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 22.04.4 LTS
Release:        22.04
Codename:       jammy
```

```
%env PYTHONPATH=
```

```
env: PYTHONPATH=
```

```
!python --version
```

```
Python 3.11.11
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
!chmod +x Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
!bash ./Miniconda3-py311_24.11.1-0-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.11/site-packages/')
```

```
--2025-02-06 09:39:24--  https://repo.anaconda.com/miniconda/Miniconda3-py311_24.11.1-0-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: 145900576 (139M) [application/octet-stream]
Saving to: 'Miniconda3-py311_24.11.1-0-Linux-x86_64.sh'

Miniconda3-py311_24 100%[===================>] 139.14M   126MB/s    in 1.1s

2025-02-06 09:39:25 (126 MB/s) - 'Miniconda3-py311_24.11.1-0-Linux-x86_64.sh' saved [145900576/145900576]

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
```

```
Channels:
 - defaults
Platform: linux-64
Collecting package metadata (repodata.json): done
Solving environment: done

## Package Plan ##

  environment location: /usr/local

  added / updated specs:
    - conda


The following packages will be downloaded:

    package                    |            build
    ---------------------------|-----------------
    ca-certificates-2024.12.31 |       h06a4308_0         128 KB
    certifi-2025.1.31          |  py311h06a4308_0         163 KB
    ------------------------------------------------------------
                                           Total:         291 KB

The following packages will be UPDATED:

  ca-certificates                    2024.11.26-h06a4308_0 --> 2024.12.31-h06a4308_0
  certifi                          2024.8.30-py311h06a4308_0 --> 2025.1.31-py311h06a4308_0



Downloading and Extracting Packages:
```

```
    certifi-2025.1.31    | 163 KB    | :   0% 0/1 [00:00<?, ?it/s]
    ca-certificates-2024 | 128 KB    | :   0% 0/1 [00:00<?, ?it/s]
    certifi-2025.1.31    | 163 KB    | : 100% 1.0/1 [00:00<00:00, 10.06it/s]
    ca-certificates-2024 | 128 KB    | : 100% 1.0/1 [00:00<00:00,  8.30it/s]


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

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

```
conda 24.11.1
Python 3.11.11
```

```
!conda config --set channel_priority strict
```

```
CustomValidationError: Parameter channel_priority = 'stric' declared in --set parameter is invalid.
'stric' is not a valid ChannelPriority
Valid choices for channel_priority: 'strict', 'flexible', 'disabled'
```

```
!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
```

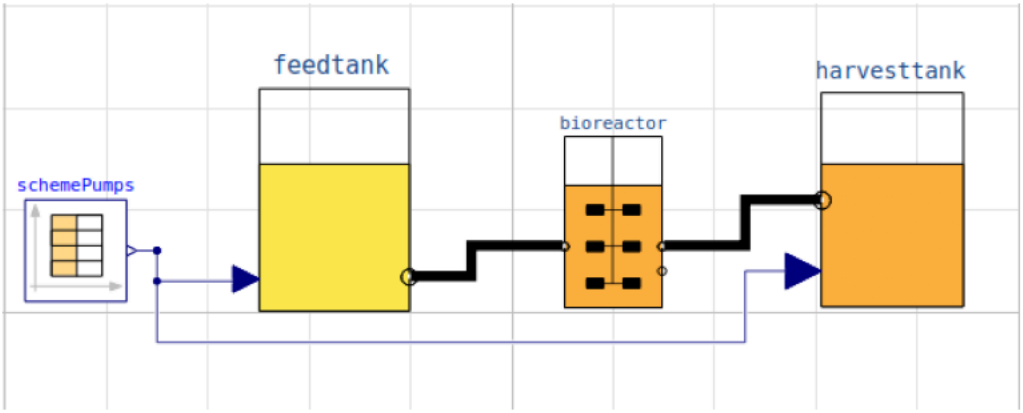
```
run -i BPL_TEST2_Chemostat_explore.py
```

```
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.
```

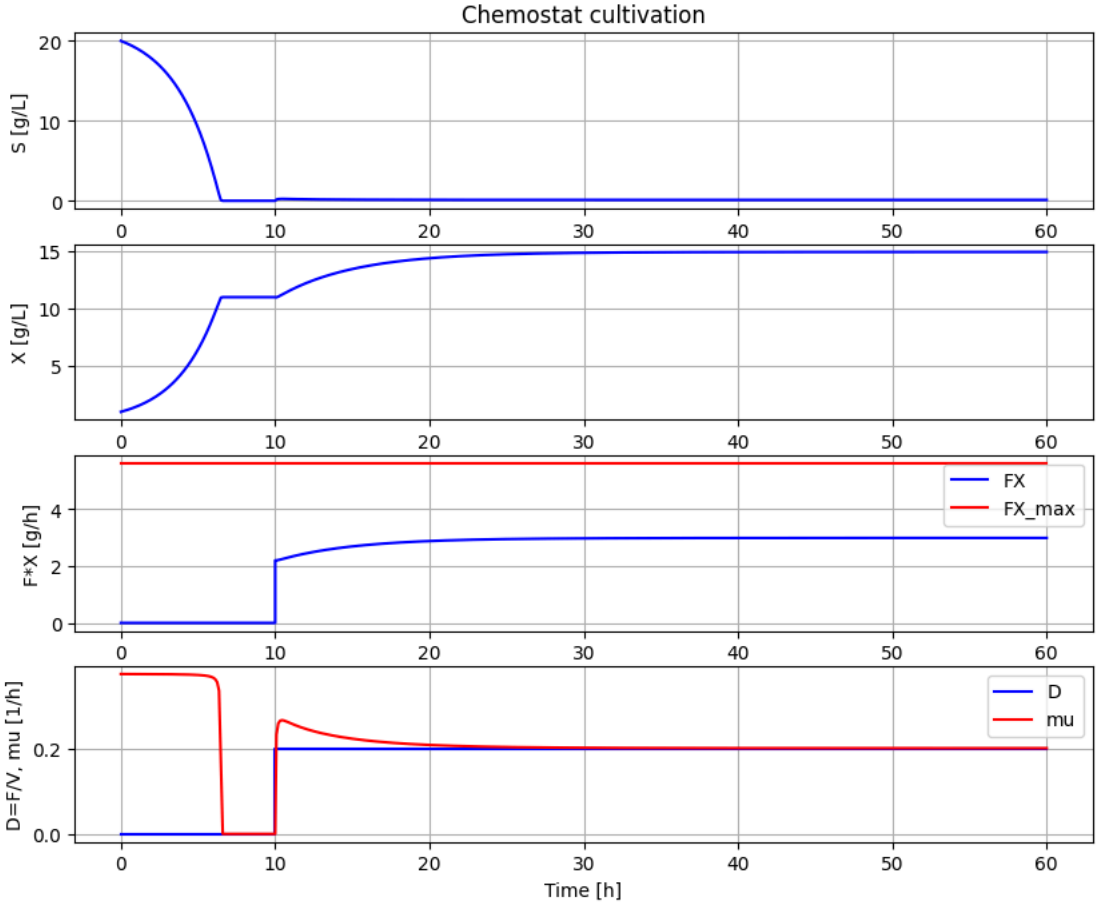



```
describe('culture')
```

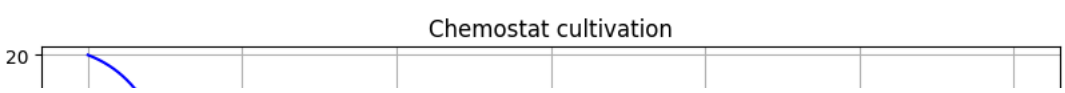
```
Simplified text book model - only substrate S and cell concentration X
```

```
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)
```

```
Could not find cannot import name 'dopri5' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/__i
Could not find cannot import name 'rodas' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/__in
Could not find cannot import name 'odassl' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/__i
Could not find ODEPACK functions.
Could not find RADAR5
Could not find GLIMDA.
```




```
# 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: 3.11.11
 -Scipy: not installed in the notebook
 -PyFMI: 2.16.3
 -FMU by: OpenModelica Compiler OpenModelica 1.25.0~dev-133-ga5470be
 -FMI: 2.0
 -Type: FMUModelME2
 -Name: BPL.Examples_TEST2.Chemostat
 -Generated: 2024-11-06T21:37:41Z
 -MSL: 3.2.3
 -Description: Bioprocess Library version 2.3.0
 -Interaction: FMU-explore version 1.0.0
```

Start coding or generate with AI.