

✓ BPL_CHO_Perfusion_cspr_opennloop 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.

```
!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/')
```

```
➔ --2024-05-24 07:19:53-- https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linu
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.158, 2606:4700:
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 135MB/s in 1.0s
```

```
2024-05-24 07:19:54 (135 MB/s) - 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh' saved [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, 3.76it/s]
openssl-3.0.13	5.2 MB	: 0% 0.002992912657148922/1 [00:00<00:51, 51.62s/it]
conda-24.5.0	1.2 MB	: 1% 0.01293349794914382/1 [00:00<00:12, 12.75s/it]
conda-24.5.0	1.2 MB	: 100% 1.0/1 [00:00<00:00, 1.85it/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
```

```
#!/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 DeprecationWarnings for 'np.float as alias' is needed – wish I could make filter m  
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_opennloop - demo

Author: Jan Peter Axelson

```
run -i BPL_CHO_perfusion_cspr_opennloop_explore_fmpy.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()

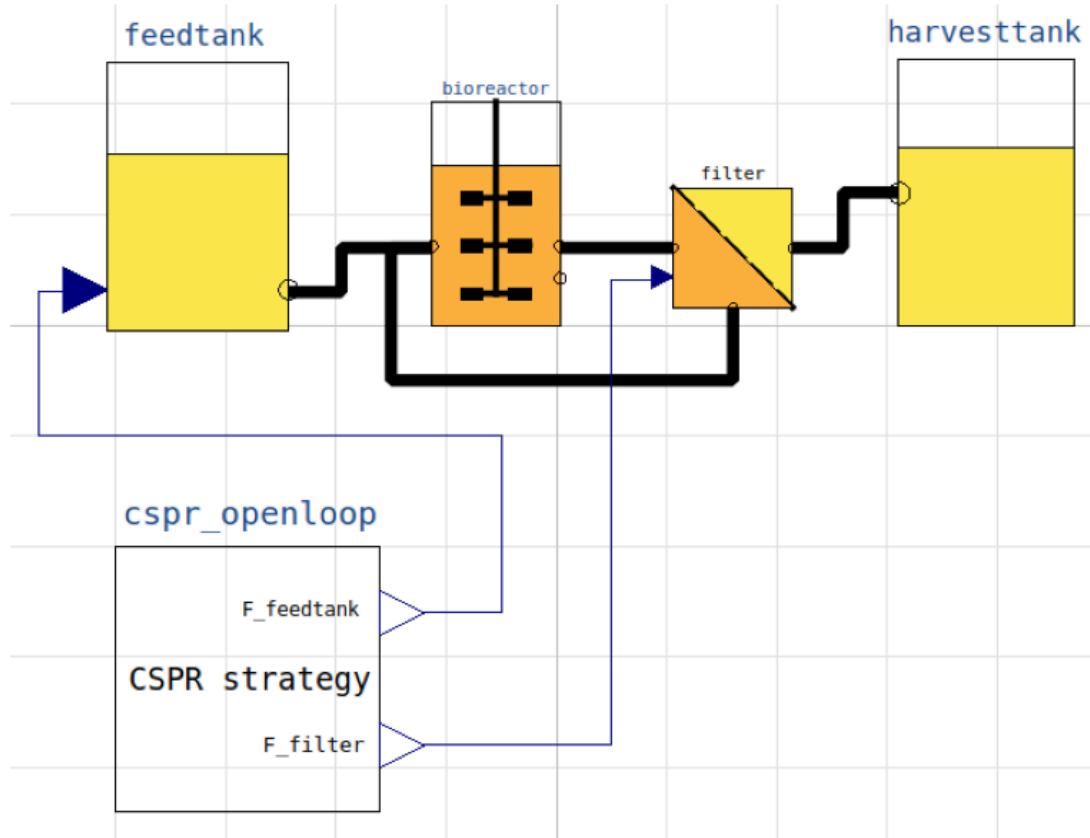
```
%matplotlib inline  
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

✓ 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 values 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

➡ Reactor culture CHO-MAb – cell line HB-58 American Culture Collection ATCC

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

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

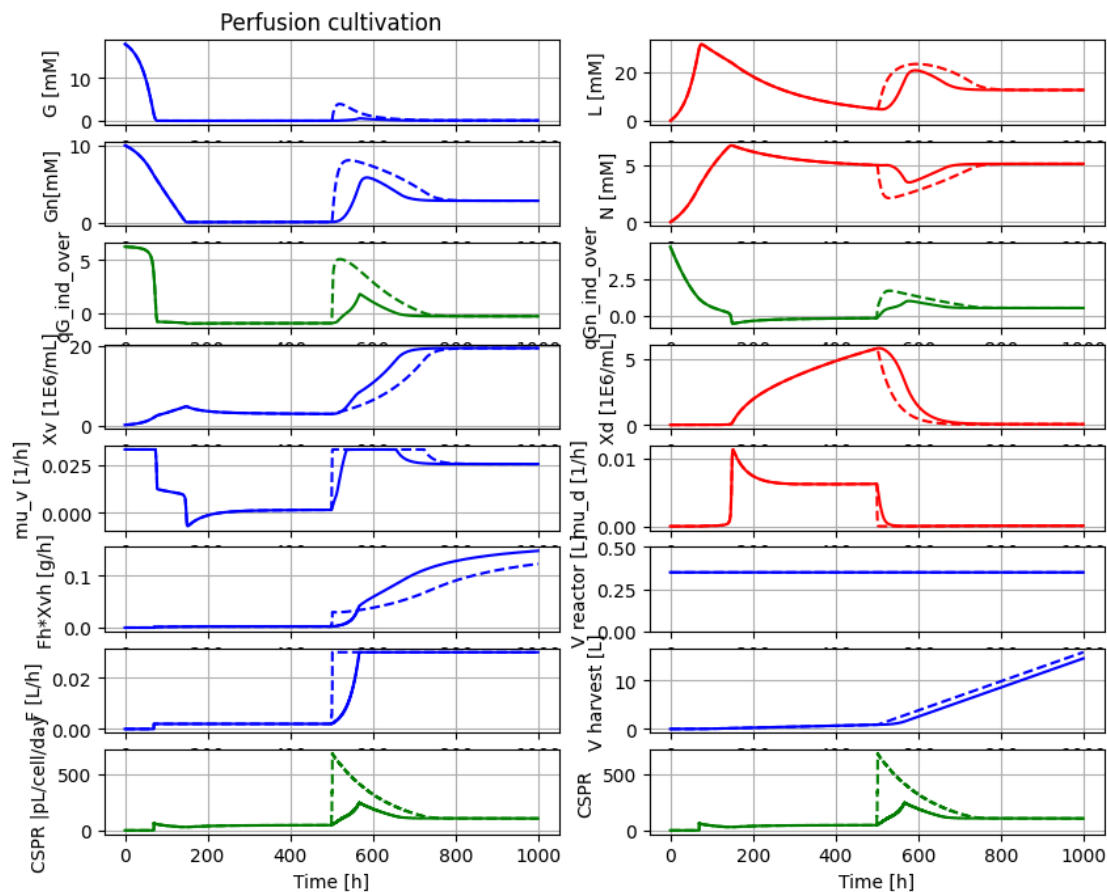
➡ MSL: 3.2.3 – used components: RealInput, RealOutput, CombiTimeTable, Types

```
newplot('Perfusion cultivation', plotType='Extended')
```

```

par(samplePeriod=1); par(F1=0.0020)           # General parameters
par(mu_ref=0.04); simu()                       # First simulation (solid)
par(mu_ref=1); simu()                         # Second simulation (dashed)

```



```
model_get('CSpr')
```

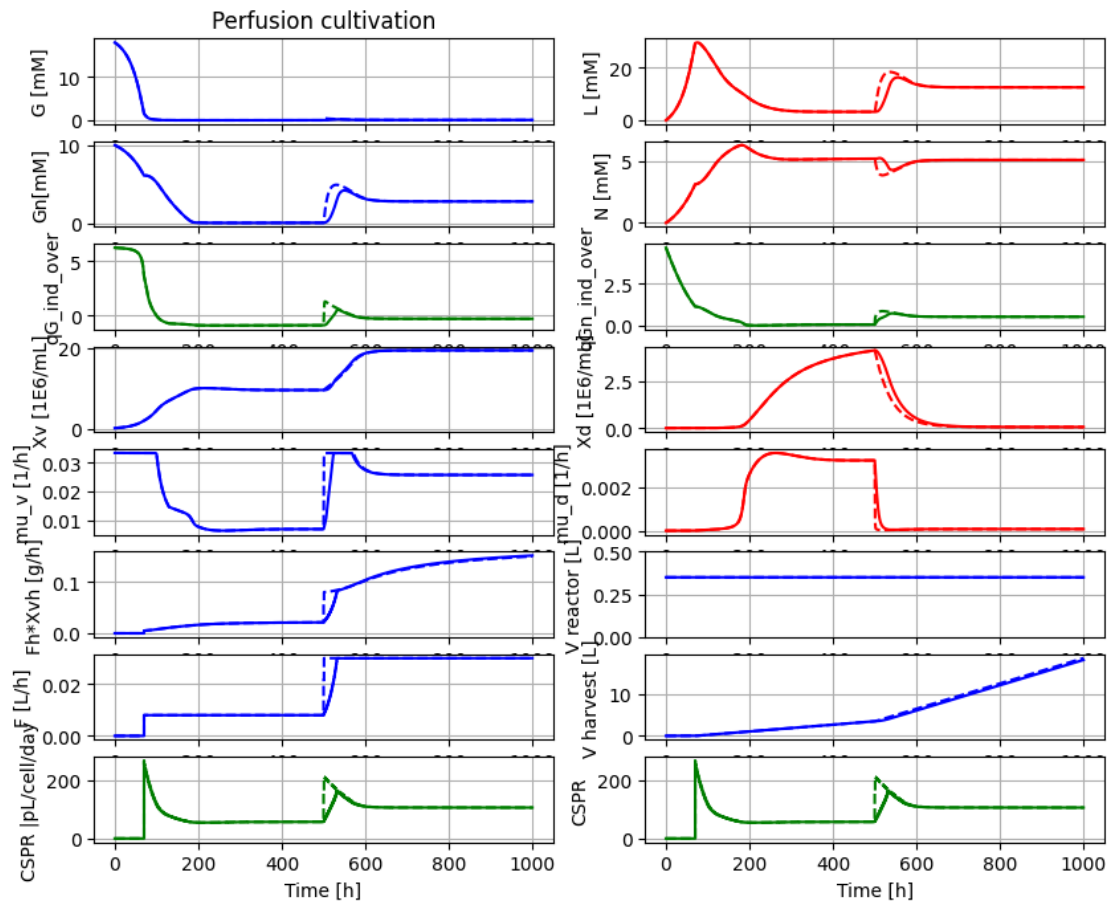


```
105.41563602162672
```

We see here the shorter settling time for cell conc X_v when the slower exponential increase of perfusion rate is used, compared to an abrupt change.

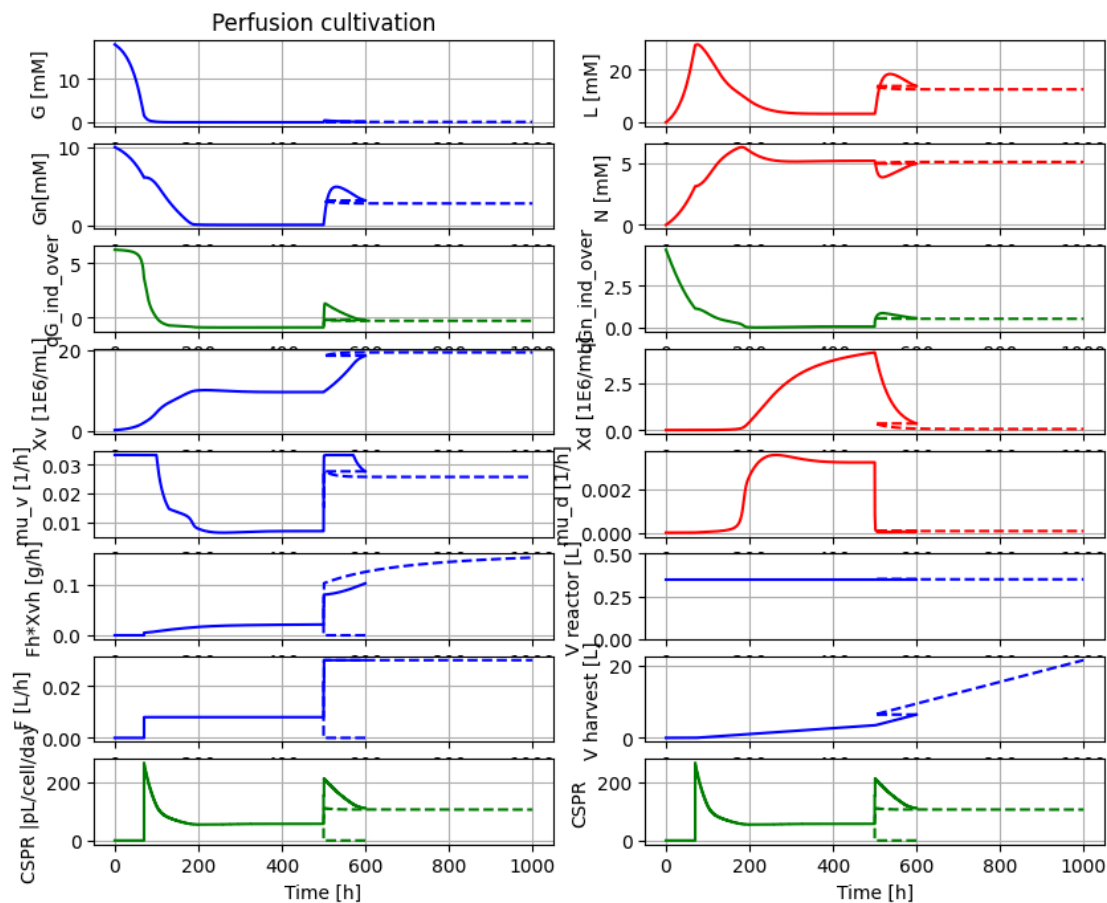
```
newplot('Perfusion cultivation', plotType='Extended')
```

```
par(samplePeriod=1); par(F1=0.0080)      # General parameters
par(mu_ref=0.04); simu()                  # First simulation (solid)
par(mu_ref=1); simu()                     # Second simulation (dashed)
```



We see that a somewhat smaller change in perfusion rate make the difference in settling time of X_v for the two strategies to almost disappear.

```
newplot('Perfusion cultivation', plotType='Extended')
simu(600)
simu(400,'cont')
```



```
describe('feedtank.W')
```



Reactor broth weight : 78.915 [kg]

```
describe('feedtank.V')
```



Feed volume : 78.577 [L]

```
78.915/78.577
```



1.0043015131654303

```
describe('bioreactor.broth_decay.k_decay')
```



Rate of decay of viable cells : 0.0 [1E9 cells/(L*h)]

```
describe('k_lysis')
```



Specific rate of lysis of dead cells : 0.0 [1/h]

```
disp('culture')
```




```
qG_max1 : 0.297  
qG_max2 : 0.038  
nGn_max1 : 0.124
```