BPL_TEST2_Chemostat script with FMPy

The key library FMPy 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=
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linux-x86_64.
!chmod +x Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
!bash ./Miniconda3-py312_24.3.0-0-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.12/site-packages/')
```

```
--2024-05-15 11:38:40--  https://repo.anaconda.com/miniconda/Miniconda3-py312
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.1
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... conn
HTTP request sent, awaiting response... 200 OK
Length: 143351488 (137M) [application/octet-stream]
Saving to: ‘Miniconda3-py312_24.3.0-0-Linux-x86_64.sh’

Miniconda3-py312_24 100%[===================>] 136.71M   105MB/s    in 1.3s

2024-05-15 11:38:42 (105 MB/s) - ‘Miniconda3-py312_24.3.0-0-Linux-x86_64.sh’ s

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
    ---------------------------|-----------------
    conda-24.5.0               |  py312h06a4308_0         1.2 MB
    frozendict-2.4.2           |  py312h06a4308_0          36 KB
    openssl-3.0.13             |       h7f8727e_1         5.2 MB
    ------------------------------------------------------------
                                           Total:         6.5 MB

The following NEW packages will be INSTALLED:

  frozendict         pkgs/main/linux-64::frozendict-2.4.2-py312h06a4308_0

The following packages will be UPDATED:

  conda                               24.3.0-py312h06a4308_0 --> 24.5.0-py312h0
  openssl                                3.0.13-h7f8727e_0 --> 3.0.13-h7f872


Downloading and Extracting Packages:
openssl-3.0.13       | 5.2 MB    | :   0% 0/1 [00:00<?, ?it/s]
conda-24.5.0         | 1.2 MB    | :   0% 0/1 [00:00<?, ?it/s]

openssl-3.0.13       | 5.2 MB    | :   0% 0.002997347135570501/1 [00:00<00:48
conda-24.5.0         | 1.2 MB    | :   1% 0.01293349794914382/1 [00:00<00:12,

frozendict-2.4.2     | 36 KB     | :  44% 0.43853215920344746/1 [00:00<00:00,

openssl-3.0.13       | 5.2 MB    | : 100% 1.0/1 [00:00<00:00,  1.41it/s]
conda-24.5.0         | 1.2 MB    | : 100% 1.0/1 [00:00<00:00,  1.36it/s]



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

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

```
conda 24.5.0
Python 3.12.2
```

```
!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

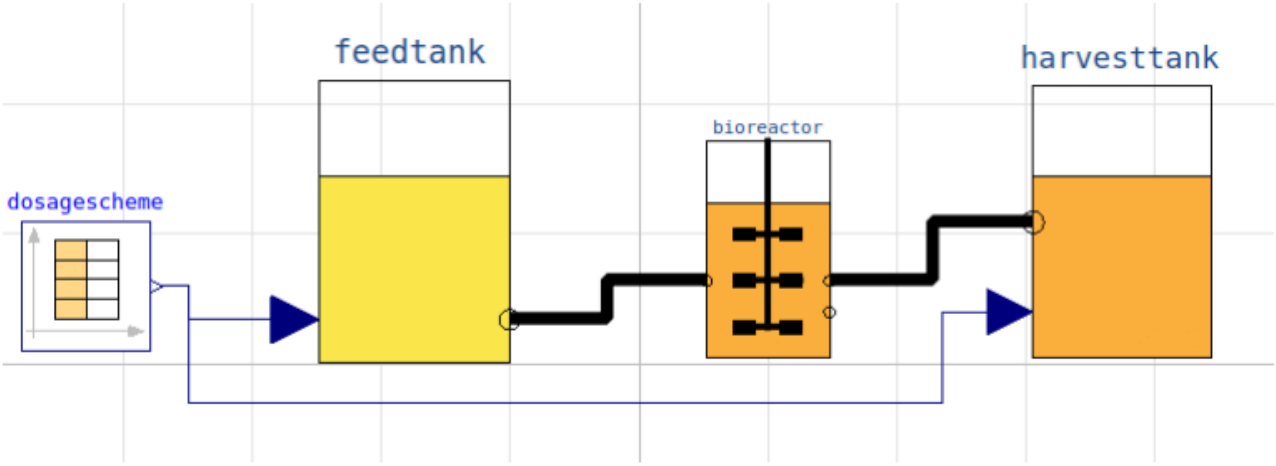
```
run -i BPL_TEST2_Chemostat_fmpy_explore.py
```

```
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 simulati
     - describe()  - describe culture, broth, parameters, variables with values/u

    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()
```

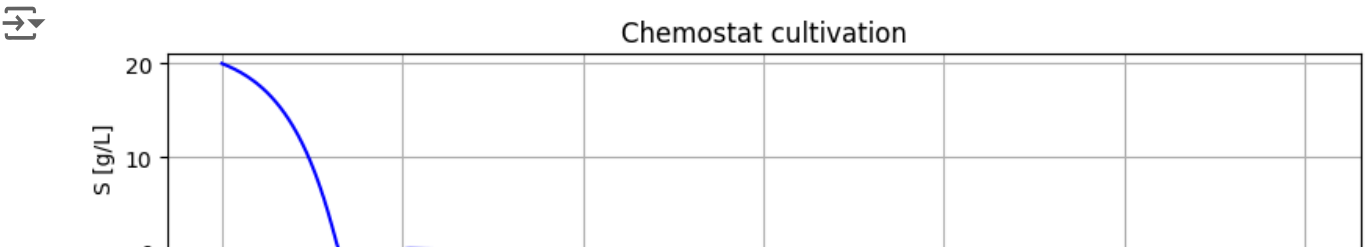
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

```
process_diagram()
```

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




```
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)
```




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

```
['bioreactor', 'bioreactor.culture', 'D', 'dosagescheme', 'feedtank', 'harves
```

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

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

```
system_info()
```

```
System information
 -OS: Linux
 -Python: 3.10.12
 -Scipy: not installed in the notebook
 -FMPy: 0.3.20
 -FMU by: OpenModelica Compiler OpenModelica 1.21.0
 -FMI: 2.0
 -Type: ME
 -Name: BPL_TEST2.Chemostat
 -Generated: 2024-03-05T09:09:17Z
 -MSL: 3.2.3
 -Description: Bioprocess Library version 2.2.0
 -Interaction: FMU-explore for FMPy version 1.0.0
```