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
                     22.04
    Release:
    Codename:
                     jammy
%env PYTH0NPATH=
    env: PYTHONPATH=
!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 svs
sys.path.append('/usr/local/lib/python3.10/site-packages/')
    --2024-03-05 20:53:03-- <a href="https://repo.anaconda.com/miniconda/Miniconda3-py310">https://repo.anaconda.com/miniconda/Miniconda3-py310</a> 23.1.0-1-Linux-x86 64.sh
    Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.130.3, 104.16.131.3, 2606:4700::6810:8303, ...
    Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.130.3|: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'
    132MB/s
                                                                          in 0.5s
    2024-03-05 20:53:04 (132 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 24.1.2 Python 3.10.13

!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:
```

```
- change of parameters and initial values
- par()
```

- change initial values only - init()

- simu() - simulate and plot

- newplot() - make a new plot

- show() - show plot from previous simulation

- display parameters and initial values from the last simulation - disp() - describe() - describe culture, broth, parameters, variables with values/units

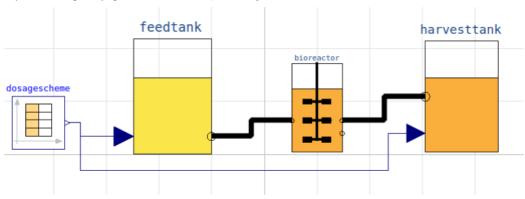
Note that both disp() and describe() takes values from the last simulation and the command process_diagram() brings up the main configuration

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

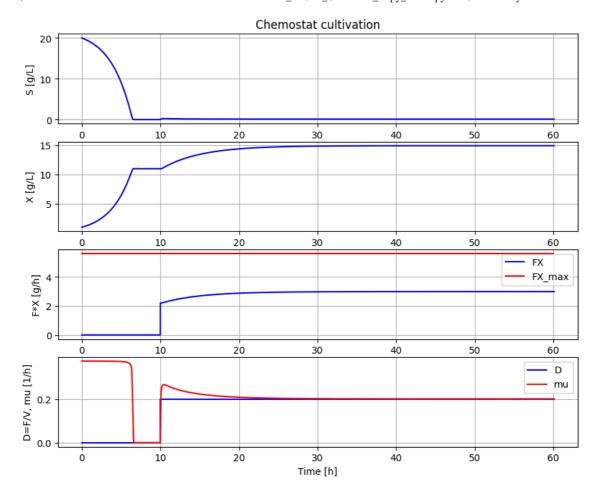
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

process_diagram()

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



```
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', 'harvesttank']

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: 0.3.19
   -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 2.1.2 prel
```

-Interaction: FMU-explore for FMPy version 0.9.9