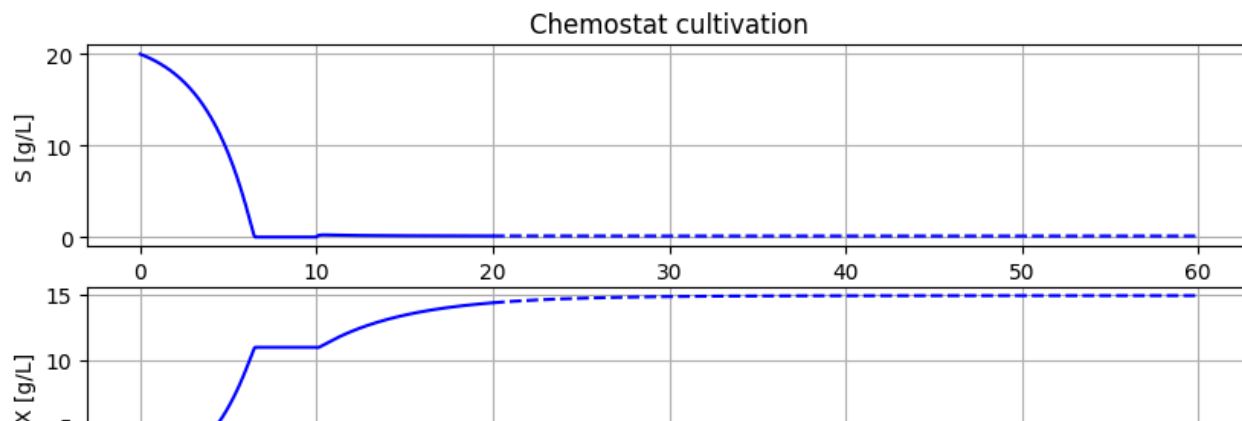
> Simplified text book model – only substrate S and cell concentration X

```
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)
```

```
Could not find cannot import name 'dopri5' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/
Could not find cannot import name 'rodas' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/a
Could not find cannot import name 'odassl' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/
Could not find ODEPACK functions.
Could not find RADAR5
Could not find GLIMDA.
```


Chemostat cultivation

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

Chemostat cultivation


```
# 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']

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

MSL: 3.2.3 – used components: RealInput, RealOutput, CombiTimeTable, Types

```
system_info()
```

```
System information
 –OS: Linux
 –Python: 3.10.12
```