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```
# BPL_CHO_Perfusion_cspr_openloop script with FMPy

The key library FMPy is installed.

After the installation a small application BPL_CHO_Fedbatch is
loaded and run. You can continue with this example if you like
```

BPL_CHO_Perfusion_cspr_openloop script with FMPy

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```
!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.sh
!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/')
```

⇥ --2024-05-23 08:12:13-- https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
    Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.158, 2606:4700::6810:20f1, ...
    Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... connected.
    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   187MB/s   in 0.7s

    2024-05-23 08:12:14 (187 MB/s) - 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh' saved [143351488/143351488]

    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_2 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-py312h06a4308_0
      openssl                                3.0.13-h7f8727e_0 --> 3.0.13-h7f8727e_2



    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]

    frozendict-2.4.2      | 36 KB     | :    0% 0/1 [00:00<?, ?it/s]

    frozendict-2.4.2      | 36 KB     | :   44% 0.43853215920344746/1 [00:00<00:00,  1.79it/s]
    openssl-3.0.13        | 5.2 MB    | :    0% 0.0029929126657148922/1 [00:00<01:31, 91.48s/it]

    openssl-3.0.13        | 5.2 MB    | : 100% 1.0/1 [00:00<00:00,  3.26it/s]
    conda-24.5.0          | 1.2 MB    | : 100% 1.0/1 [00:00<00:00,  1.24it/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
```

```
#!conda install matplotlib --yes

#!conda install scipy --yes

#!conda install openpyxl --yes

#!conda install xlrd --yes
```

⌄ BPL_CHO_Perfusion_cspr_openloop setup

Now specific installation and the run simulations. Start with connecting to Github. Then upload the two files:

- FMU - BPL_CHO_Perfusion_cspr_openloop_linux_om_me.fmu
- Setup-file - BPL_CHO_Perfusion_cspr_openloop_fmpy_explore

```
# 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_CHO_Perfusion
```

> Cloning into 'BPL_CHO_Perfusion'...

```
%cd BPL_CHO_Perfusion
```

> /content/BPL_CHO_Perfusion

⌄ BPL_CHO_Perfusion_cspr_openloop - demo

Author: Jan Peter Axelson

```
run -i BPL_CHO_perfusion_cspr_openloop_explore_fmpy.py
```

> Linux - run FMU pre-comiled 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]
```

⌄ 1 About the process model

We can get information about the process and liquid phase by the command describe(). Here is no gas-phase included. This command can also be used to bring up information about a specific variable or parameter. However, you should use describe() after a simulation to get the valued used during the simulation.

```
process_diagram()
```

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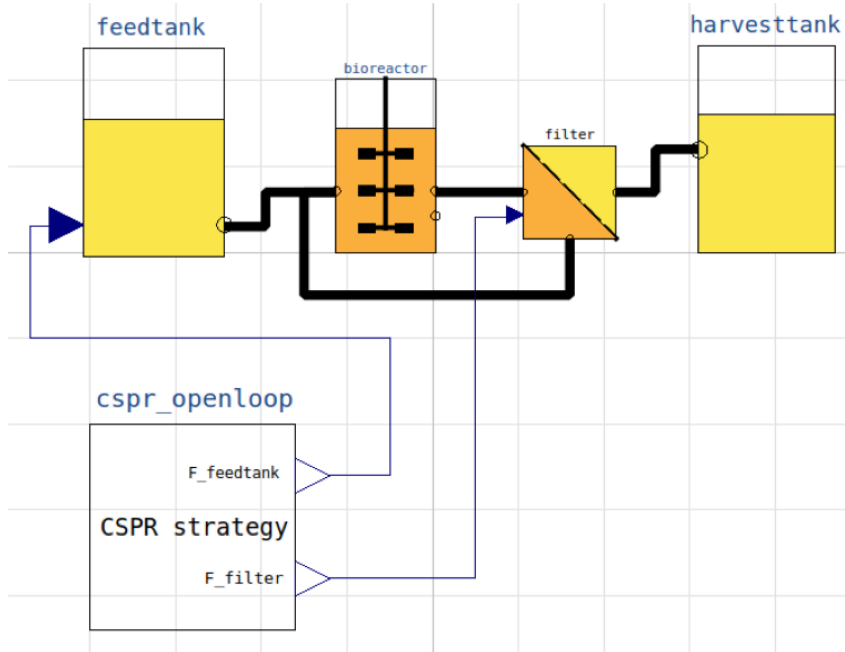

```
describe('culture'); print(); #describe('liquidphase')                    # Pump schedule parameter
```

⎯⎯ Reactor culture CHO—MAb — cell line HB—58 American Culture Collection ATCC

The molecular weight of the recombinant protein (MAb) is somewhat arbitrarly chosen and the value not used in the simulations.

```
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_CHO.Perfusion_cspr_openloop
  —Generated: 2024-05-20T19:01:47Z
  —MSL: 3.2.3
  —Description: Bioprocess Library version 2.2.0
  —Interaction: FMU—explore for FMPy version 1.0.0
```