

## ✓ 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/')
```

```
⇒ --2024-08-13 08:45:32-- 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... con
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 98.5MB/s in 1.4s
```

```
2024-08-13 08:45:34 (98.5 MB/s) - 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh'
```

```
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
```

```
⇒
```

openssl-3.0.14	5.2 MB	:	0%	0/1	[00:00<?, ?it/s]
conda-24.7.1	1.2 MB	:	0%	0/1	[00:00<?, ?it/s]
certifi-2024.7.4	159 KB	:	0%	0/1	[00:00<?, ?it/s]
ca-certificates-2024	127 KB	:	0%	0/1	[00:00<?, ?it/s]
frozendict-2.4.2	36 KB	:	0%	0/1	[00:00<?, ?it/s]
certifi-2024.7.4	159 KB	:	10%	0.10045740493212503/1	[00:00<00:01,
conda-24.7.1	1.2 MB	:	1%	0.013060714305643354/1	[00:00<00:18
ca-certificates-2024	127 KB	:	13%	0.12647440251960723/1	[00:00<00:01,
frozendict-2.4.2	36 KB	:	44%	0.43853215920344746/1	[00:00<00:00,
certifi-2024.7.4	159 KB	:	100%	1.0/1	[00:00<00:00, 3.87it/s]
openssl-3.0.14	5.2 MB	:	0%	0.003006342237126712/1	[00:00<01:47
ca-certificates-2024	127 KB	:	100%	1.0/1	[00:00<00:00, 3.56it/s]
ca-certificates-2024	127 KB	:	100%	1.0/1	[00:00<00:00, 3.56it/s]
frozendict-2.4.2	36 KB	:	100%	1.0/1	[00:00<00:00, 2.77it/s]
openssl-3.0.14	5.2 MB	:	92%	0.9169343823236471/1	[00:00<00:00,
conda-24.7.1	1.2 MB	:	100%	1.0/1	[00:00<00:00, 1.50it/s]

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

!conda --version  
!python --version

 conda 24.7.1  
Python 3.12.2

```
!conda install -c conda-forge fmpy --yes # Install the key package
```



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 1.23.0-dev
```

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)

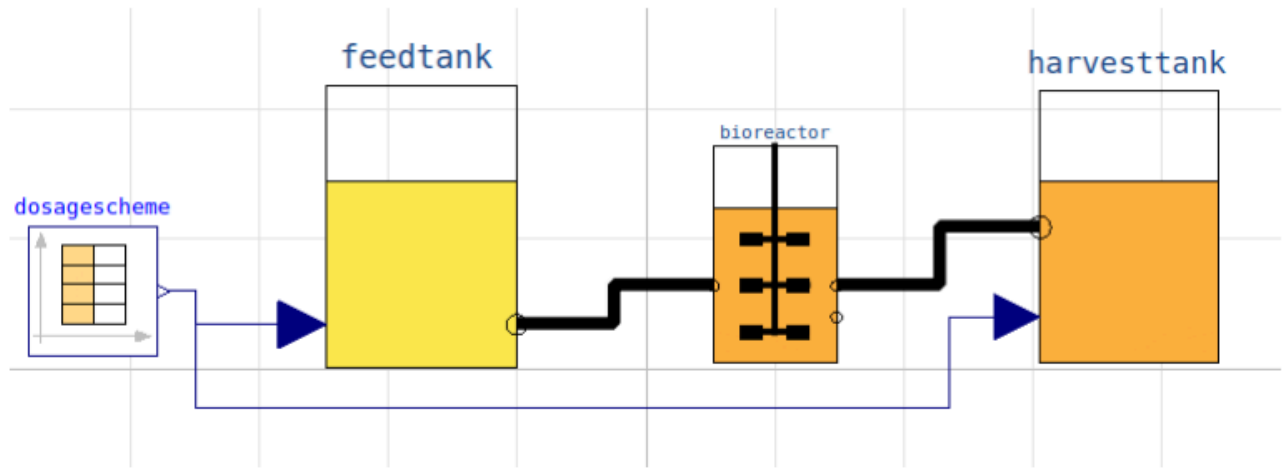
Key system information is listed with the command system\_info()

```
%matplotlib inline
```

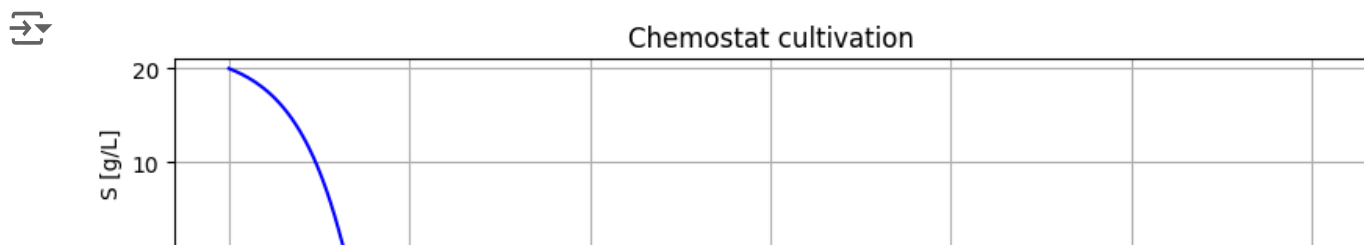
```
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

```
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)
```



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

```
➡ ['bioreactor', 'bioreactor.culture', 'D', 'dosagescheme', 'feedtank', 'harvest']
```

```
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 1.23.0~dev.beta.1-1-g379f714
-FMI: 2.0
-Type: ME
-Name: BPL_TEST2.Chemostat
-Generated: 2024-05-20T18:13:12Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.2.0
-Interaction: FMU-explore for FMPy version 1.0.1
```

Start coding or generate with AI.