⌄ 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 22.04.4 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/')
```

⇥ --2025-02-07 20:17:33-- 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.1'

    Miniconda3-py311_24 100%[===================>] 139.14M   110MB/s   in 1.3s

    2025-02-07 20:17:34 (110 MB/s) - 'Miniconda3-py311_24.11.1-0-Linux-x86_64.sh.1' 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]
    certifi-2025.1.31     | 163 KB    | : 100% 1.0/1 [00:00<00:00, 11.93it/s]
    ca-certificates-2024 | 128 KB    | : 100% 1.0/1 [00:00<00:00, 12.03it/s]
    ca-certificates-2024 | 128 KB    | : 100% 1.0/1 [00:00<00:00,  9.48it/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
```

```
!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
```

```
fatal: destination path 'BPL_TEST2_Chemostat' already exists and is not an empty directory.
---------------------------------------------------------------------------
CalledProcessError                        Traceback (most recent call last)
<ipython-input-9-abd5d26245bd> in <cell line: 0>()
----> 1 get_ipython().run_cell_magic('bash', '', 'git clone
https://github.com/janpeter19/BPL_TEST2_Chemostat\n')

                            ↕ 4 frames
<decorator-gen-103> in shebang(self, line, cell)

/usr/local/lib/python3.11/dist-packages/IPython/core/magics/script.py in shebang(self, line, cell)
    243             sys.stderr.flush()
    244         if args.raise_error and p.returncode!=0:
--> 245             raise CalledProcessError(p.returncode, cell, output=out, stderr=err)
    246
    247     def _run_script(self, p, cell, to_close):

CalledProcessError: Command 'b'git clone https://github.com/janpeter19/BPL_TEST2_Chemostat\n'' returned non-
zero exit status 128.
```

Next steps: (**Explain error**)

```
%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

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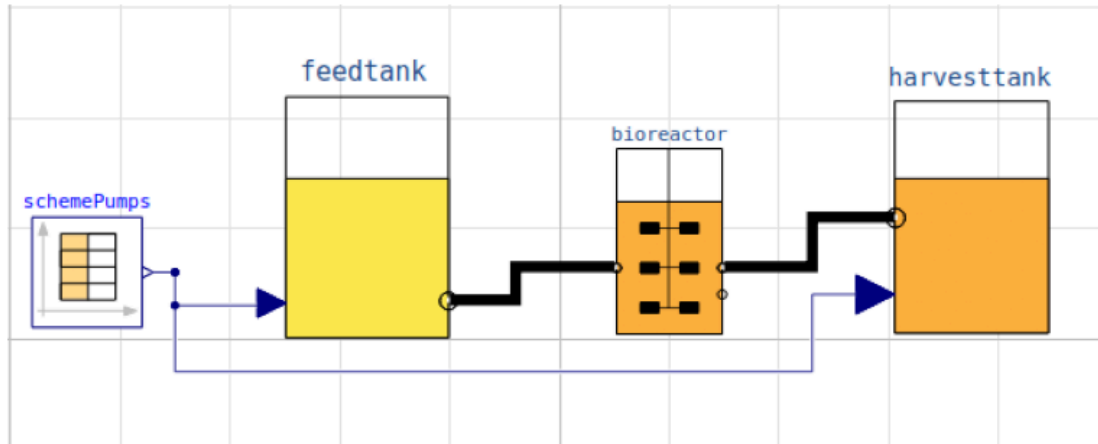
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```
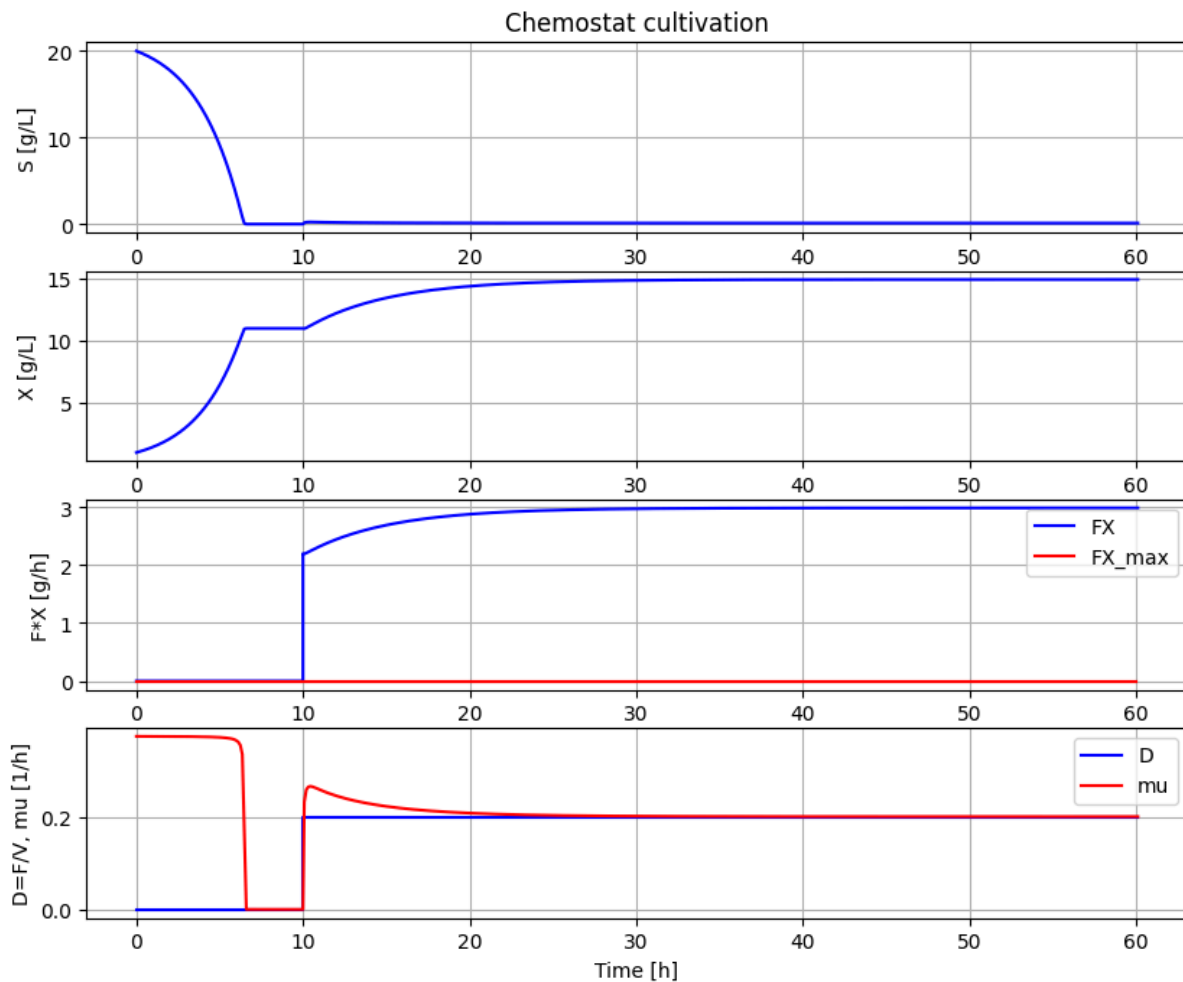
```
process_diagram()
```

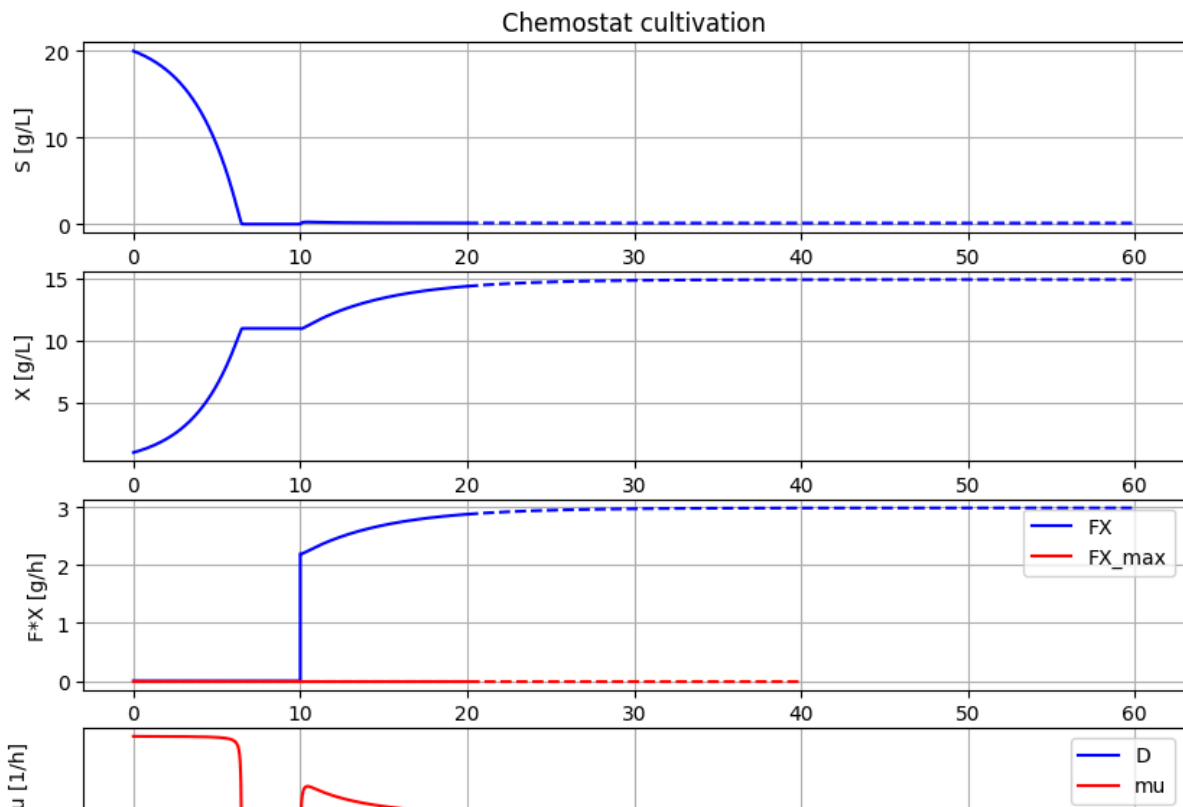⇥ No processDiagram.png file in the FMU, but try the file on disk.


```
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)
```



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

Chemostat cultivation

```
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: 3.11.11
 -Scipy: not installed in the notebook
 -FMPy: 0.3.19
 -FMU by: OpenModelica Compiler OpenModelica 1.25.0~dev-133-ga5470be
 -FMI: 2.0
 -Type: ME
 -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 for FMPy version 1.0.1
```

Start coding or generate with AI.