

## BPL\_TEST2\_Perfusion script with PyFMI ver 2.9.8

The key library PyFMI v2.9.8 is installed.

After the installation a small application BPL\_TEST2\_Perfusion is loaded and run. You can continue with this example if you like.

In [ ]: !lsb\_release -a # Actual VM Ubuntu version used by Google

No LSB modules are available.

Distributor ID: Ubuntu

Description: Ubuntu 20.04.5 LTS

Release: 20.04 Codename: focal

In [ ]: %env PYTHONPATH=

env: PYTHONPATH=

!wget https://repo.anaconda.com/miniconda/Miniconda3-py38\_22.11.1-1-Linux
!chmod +x Miniconda3-py38\_22.11.1-1-Linux-x86\_64.sh
!bash ./Miniconda3-py38\_22.11.1-1-Linux-x86\_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.8/site-packages/')

```
--2023-01-25 10:17:20-- https://repo.anaconda.com/miniconda/Miniconda3-
       py38_22.11.1-1-Linux-x86_64.sh
       Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.131.3, 104.16.
       130.3, 2606:4700::6810:8203, ...
       Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.131.3|:443...
       connected.
       HTTP request sent, awaiting response... 200 OK
       Length: 64630241 (62M) [application/x-sh]
       Saving to: 'Miniconda3-py38 22.11.1-1-Linux-x86 64.sh'
       Miniconda3-py38 22. 100%[============] 61.64M
                                                             124MB/s
                                                                        in
       0.5s
       2023-01-25 10:17:21 (124 MB/s) - 'Miniconda3-py38_22.11.1-1-Linux-x86_6
       4.sh' saved [64630241/64630241]
       PREFIX=/usr/local
       Unpacking payload ...
       Installing base environment...
       Downloading and Extracting Packages
       Downloading and Extracting Packages
       Preparing transaction: -
                                     / - \
                                 \
       Executing transaction: / - \
                                           / - \ |
                                       \ | /
                         - \
       installation finished.
In [ ]: !conda update -n base -c defaults conda --yes
```

The following packages will be downloaded:

```
package
ca-certificates-2023.01.10 | h06a4308 0
                                       120 KB
conda-23.1.0 | py38h06a4308_0
conda-package-handling-2.0.2| py38h06a4308_0
                                      942 KB
                                       267 KB
26 KB
conda-package-streaming-0.7.0| py38h06a4308_0
                                      1.4 MB
cryptography-38.0.4 | py38h9ce1e76_0
                                       1.2 MB
                   h5082296_0
sqlite-3.40.1
urllib3-1.26.14
                                       196 KB
                   | py38h06a4308 0
xz-5.2.10
                       h5eee18b 1
                                       429 KB
                   | py38h5eee18b_0 434 KB
zstandard-0.18.0
                 -----
                            Total: 4.9 MB
```

The following NEW packages will be INSTALLED:

```
conda-package-str~ pkgs/main/linux-64::conda-package-streaming-0.7.0-p
y38h06a4308_0
zstandard pkgs/main/linux-64::zstandard-0.18.0-py38h5eee18b_0
```

The following packages will be UPDATED:

```
ca-certificates
                                      2022.10.11-h06a4308 0 --> 2023.01.
10-h06a4308 0
  conda
                                     22.11.1-py38h06a4308 4 --> 23.1.0-p
y38h06a4308 0
  conda-package-han~
                                       1.9.0-py38h5eee18b 1 --> 2.0.2-py
38h06a4308 0
  cryptography
                                      38.0.1-py38h9ce1e76 0 --> 38.0.4-p
y38h9ce1e76_0
                                           3.40.0-h5082296 0 --> 3.40.1-h
  sqlite
5082296 0
                                     1.26.13-py38h06a4308 0 --> 1.26.14-
  urllib3
py38h06a4308 0
                                           5.2.8-h5eee18b 0 --> 5.2.10-h
 ΧZ
5eee18b 1
```

```
Downloading and Extracting Packages ca-certificates-2023 | 120 KB | : 0% 0/1 [00:00<?, ?it/s] sqlite-3.40.1 | 1.2 MB | : 0% 0/1 [00:00<?, ?it/s] urllib3-1.26.14 | 196 KB | : 0% 0/1 [00:00<?, ?it/s]
```

```
conda-package-handli | 267 KB | : 0% 0/1 [00:00<?, ?it/s]</pre>
```

zstandard-0.18.0 | 434 KB | : 0% 0/1 [00:00<?, ?it/s]

conda-package-stream | 26 KB | : 0% 0/1 [00:00<?, ?it/s]

conda-23.1.0 | 942 KB | : 0% 0/1 [00:00<?, ?it/s]

xz-5.2.10 | 429 KB | : 0% 0/1 [00:00<?, ?it/s]

cryptography-38.0.4 | 1.4 MB | : 0% 0/1 [00:00<?, ?it/s]

sqlite-3.40.1 | 1.2 MB | : 17% 0.1743092837501637/1 [00:00<0

0:00, 1.72it/s]

urllib3-1.26.14 | 196 KB | : 57% 0.5716592813386302/1 [00:00<0

0:00, 5.53it/s]

zstandard-0.18.0 | 434 KB | : 15% 0.1476335293190061/1 [00:00<0

0:00, 1.41it/s]

conda-23.1.0 | 942 KB | : 2% 0.016977341093890375/1 [00:00<

00:07, 7.42s/it]

xz-5.2.10 | 429 KB | : 4% 0.037267448076008854/1 [00:00<

00:03, 3.58s/it]

```
conda-package-stream | 26 KB | : 61% 0.6093197961991893/1 [00:00<0
0:00, 4.42it/s]
ca-certificates-2023 | 120 KB | : 100% 1.0/1 [00:00<00:00, 4.95it/s]
conda-package-handli | 267 KB
                               | : 100% 1.0/1 [00:00<00:00, 4.12it/s]
conda-package-handli | 267 KB
                               | : 100% 1.0/1 [00:00<00:00, 4.12it/s]
urllib3-1.26.14
                    | 196 KB
                                | : 100% 1.0/1 [00:00<00:00, 5.53it/s]
zstandard-0.18.0
                                | : 100% 1.0/1 [00:00<00:00, 3.05it/s]
                    | 434 KB
zstandard-0.18.0
                    | 434 KB
                                | : 100% 1.0/1 [00:00<00:00, 3.05it/s]
conda-package-stream | 26 KB
                               | : 100% 1.0/1 [00:00<00:00, 4.42it/s]
sqlite-3.40.1
                    | 1.2 MB
                               | : 100% 1.0/1 [00:00<00:00, 2.23it/s]
                                | : 100% 1.0/1 [00:00<00:00, 2.23it/s]
sqlite-3.40.1
                    | 1.2 MB
xz-5.2.10
                    | 429 KB | : 100% 1.0/1 [00:00<00:00, 2.04it/s]
xz-5.2.10
                    | 429 KB | : 100% 1.0/1 [00:00<00:00, 2.04it/s]
```

| 942 KB | : 100% 1.0/1 [00:00<00:00, 1.70it/s]

conda-23.1.0

```
conda-23.1.0 | 942 KB | : 100% 1.0/1 [00:00<00:00, 1.70it/s]
```

```
cryptography-38.0.4 | 1.4 MB | : 100% 1.0/1 [00:00<00:00, 1.47it/s]
```

```
Preparing transaction: - done
Verifying transaction: | / done
Executing transaction: \ | done
```

```
In [ ]: !conda --version
!python --version
```

conda 23.1.0 Python 3.8.15

In [ ]: !conda install -c conda-forge pyfmi --yes # Install the key package

## Package Plan ##

environment location: /usr/local

added / updated specs:

- pyfmi

The following packages will be downloaded:

package	build	
_libgcc_mutex-0.1	-    conda_forge	3 KB conda-
forge		
_openmp_mutex-4.5	2_kmp_llvm	6 KB conda-
forge		
appdirs-1.4.4	pyh9f0ad1d_0	13 KB conda-
forge		
assimulo-3.3	py38h71f17ff_1	2.4 MB conda-
forge		
ca-certificates-2022.12.7	ha878542_0	143 KB conda-
forge		
certifi-2022.12.7	pyhd8ed1ab_0	147 KB conda-
forge		
fmilib-2.4.1	h27087fc_0	545 KB conda-
forge	1 50500 0 0	006.140
gmp-6.2.1	h58526e2_0	806 KB conda-
forge	1 1 5404 12 1000	22 C MD
icu-58.2	hf484d3e_1000	22.6 MB conda-
forge	110 1: 04	12 1/0
libblas-3.9.0	16_linux64_openblas	13 KB cond
a-forge	116 1564	12 KD
libcblas-3.9.0	16_linux64_openblas	13 KB cond
a-forge	heEd4601 10	O21 KD condo
libgcc-ng-12.2.0	h65d4601_19	931 KB conda-
forge	l 6007020 10	22 VD condo
libgfortran-ng-12.2.0	h69a702a_19	22 KB conda-
<pre>forge     libgfortran5-12.2.0</pre>	l h227069a 10	1.8 MB conda-
forge	h337968e_19	1.0 MD COMUA-
libhwloc-2.8.0	h32351e8 1	3.0 MB conda-
forge	1 113533160_1	J. W PID CUITUR-
liblapack-3.9.0	16 linux64 openblas	13 KB cond
CIDCapack-3.3.0	Tro_crimyo4_obelincas	TO KD COUR

a-forge					
libopenblas-0.3.21	pthreads_h78a6416_3		3 10.1 M	10.1 MB cond	
a-forge		1.4661767.10	4 2 45		
libstdcxx-ng-12.2.0		h46fd767_19	4.3 MB	conda-	
forge		174 7540 0	710 1/0		
libxml2-2.9.14	!	h74e7548_0	718 KB		
libxslt-1.1.35	ļ	h4e12654_0	453 KB		
llvm-openmp-14.0.6	ļ	h9e868ea_0	4.4 MB		
lxml-4.9.1	ļ	py38h1edc446_0	1.3 MB		
metis-5.1.0		h58526e2_1006	4.1 MB	conda-	
forge					
mpfr-4.1.0		h9202a9a_1	2.6 MB	conda-	
forge					
numpy-1.24.1		py38hab0fcb9_0	6.3 MB	conda-	
forge					
openssl-1.1.1s		h0b41bf4_1	1.9 MB	conda-	
forge					
packaging-23.0		pyhd8ed1ab_0	40 KB	conda-	
forge					
pooch-1.6.0		pyhd8ed1ab_0	44 KB	conda-	
forge					
pyfmi-2.9.8		py38h26c90d9_1	12.7 MB	conda-	
forge					
python abi-3.8		2 cp38	4 KB	conda-	
forge	-				
scipy-1.10.0	- 1	py38h10c12cc 0	23.5 MB	conda-	
forge	•	_			
suitesparse-5.10.1		h9e50725 1	2.4 MB	conda-	
forge	•	_			
sundials-6.4.1	- 1	h89a52a3 0	1.2 MB	conda-	
forge	'				
tbb-2021.7.0	- 1	h924138e 1	1.5 MB	conda-	
forge	'				
		Total:	109.6 MB		

## The following NEW packages will be INSTALLED:

```
conda-forge/noarch::appdirs-1.4.4-pyh9f0ad1d 0
  appdirs
  assimulo
                     conda-forge/linux-64::assimulo-3.3-py38h71f17ff_1
                     conda-forge/linux-64::fmilib-2.4.1-h27087fc 0
  fmilib
                     conda-forge/linux-64::gmp-6.2.1-h58526e2 0
  gmp
                     conda-forge/linux-64::icu-58.2-hf484d3e 1000
  icu
                     conda-forge/linux-64::libblas-3.9.0-16_linux64_open
  libblas
blas
  libcblas
                     conda-forge/linux-64::libcblas-3.9.0-16_linux64_ope
nblas
  libgfortran-ng
                     conda-forge/linux-64::libgfortran-ng-12.2.0-h69a702
a 19
                     conda-forge/linux-64::libgfortran5-12.2.0-h337968e
  libgfortran5
  libhwloc
                     conda-forge/linux-64::libhwloc-2.8.0-h32351e8 1
                     conda-forge/linux-64::liblapack-3.9.0-16 linux64 op
  liblapack
enblas
  libopenblas
                     conda-forge/linux-64::libopenblas-0.3.21-pthreads h
78a6416 3
  libxml2
                     pkgs/main/linux-64::libxml2-2.9.14-h74e7548 0
  libxslt
                     pkgs/main/linux-64::libxslt-1.1.35-h4e12654 0
                     pkgs/main/linux-64::llvm-openmp-14.0.6-h9e868ea 0
  llvm-openmp
  lxml
                     pkgs/main/linux-64::lxml-4.9.1-py38h1edc446 0
```

```
conda-forge/linux-64::metis-5.1.0-h58526e2 1006
metis
                   conda-forge/linux-64::mpfr-4.1.0-h9202a9a 1
mpfr
                   conda-forge/linux-64::numpy-1.24.1-py38hab0fcb9 0
numpy
                   conda-forge/noarch::packaging-23.0-pyhd8ed1ab 0
packaging
                   conda-forge/noarch::pooch-1.6.0-pyhd8ed1ab 0
pooch
                   conda-forge/linux-64::pyfmi-2.9.8-py38h26c90d9 1
pyfmi
                   conda-forge/linux-64::python abi-3.8-2 cp38
python abi
                   conda-forge/linux-64::scipy-1.10.0-py38h10c12cc 0
scipy
                   conda-forge/linux-64::suitesparse-5.10.1-h9e50725 1
suitesparse
sundials
                   conda-forge/linux-64::sundials-6.4.1-h89a52a3 0
                   conda-forge/linux-64::tbb-2021.7.0-h924138e 1
tbb
```

The following packages will be REMOVED:

```
libgomp-11.2.0-h1234567 1
```

The following packages will be UPDATED:

The following packages will be SUPERSEDED by a higher-priority channel:

```
Downloading and Extracting Packages
```

```
libxml2-2.9.14
                     | 718 KB
                                  | :
                                        0% 0/1 [00:00<?, ?it/s]
                     | 40 KB
packaging-23.0
                                  | :
                                        0% 0/1 [00:00<?, ?it/s]
pooch-1.6.0
                     | 44 KB
                                  1 :
                                        0% 0/1 [00:00<?, ?it/s]
mpfr-4.1.0
                     | 2.6 MB
                                  | :
                                        0% 0/1 [00:00<?, ?it/s]
                                        0% 0/1 [00:00<?, ?it/s]
pyfmi-2.9.8
                     | 12.7 MB
                                  1 :
```

libcblas-3.9.0 | 13 KB | : 0% 0/1 [00:00<?, ?it/s]

lxml-4.9.1 | 1.3 MB | : 0% 0/1 [00:00<?, ?it/s]

icu-58.2 | 22.6 MB | : 0% 0/1 [00:00<?, ?it/s]

gmp-6.2.1 | 806 KB | : 0% 0/1 [00:00<?, ?it/s]

tbb-2021.7.0 | 1.5 MB | : 0% 0/1 [00:00<?, ?it/s]

\_openmp\_mutex-4.5 | 6 KB | : 0% 0/1 [00:00<?, ?it/s]

scipy-1.10.0 | 23.5 MB | : 0% 0/1 [00:00<?, ?it/s]

certifi-2022.12.7 | 147 KB | : 0% 0/1 [00:00<?, ?it/s]

liblapack-3.9.0 | 13 KB | : 0% 0/1 [00:00<?, ?it/s]

libgfortran-ng-12.2. | 22 KB | : 0% 0/1 [00:00<?, ?it/s]

python\_abi-3.8 | 4 KB | : 0% 0/1 [00:00<?, ?it/s]

libxslt-1.1.35 | 453 KB | : 0% 0/1 [00:00<?, ?it/s]

llvm-openmp-14.0.6 | 4.4 MB | : 0% 0/1 [00:00<?, ?it/s]

libhwloc-2.8.0 | 3.0 MB | : 0% 0/1 [00:00<?, ?it/s]

libxml2-2.9.14 | 718 KB | : 13% 0.1336825528928924/1 [00:00<0 0:00, 1.33it/s]

pooch-1.6.0 | 44 KB | : 37% 0.36539619527643347/1 [00:00<0

mpfr-4.1.0 | 2.6 MB | : 1% 0.0060485553093571716/1 [00:00

 $Io calhost: 8888/nbconvert/html/BPL\_TEST2\_Perfusion/BPL\_TEST2\_Perfusion\_colab\_me.ipynb?download=falseter and the state of the state o$ 

0:00, 3.62it/s]

libcblas-3.9.0 | 13 KB | : 100% 1.0/1 [00:00<00:00, 7.13it/s]

lxml-4.9.1 | 1.3 MB | : 1% 0.012074003382548555/1 [00:00<

00:13, 13.68s/it]

pyfmi-2.9.8 | 12.7 MB | : 0% 0.0012299889380572495/1 [00:00

<02:18, 138.84s/it]

gmp-6.2.1 | 806 KB | : 2% 0.019840539414665338/1 [00:00<

00:08, 8.71s/it]

mpfr-4.1.0 | 2.6 MB | : 79% 0.7863121902164323/1 [00:00<0

0:00, 4.52it/s]

icu-58.2 | 22.6 MB | : 0% 0.0006924013097812081/1 [00:00

<05:06, 306.75s/it]

packaging-23.0 | 40 KB | : 100% 1.0/1 [00:00<00:00, 3.94it/s] | : 100% 1.0/1 [00:00<00:00, 3.94it/s] packaging-23.0 | 40 KB

pyfmi-2.9.8 | 12.7 MB | : 7% 0.07379933628343498/1 [00:00<0

0:02, 3.04s/it]

tbb-2021.7.0 | 1.5 MB | : 1% 0.010517220793593123/1 [00:00< 00:25, 25.61s/it]

\_openmp\_mutex-4.5 | 6 KB | : 100% 1.0/1 [00:00<00:00, 3.39it/s]

icu-58.2 | 22.6 MB | : 7% 0.06993253228790201/1 [00:00<0 0:03, 3.60s/it]

certifi-2022.12.7 | 147 KB | : 11% 0.10862920603348251/1 [00:00<0 0:02, 3.05s/it]

pooch-1.6.0 | 44 KB | : 100% 1.0/1 [00:00<00:00, 2.55it/s]

pooch-1.6.0 | 44 KB | : 100% 1.0/1 [00:00<00:00, 2.55it/s]

liblapack-3.9.0 | 13 KB | : 100% 1.0/1 [00:00<00:00, 2.65it/s]

libgfortran-ng-12.2. | 22 KB | : 72% 0.7159587484705471/1 [00:00<0 0:00, 1.79it/s]

python\_abi-3.8 | 4 KB | : 100% 1.0/1 [00:00<00:00, 2.43it/s]

icu-58.2 | 22.6 MB | : 14% 0.1357106567171168/1 [00:00<0 0:02, 2.55s/it]

llvm-openmp-14.0.6 | 4.4 MB | : 0% 0.0035718910660429226/1 [00:00 <02:23, 143.88s/it]

scipy-1.10.0 | 23.5 MB | : 11% 0.1085740367907962/1 [00:00<0 0:03, 3.51s/it]

icu-58.2 | 22.6 MB | : 19% 0.18556355102136377/1 [00:00<0 0:01, 2.35s/it]

libxslt-1.1.35 | 453 KB | : 4% 0.03535018997706466/1 [00:00<0 0:14, 14.98s/it]

libxml2-2.9.14 | 718 KB | : 100% 1.0/1 [00:00<00:00, 1.70it/s]

pyfmi-2.9.8 | 12.7 MB | : 47% 0.47354574115204107/1 [00:00<0 0:00, 1.07it/s]

libhwloc-2.8.0 | 3.0 MB | : 1% 0.005266267282350226/1 [00:00< 01:53, 113.76s/it]

llvm-openmp-14.0.6 | 4.4 MB | : 27% 0.27146372101926214/1 [00:00<0 0:01, 1.70s/it]

icu-58.2 | 22.6 MB | : 25% 0.24857207021145372/1 [00:00<0 0:01, 2.04s/it]

scipy-1.10.0 | 23.5 MB | : 15% 0.15120433344485115/1 [00:00<0 0:02, 3.19s/it]

pyfmi-2.9.8 | 12.7 MB | : 64% 0.6371342699136553/1 [00:00<0 0:00, 1.23it/s]

libhwloc-2.8.0 | 3.0 MB | : 50% 0.49502912454092124/1 [00:00<0 0:00, 1.05s/it]

llvm-openmp-14.0.6 | 4.4 MB | : 65% 0.6536560650858548/1 [00:00<0 0:00, 1.35it/s]

icu-58.2 | 22.6 MB | : 33% 0.3254286155971678/1 [00:00<0 0:01, 1.74s/it]

scipy-1.10.0 | 23.5 MB | : 22% 0.217814171966812/1 [00:00<00: 01, 2.44s/it]

... (more hidden) ...

pyfmi-2.9.8 | 12.7 MB | : 77% 0.7650531194716093/1 [00:00<0 0:00, 1.14it/s]

icu-58.2 | 22.6 MB | : 40% 0.40436236491222555/1 [00:00<0 0:00, 1.57s/it]

... (more hidden) ...

pyfmi-2.9.8 | 12.7 MB | : 94% 0.9397115486757387/1 [00:00<0 0:00, 1.27it/s]

icu-58.2 | 22.6 MB | : 49% 0.4929897325642202/1 [00:00<0 0:00, 1.43s/it]

... (more hidden) ...

icu-58.2 | 22.6 MB | : 56% 0.5649994687814658/1 [00:01<0 0:00, 1.44s/it]

scipy-1.10.0 | 23.5 MB | : 44% 0.4369605407040632/1 [00:01<0 0:00, 1.61s/it]

icu-58.2 | 22.6 MB | : 64% 0.6363168036889303/1 [00:01<0 0:00, 1.51s/it]

scipy-1.10.0 | 23.5 MB | : 56% 0.5648514306662281/1 [00:01<0 0:00, 1.74s/it]

icu-58.2 | 22.6 MB | : 70% 0.7041721320474886/1 [00:01<0 0:00, 1.82s/it]

scipy-1.10.0 | 23.5 MB | : 64% 0.6367900562699458/1 [00:01<0 0:00, 1.63s/it]

icu-58.2 | 22.6 MB | : 78% 0.7824134800527651/1 [00:01<0 0:00, 1.68s/it]

icu-58.2 | 22.6 MB | : 86% 0.864809235916729/1 [00:01<00: 00, 1.54s/it]

scipy-1.10.0 | 23.5 MB | : 78% 0.7800012090921616/1 [00:01<0 0:00, 1.50s/it]

icu-58.2 | 22.6 MB | : 94% 0.9368189721339746/1 [00:01<0 0:00, 1.50s/it]

scipy-1.10.0 | 23.5 MB | : 96% 0.9611799698718951/1 [00:01<0 0:00, 1.27s/it]

gmp-6.2.1 | 806 KB | : 100% 1.0/1 [00:01<00:00, 1.83s/it]

gmp-6.2.1 | 806 KB | : 100% 1.0/1 [00:01<00:00, 1.83s/it]

lxml-4.9.1 | 1.3 MB | : 100% 1.0/1 [00:01<00:00, 1.92s/it]

lxml-4.9.1 | 1.3 MB | : 100% 1.0/1 [00:01<00:00, 1.92s/it]

\_openmp\_mutex-4.5 | 6 KB | : 100% 1.0/1 [00:01<00:00, 3.39it/s]

certifi-2022.12.7 | 147 KB | : 100% 1.0/1 [00:01<00:00, 1.95s/it]

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tbb-2021.7.0 | 1.5 MB | : 100% 1.0/1 [00:02<00:00, 1.98s/it]

tbb-2021.7.0 | 1.5 MB | : 100% 1.0/1 [00:02<00:00, 1.98s/it]

liblapack-3.9.0 | 13 KB | : 100% 1.0/1 [00:02<00:00, 2.65it/s]

libgfortran-ng-12.2. | 22 KB | : 100% 1.0/1 [00:02<00:00, 2.52s/it]

libgfortran-ng-12.2. | 22 KB | : 100% 1.0/1 [00:02<00:00, 2.52s/it]

python\_abi-3.8 | 4 KB | : 100% 1.0/1 [00:02<00:00, 2.43it/s]

libxslt-1.1.35 | 453 KB | : 100% 1.0/1 [00:02<00:00, 2.08s/it]

libxslt-1.1.35 | 453 KB | : 100% 1.0/1 [00:02<00:00, 2.08s/it]

mpfr-4.1.0 | 2.6 MB | : 100% 1.0/1 [00:02<00:00, 4.52it/s]

llvm-openmp-14.0.6 | 4.4 MB | : 100% 1.0/1 [00:02<00:00, 3.04s/it]

llvm-openmp-14.0.6 | 4.4 MB | : 100% 1.0/1 [00:02<00:00, 3.04s/it]

libhwloc-2.8.0 | 3.0 MB | : 100% 1.0/1 [00:03<00:00, 3.37s/it]

libhwloc-2.8.0 | 3.0 MB | : 100% 1.0/1 [00:03<00:00, 3.37s/it]

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pyfmi-2.9.8 | 12.7 MB | : 100% 1.0/1 [00:05<00:00, 1.27it/s]

scipy-1.10.0 | 23.5 MB | : 100% 1.0/1 [00:12<00:00, 1.27s/it]

icu-58.2 | 22.6 MB | : 100% 1.0/1 [00:14<00:00, 1.50s/it]

## Notes of BPL\_TEST2\_Perfusion

This notebook explore perfusion cultivation in comparison with ordinary continuous cultivation (chemostat) and use comparable settings to earlier notebook. Further you see here examples of interaction with the simplified commands par(), init(), simu() etc as well

as direct interaction with the FMU which is called "model" here. The last simulation is always available in the workspace and called "sim\_res". Note that describe() brings mainly up from descriptive information from the Modelica code from the FMU but is complemented by some information given in the Python setup file.

Now specific installation run a simulation and notebook for that Start with connecting to Github. Then upload the two files:

- FMU BPL TEST2 Perfusion linux om me.fmu
- Setup-file BPL TEST2 Perfusion explore.py

```
In [1]: %bash
git clone https://github.com/janpeter19/BPL_TEST2_Perfusion
```

```
bash: line 1: git: command not found
                                          Traceback (most recent call la
CalledProcessError
st)
Cell In[1], line 1
----> 1 get ipython().run cell magic('bash', '', 'git clone https://gith
ub.com/janpeter19/BPL TEST2 Perfusion\n')
File ~/miniconda3/envs/pyfmi/lib/python3.8/site-packages/IPython/core/in
teractiveshell.py:2422, in InteractiveShell.run_cell_magic(self, magic_n
ame, line, cell)
  2420 with self.builtin trap:
  2421
           args = (magic_arg_s, cell)
           result = fn(*args, **kwargs)
-> 2422
   2423 return result
File ~/miniconda3/envs/pyfmi/lib/python3.8/site-packages/IPython/core/ma
gics/script.py:153, in ScriptMagics. make script magic.<locals>.named sc
ript magic(line, cell)
   151 else:
   152
           line = script
--> 153 return self.shebang(line, cell)
File ~/miniconda3/envs/pyfmi/lib/python3.8/site-packages/IPython/core/ma
gics/script.py:305, in ScriptMagics.shebang(self, line, cell)
    300 if args.raise_error and p.returncode != 0:
           # If we get here and p.returncode is still None, we must hav
   302
           # killed it but not yet seen its return code. We don't wait
for it,
   303
           # in case it's stuck in uninterruptible sleep. -9 = SIGKILL
   304
            rc = p.returncode or -9
            raise CalledProcessError(rc, cell)
--> 305
CalledProcessError: Command 'b'git clone https://github.com/janpeter19/B
PL TEST2 Perfusion\n'' returned non-zero exit status 127.
```

```
In [ ]: %cd BPL_TEST2_Perfusion
In [23]: run -i BPL_TEST2_Perfusion_explore_me.py
```

Linux - run FMU pre-comiled OpenModelica 1.21.0

```
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 simulati on

Brief information about a command by help(), eg help(simu) Key system information is listed with the command system\_info() <Figure size 984.252x787.402 with 0 Axes>

```
In [24]: %matplotlib inline
   plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]

In [25]: # Process parameters used throughout
   par(Y=0.5, qSmax=0.75, Ks=0.1) # Cul
   par(filter_eps=0.10, filter_alpha_X=0.02, filter_alpha_S=0.10) # Fil
   par(S_in=30.0) # Inl
   init(V_0=1.0, VX_0=1.0) # Proceed throughout
   par(S_in=30.0) # Proceed throughout
   par(S_in
```

Out[26]: {'V 0': 1.0,

'VX 0': 1.0,

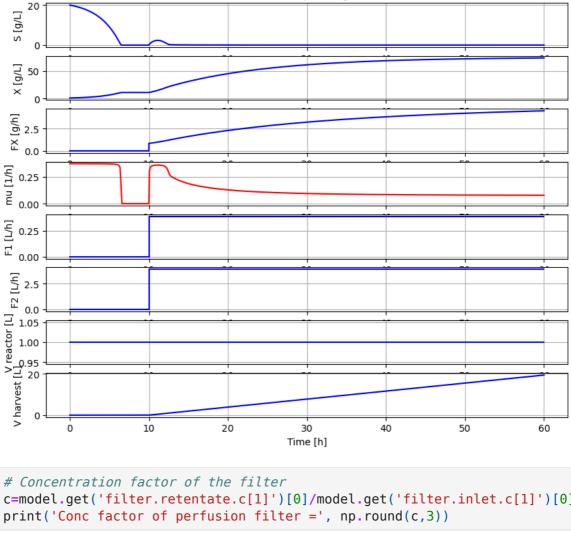
```
'VS 0': 100.0,
           'Y': 0.5,
           'qSmax': 0.75,
           'Ks': 0.1,
           'filter eps': 0.1,
           'filter alpha X': 0.02,
           'filter alpha S': 0.1,
           'S in': 30.0,
           'harvesttank V 0': 0.0,
           'harvesttank X 0': 0.0,
           'harvesttank S 0': 0.0,
           'pump1 t0': 0.0,
           'pump1 F0': 0.0,
           'pump1 t1': 17.0,
           'pump1 F1': 4.0,
           'pump1_t2': 50.0,
           'pump1_F2': 4.0,
           'pump1_t3': 993.0,
           'pump1 F3': 4.0,
           'pump1_t4': 994.0,
           'pump1 F4': 4.0,
           'pump2 t0': 0.0,
           'pump2_F0': 0.0,
           'pump2_t1': 17.0,
           'pump2 F1': 4.0,
           'pump2 t2': 50.0,
           'pump2_F2': 4.0,
           'pump2 t3': 993.0,
           'pump2 F3': 4.0,
           'pump2 t4': 994.0,
           'pump2 F4': 4.0}
In [27]: # Simulation of process with flow rate clot to wash-out for chemostat
         init(VS 0=20)
                                                                    # Process initia
         par(pump1_t1=10, pump2_t1=10)
                                                                    # Pump schedule
         par(pump1 F1=2.5*0.155, pump2 F1=2.5*0.155/eps)
         par(pump1 t2=940, pump2 t2=940, pump1 t3=950, pump2 t3=950, pump1 t4=960,
         newplot(title='Perfusion cultivation - flow rate corresponding to maximal
         simu(60)
                            | warning | The default linear solver fails, the fallb
         ack solver with total pivoting is started at time 0.000000. That might r
         aise performance issues, for more information use -lv LOG LS.
                            | warning | The default linear solver fails, the fallb
         ack solver with total pivoting is started at time 0.000000. That might r
         aise performance issues, for more information use -lv LOG LS.
         stdout
                            | warning | The default linear solver fails, the fallb
         ack solver with total pivoting is started at time 0.000000. That might r
         aise performance issues, for more information use -lv LOG LS.
                            | warning | The default linear solver fails, the fallb
```

ack solver with total pivoting is started at time 0.000000. That might r

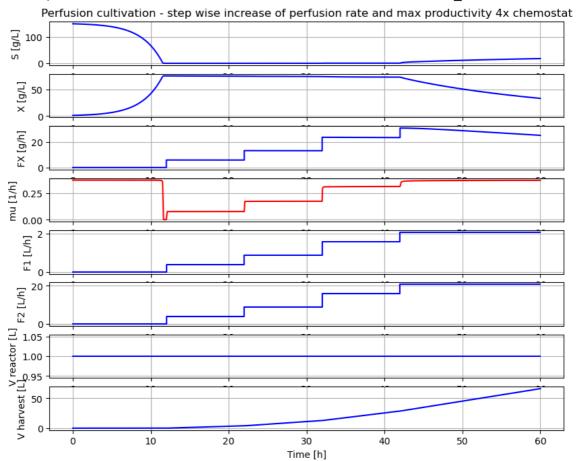
aise performance issues, for more information use -lv LOG LS.

stdout

Perfusion cultivation - flow rate corresponding to maximal rate for chemostat



```
In [28]: # Concentration factor of the filter
         c=model.get('filter.retentate.c[1]')[0]/model.get('filter.inlet.c[1]')[0]
         Conc factor of perfusion filter = 1.089
         c data=sim res['filter.retentate.c[1]']/sim res['filter.inlet.c[1]']
In [29]:
         print('Conc factor variation', np.round(min(c_data[151:]), 3), np.round(min(c_data[151:]), 3)
         Conc factor variation 1.089 1.089
         /tmp/ipykernel 3163/3491953895.py:1: RuntimeWarning: invalid value encou
         ntered in divide
           c_data=sim_res['filter.retentate.c[1]']/sim_res['filter.inlet.c[1]']
In [30]:
        # Simulation of process with step-wise increase of pefusion rate until wa
         # This means that re-circulation rate change at the same time as the perf
         init(VS 0=150)
                                                                    # Process initia
         par(pump1_t1=12, pump2_t1=12)
                                                                    # Pump schedule
         par(pump1_F1=2.5*0.155, pump2_F1=2.5*0.155/eps)
         par(pump1_t2=22, pump2_t2=22)
         par(pump1 F2=2.5*0.35, pump2 F2=2.5*0.35/eps)
         par(pump1 t3=32, pump2 t3=32)
         par(pump1 F3=2.5*0.63, pump2 F3=2.5*0.63/eps)
         par(pump1 t4=42, pump2 t4=42)
         par(pump1 F4=2.5*0.83, pump2 F4=2.5*0.83/eps)
         newplot(title='Perfusion cultivation - step wise increase of perfusion ra
         simu(60)
```



In [31]: # Simulation without a plot and just to check typical values at high prod
simu(40)
c\_data=sim\_res['filter.retentate.c[1]']/sim\_res['filter.inlet.c[1]']
print('Conc factor variation', np.round(min(c\_data[190:]), 3), 'to', np.r

Out[37]: -14.174999999999999

```
/tmp/ipykernel 3163/3195256660.py:3: RuntimeWarning: invalid value encou
         ntered in divide
           c data=sim res['filter.retentate.c[1]']/sim res['filter.inlet.c[1]']
In [32]: #describe('cstrProdMax')
In [33]: # The maximal biomass productivity before washout is obtained aroudn 40 h
         np.round(model.get('harvesttank.inlet.F')[0]*model.get('harvesttank.inlet
Out[33]: 23.5
In [34]: # Thus perfusion (with this filter) brings a productivity improvement of
         np.round(23.5/5.6,1)
Out[34]: 4.2
In [35]: # Finally we check the filter flow rates at time 40 hour - note the negat
         model.get('filter.inlet.F')[0]
Out[35]: 15.74999999999998
In [36]: model.get('filter.filtrate.F')[0]
Out[36]: -1.575
In [37]: model.get('filter.retentate.F')[0]
```

## Summary

- The perfusion filter had a concentration factor of cells around 1.08 and re-cycling flow was set to a factor 10 higher than the perfusion rate and changed when perfusion rate was change to keep the ratio factor 10.
- The first simulation showed that by cell retention using perfusion filter the process could be run at a perfusion flow rate at the maximal flow rate possible for corresponding chemostat culture and cell concetration increased steadily.
- The second simulation showed that with a proper startup cell concentration, the cell concentration remained constant when perfusion rate increased in a similar way as what we see in a chemostat.
- The second simulation also showed that biomass productivity in this case was increased by a factor 4.2 compared to chemostat.
- If the perfusion rate increased to higher levels washout started but the decrase of cell concentration was slow.

Some of you who read this may have your perfusion experience with CHO-cultures. For such cultures the cell concentration do increase with increase of perfusion rate and there are understood reasons for that. But for this simplified process as well as microbial processes they typically keep cell concentration constant when flow rate is chaged, and that under quite wide conditions. I will try come back to this phenomena in a later notebook.

```
# List of components in the process setup and also a couple of other thin
In [38]:
         describe('parts')
         ['bioreactor', 'bioreactor.culture', 'D', 'feedtank', 'filter', 'harvest
         tank', 'schemePump1', 'schemePump2']
        describe('MSL')
In [39]:
         MSL: 3.2.3 - used components: RealInput, RealOutput, CombiTimeTable, Typ
         es
In [40]: system info()
         System information
          -OS: Linux
          -Python: 3.8.16
          -Scipy: not installed in the notebook
          -PyFMI: 2.9.8
          -FMU by: OpenModelica Compiler OpenModelica 1.21.0~dev-185-q9d983b8
          -FMI: 2.0
          -Type: FMUModelME2
          -Name: BPL TEST2.Perfusion
          -Generated: 2023-01-25T11:02:31Z
          -MSL: 3.2.3
          -Description: Bioprocess Library version 2.1.1-beta
          -Interaction: FMU-explore version 0.9.6
 In [ ]:
```