BPL_TEST2_Perfusion script with PyFMI ver 2.7.4

The key library PyFMI v2.7.4 is installed and downgrading is done Numpy v1.19.1. To simplify this we first install conda.

After the installation a small application BPL_TEST2_Perfusion 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 18.04.6 LTS
Release:        18.04
Codename:       bionic
```

```
%env PYTHONPATH=
```

```
env: PYTHONPATH=
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py37_4.12.0-Linux-x86_64.sh
!chmod +x Miniconda3-py37_4.12.0-Linux-x86_64.sh
!bash ./Miniconda3-py37_4.12.0-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.7/site-packages/')
```

```
        - ruamel_yaml==0.15.100=py37h27cfd23_0
        - setuptools==61.2.0=py37h06a4308_0
        - six==1.16.0=pyhd3eb1b0_1
        - sqlite==3.38.2=hc218d9a_0
        - tk==8.6.11=h1ccaba5_0
        - tqdm==4.63.0=pyhd3eb1b0_0
        - urllib3==1.26.8=pyhd3eb1b0_0
        - wheel==0.37.1=pyhd3eb1b0_0
        - xz==5.2.5=h7b6447c_0
        - yaml==0.2.5=h7b6447c_0
        - zlib==1.2.12=h7f8727e_1


    The following NEW packages will be INSTALLED:

      _libgcc_mutex      pkgs/main/linux-64::_libgcc_mutex-0.1-main
      _openmp_mutex      pkgs/main/linux-64::_openmp_mutex-4.5-1_gnu
      brotlipy           pkgs/main/linux-64::brotlipy-0.7.0-py37h27cfd23_1003
      ca-certificates    pkgs/main/linux-64::ca-certificates-2022.3.29-h06a4308_1
      certifi            pkgs/main/linux-64::certifi-2021.10.8-py37h06a4308_2
      cffi               pkgs/main/linux-64::cffi-1.15.0-py37hd667e15_1
      charset-normalizer pkgs/main/noarch::charset-normalizer-2.0.4-pyhd3eb1b0_0
      colorama           pkgs/main/noarch::colorama-0.4.4-pyhd3eb1b0_0
      conda              pkgs/main/linux-64::conda-4.12.0-py37h06a4308_0
      conda-content-tru~ pkgs/main/noarch::conda-content-trust-0.1.1-pyhd3eb1b0_0
      conda-package-han~ pkgs/main/linux-64::conda-package-handling-1.8.1-py37h7f8
      cryptography       pkgs/main/linux-64::cryptography-36.0.0-py37h9ce1e76_0
      idna               pkgs/main/noarch::idna-3.3-pyhd3eb1b0_0
```

```
  idna                pkgs/main/noarch::idna-3.3-pyhd3eb1b0_0
  ld_impl_linux-64    pkgs/main/linux-64::ld_impl_linux-64-2.35.1-h7274673_9
  libffi              pkgs/main/linux-64::libffi-3.3-he6710b0_2
  libgcc-ng           pkgs/main/linux-64::libgcc-ng-9.3.0-h5101ec6_17
  libgomp             pkgs/main/linux-64::libgomp-9.3.0-h5101ec6_17
  libstdcxx-ng        pkgs/main/linux-64::libstdcxx-ng-9.3.0-hd4cf53a_17
  ncurses             pkgs/main/linux-64::ncurses-6.3-h7f8727e_2
  openssl             pkgs/main/linux-64::openssl-1.1.1n-h7f8727e_0
  pip                 pkgs/main/linux-64::pip-21.2.2-py37h06a4308_0
  pycosat             pkgs/main/linux-64::pycosat-0.6.3-py37h27cfd23_0
  pycparser           pkgs/main/noarch::pycparser-2.21-pyhd3eb1b0_0
  pyopenssl           pkgs/main/noarch::pyopenssl-22.0.0-pyhd3eb1b0_0
  pysocks             pkgs/main/linux-64::pysocks-1.7.1-py37_1
  python              pkgs/main/linux-64::python-3.7.13-h12debd9_0
  readline            pkgs/main/linux-64::readline-8.1.2-h7f8727e_1
  requests            pkgs/main/noarch::requests-2.27.1-pyhd3eb1b0_0
  ruamel_yaml         pkgs/main/linux-64::ruamel_yaml-0.15.100-py37h27cfd23_0
  setuptools          pkgs/main/linux-64::setuptools-61.2.0-py37h06a4308_0
  six                 pkgs/main/noarch::six-1.16.0-pyhd3eb1b0_1
  sqlite              pkgs/main/linux-64::sqlite-3.38.2-hc218d9a_0
  tk                  pkgs/main/linux-64::tk-8.6.11-h1ccaba5_0
  tqdm                pkgs/main/noarch::tqdm-4.63.0-pyhd3eb1b0_0
  urllib3             pkgs/main/noarch::urllib3-1.26.8-pyhd3eb1b0_0
  wheel               pkgs/main/noarch::wheel-0.37.1-pyhd3eb1b0_0
  xz                  pkgs/main/linux-64::xz-5.2.5-h7b6447c_0
  yaml                pkgs/main/linux-64::yaml-0.2.5-h7b6447c_0
  zlib                pkgs/main/linux-64::zlib-1.2.12-h7f8727e_1


Preparing transaction: done
Executing transaction: done
```

```
!conda update -n base -c defaults conda --yes
```

```
  colorama-0.4.4-pyhd3eb1b0_0
  conda-content-trust-0.1.1-pyhd3eb1b0_0
  six-1.16.0-pyhd3eb1b0_1

The following packages will be UPDATED:

  _openmp_mutex                                4.5-1_gnu --> 5.1-1_gnu
  ca-certificates                    2022.3.29-h06a4308_1 --> 2022.07.19-h06
  certifi                         2021.10.8-py37h06a4308_2 --> 2022.9.24-py37
  cffi                               1.15.0-py37hd667e15_1 --> 1.15.1-py37h74
  conda                              4.12.0-py37h06a4308_0 --> 22.9.0-py37h06
  conda-package-han~                  1.8.1-py37h7f8727e_0 --> 1.9.0-py37h5ee
  cryptography                       36.0.0-py37h9ce1e76_0 --> 37.0.1-py37h9c
  ld_impl_linux-64                       2.35.1-h7274673_9 --> 2.38-h1181459_
  libgcc-ng                              9.3.0-h5101ec6_17 --> 11.2.0-h123456
  libgomp                                9.3.0-h5101ec6_17 --> 11.2.0-h123456
  libstdcxx-ng                           9.3.0-hd4cf53a_17 --> 11.2.0-h123456
  ncurses                                   6.3-h7f8727e_2 --> 6.3-h5eee18b_3
  openssl                                1.1.1n-h7f8727e_0 --> 1.1.1q-h7f8727
  pip                                21.2.2-py37h06a4308_0 --> 22.2.2-py37h06
  requests            pkgs/main/noarch::requests-2.27.1-pyh~ --> pkgs/main/linu
  setuptools                         61.2.0-py37h06a4308_0 --> 63.4.1-py37h06
  sqlite                                 3.38.2-hc218d9a_0 --> 3.39.3-h508229
  tk                                     8.6.11-h1ccaba5_0 --> 8.6.12-h1ccaba
  tqdm                pkgs/main/noarch::tqdm-4.63.0-pyhd3eb~ --> pkgs/main/linu
```

```
  urllib3            pkgs/main/noarch::urllib3-1.26.8-pyhd~ --> pkgs/main/linu
  xz                                  5.2.5-h7b6447c_0 --> 5.2.6-h5eee18b
  zlib                               1.2.12-h7f8727e_1 --> 1.2.12-h5eee18


Downloading and Extracting Packages
setuptools-63.4.1    | 1.1 MB    | : 100% 1.0/1 [00:00<00:00,  4.69it/s]
xz-5.2.6             | 394 KB    | : 100% 1.0/1 [00:00<00:00, 12.88it/s]
libgcc-ng-11.2.0     | 5.3 MB    | : 100% 1.0/1 [00:00<00:00,  3.98it/s]
sqlite-3.39.3        | 1.1 MB    | : 100% 1.0/1 [00:00<00:00, 13.02it/s]
pip-22.2.2           | 2.3 MB    | : 100% 1.0/1 [00:00<00:00,  3.47it/s]
toolz-0.11.2         | 49 KB     | : 100% 1.0/1 [00:00<00:00, 17.62it/s]
requests-2.28.1      | 92 KB     | : 100% 1.0/1 [00:00<00:00, 16.51it/s]
libgomp-11.2.0       | 474 KB    | : 100% 1.0/1 [00:00<00:00, 13.35it/s]
libstdcxx-ng-11.2.0  | 4.7 MB    | : 100% 1.0/1 [00:00<00:00,  4.56it/s]
tqdm-4.64.1          | 126 KB    | : 100% 1.0/1 [00:00<00:00, 14.16it/s]
urllib3-1.26.11      | 181 KB    | : 100% 1.0/1 [00:00<00:00, 14.10it/s]
zlib-1.2.12          | 103 KB    | : 100% 1.0/1 [00:00<00:00, 15.45it/s]
ca-certificates-2022 | 124 KB    | : 100% 1.0/1 [00:00<00:00, 16.94it/s]
_openmp_mutex-5.1    | 21 KB     | : 100% 1.0/1 [00:00<00:00, 16.43it/s]
conda-package-handli | 887 KB    | : 100% 1.0/1 [00:00<00:00, 11.71it/s]
ncurses-6.3          | 781 KB    | : 100% 1.0/1 [00:00<00:00,  3.60it/s]
openssl-1.1.1q       | 2.5 MB    | : 100% 1.0/1 [00:00<00:00,  7.19it/s]
certifi-2022.9.24    | 154 KB    | : 100% 1.0/1 [00:00<00:00, 14.63it/s]
cryptography-37.0.1  | 1.3 MB    | : 100% 1.0/1 [00:00<00:00,  5.79it/s]
tk-8.6.12            | 3.0 MB    | : 100% 1.0/1 [00:00<00:00,  5.70it/s]
cffi-1.15.1          | 227 KB    | : 100% 1.0/1 [00:00<00:00, 12.91it/s]
conda-22.9.0         | 878 KB    | : 100% 1.0/1 [00:00<00:00,  8.30it/s]
ld_impl_linux-64-2.3 | 654 KB    | : 100% 1.0/1 [00:00<00:00, 13.67it/s]
Preparing transaction: done
Verifying transaction: done
Executing transaction: done
```

```
!conda --version
!python --version
```

```
conda 22.9.0
Python 3.7.13
```

```
!conda install -c conda-forge pyfmi==2.7.4 --yes # Install the key package
```

```
  libblapack           conda-forge/linux-64::libblapack-3.9.0-15_linux64_openblas
  libopenblas          conda-forge/linux-64::libopenblas-0.3.20-pthreads_h78a641
  libxml2              conda-forge/linux-64::libxml2-2.9.12-h72842e0_0 None
  libxslt              conda-forge/linux-64::libxslt-1.1.33-h15afd5d_2 None
  lxml                 conda-forge/linux-64::lxml-4.8.0-py37h540881e_2 None
  metis                conda-forge/linux-64::metis-5.1.0-h58526e2_1006 None
  mpfr                 conda-forge/linux-64::mpfr-4.1.0-h9202a9a_1 None
  numpy                conda-forge/linux-64::numpy-1.21.6-py37h976b520_0 None
  pyfmi                conda-forge/linux-64::pyfmi-2.7.4-py37h161383b_0 None
  python_abi           conda-forge/linux-64::python_abi-3.7-2_cp37m None
  scipy                conda-forge/linux-64::scipy-1.7.3-py37hf2a6cf1_0 None
  suitesparse          conda-forge/linux-64::suitesparse-5.10.1-h9e50725_1 None
  sundials             conda-forge/linux-64::sundials-5.8.0-h558c624_0 None
  tbb                  conda-forge/linux-64::tbb-2021.5.0-h924138e_1 None

The following packages will be UPDATED:

  ca-certificates    pkgs/main::ca-certificates-2022.07.19~ --> conda-forge::c
  conda              pkgs/main::conda-22.9.0-py37h06a4308_0 --> conda-forge::c
```

```
  conda               pkgs/main::conda-22.9.0-py37h06a4308_0 --> conda-forge::c

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

  certifi            pkgs/main/linux-64::certifi-2022.9.24~ --> conda-forge/no
  openssl              pkgs/main::openssl-1.1.1q-h7f8727e_0 --> conda-forge::c



Downloading and Extracting Packages
libcblas-3.9.0        | 12 KB     | : 100% 1.0/1 [00:00<00:00,  8.43it/s]
libxslt-1.1.33        | 522 KB    | : 100% 1.0/1 [00:00<00:00,  3.78it/s]
conda-22.9.0          | 960 KB    | : 100% 1.0/1 [00:00<00:00,  2.81it/s]
mpfr-4.1.0            | 2.6 MB    | : 100% 1.0/1 [00:00<00:00,  1.96it/s]
gmp-6.2.1             | 806 KB    | : 100% 1.0/1 [00:00<00:00,  4.85it/s]
libgfortran-ng-12.2.  | 22 KB     | : 100% 1.0/1 [00:00<00:00, 24.39it/s]
lxml-4.8.0            | 1.4 MB    | : 100% 1.0/1 [00:00<00:00,  1.38it/s]
numpy-1.21.6          | 6.1 MB    | : 100% 1.0/1 [00:01<00:00,  1.68s/it]
python_abi-3.7        | 4 KB      | : 100% 1.0/1 [00:00<00:00, 25.34it/s]
ca-certificates-2022  | 150 KB    | : 100% 1.0/1 [00:00<00:00, 18.02it/s]
libblas-3.9.0         | 12 KB     | : 100% 1.0/1 [00:00<00:00, 25.77it/s]
openssl-1.1.1o        | 2.1 MB    | : 100% 1.0/1 [00:00<00:00,  2.27it/s]
libiconv-1.17         | 1.4 MB    | : 100% 1.0/1 [00:00<00:00,  4.42it/s]
liblapack-3.9.0       | 12 KB     | : 100% 1.0/1 [00:00<00:00, 26.79it/s]
sundials-5.8.0        | 1.0 MB    | : 100% 1.0/1 [00:00<00:00,  1.27it/s]
libopenblas-0.3.20    | 10.1 MB   | : 100% 1.0/1 [00:02<00:00,  2.05s/it]
icu-68.2              | 13.1 MB   | : 100% 1.0/1 [00:02<00:00,  2.49s/it]
assimulo-3.2.9        | 2.6 MB    | : 100% 1.0/1 [00:00<00:00,  1.05it/s]
suitesparse-5.10.1    | 2.4 MB    | : 100% 1.0/1 [00:00<00:00,  1.77it/s]
tbb-2021.5.0          | 1.9 MB    | : 100% 1.0/1 [00:00<00:00,  1.21it/s]
libxml2-2.9.12        | 772 KB    | : 100% 1.0/1 [00:00<00:00,  5.25it/s]
metis-5.1.0           | 4.1 MB    | : 100% 1.0/1 [00:00<00:00,  1.21it/s]
pyfmi-2.7.4           | 12.4 MB   | : 100% 1.0/1 [00:02<00:00,  2.46s/it]
certifi-2022.9.24     | 155 KB    | : 100% 1.0/1 [00:00<00:00, 17.27it/s]
scipy-1.7.3           | 21.8 MB   | : 100% 1.0/1 [00:04<00:00,  4.63s/it]
fmilib-2.2.3          | 532 KB    | : 100% 1.0/1 [00:00<00:00,  1.93it/s]
libgfortran5-12.2.0   | 1.8 MB    | : 100% 1.0/1 [00:00<00:00,  2.43it/s]
Preparing transaction: done
Verifying transaction: done
Executing transaction: done
Retrieving notices: ...working... done
```

```
!conda install numpy=1.19.1 --yes # Need to downgrade numpy
```

```
Collecting package metadata (current_repodata.json): done
Solving environment: failed with initial frozen solve. Retrying with flexible
Collecting package metadata (repodata.json): done
Solving environment: done

## Package Plan ##

  environment location: /usr/local

  added / updated specs:
    - numpy=1.19.1


The following packages will be downloaded:

    package                    |            build
```

```
    ---------------------------|-----------------
    blas-1.0                   |         openblas          46 KB
    numpy-1.19.1               |   py37h30dfecb_0          21 KB
    numpy-base-1.19.1          |   py37h75fe3a5_0         4.1 MB
    ------------------------------------------------------------
                                           Total:         4.2 MB

The following NEW packages will be INSTALLED:

  blas               pkgs/main/linux-64::blas-1.0-openblas None
  numpy-base         pkgs/main/linux-64::numpy-base-1.19.1-py37h75fe3a5_0 None

The following packages will be UPDATED:

  openssl            conda-forge::openssl-1.1.1o-h166bdaf_0 --> pkgs/main::ope

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

  ca-certificates    conda-forge::ca-certificates-2022.9.2~ --> pkgs/main::ca-
  certifi            conda-forge/noarch::certifi-2022.9.24~ --> pkgs/main/linu
  conda              conda-forge::conda-22.9.0-py37h89c186~ --> pkgs/main::con
  numpy              conda-forge::numpy-1.21.6-py37h976b52~ --> pkgs/main::num



Downloading and Extracting Packages
numpy-base-1.19.1    | 4.1 MB    | : 100% 1.0/1 [00:00<00:00,  1.36it/s]
numpy-1.19.1         | 21 KB     | : 100% 1.0/1 [00:00<00:00, 10.50it/s]
blas-1.0             | 46 KB     | : 100% 1.0/1 [00:00<00:00, 39.17it/s]

ChecksumMismatchError: Conda detected a mismatch between the expected content
for url 'https://repo.anaconda.com/pkgs/main/linux-64/blas-1.0-openblas.conda'
  download saved to: /usr/local/pkgs/blas-1.0-openblas.conda
  expected sha256: c85b5d0a336b5be0f415c71fd7fe2eca59e09f42221bfa684aafef5510b
  actual sha256: 5dc5483db0d9785b19e021cee418a8ee03e0ff0e5ebd0b75af4927746604e
```

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_jm_cs.fmu

- Setup-file - BPL_TEST2_Perfusion_explore.py

```
# Filter out DepracationWarnings for 'np.float as alias' is needed - wish I could m
import warnings
warnings.filterwarnings("ignore")
```

```
%%bash
git clone https://github.com/janpeter19/BPL_TEST2_Perfusion
```

```
    Cloning into 'BPL_TEST2_Perfusion'...
```

```
%cd BPL_TEST2_Perfusion
```

```
    /content/BPL_TEST2_Perfusion
```

```
run -i BPL_TEST2_Perfusion_explore.py
```

```
    Linux - run FMU pre-comiled JModelica 2.4

    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 simulatic
     - describe()  - describe culture, broth, parameters, variables with values /

    Note that both disp() and describe() takes values from the last simulation

    Brief information about a command by help(), eg help(simu)
    Key system information is listed with the command system_info()
```

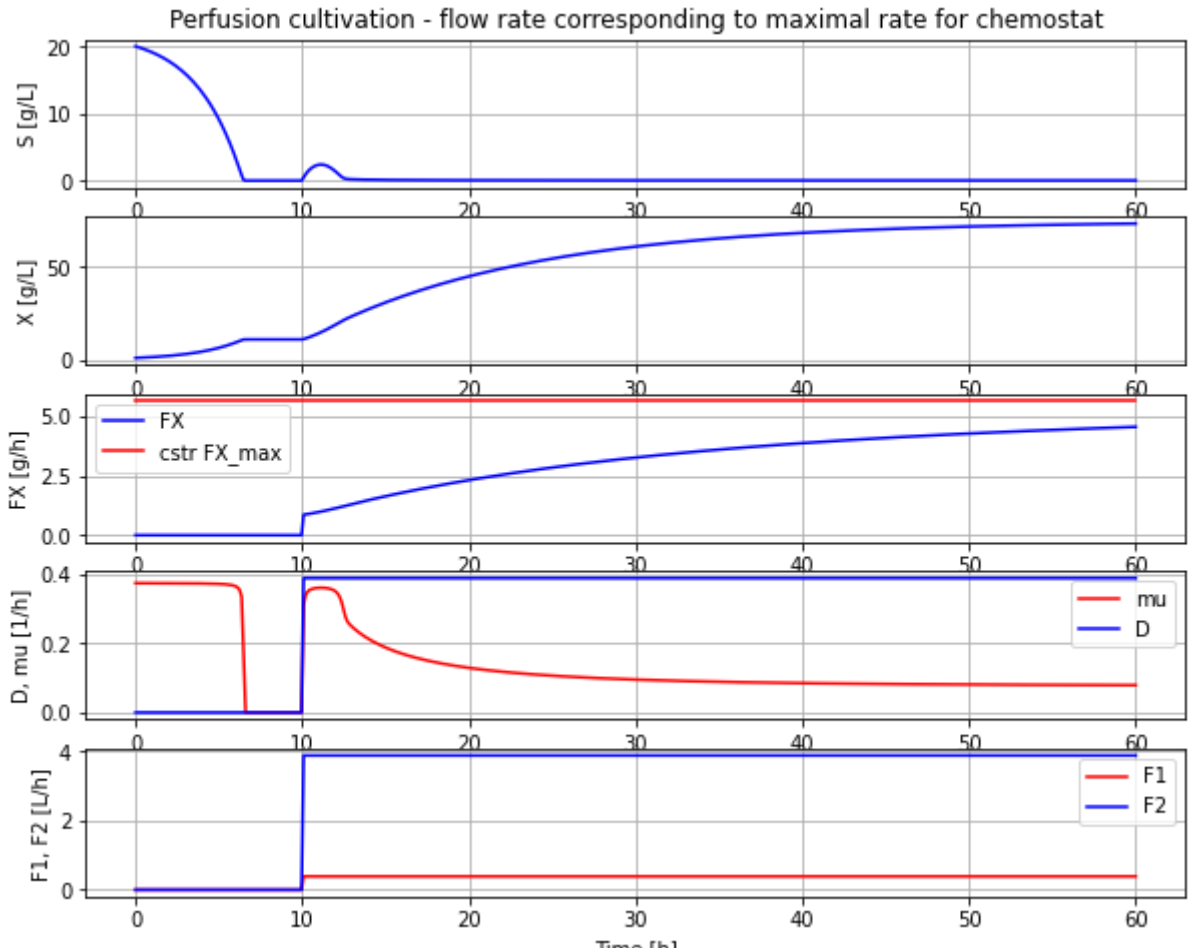
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

```
# Process parameters used throughout
par(Y=0.5, qSmax=0.75, Ks=0.1)                                          # Culture
par(filter_eps=0.10, filter_alpha_X=0.02, filter_alpha_S=0.10)      # Filter
par(S_in=30.0)                                                          # Inlet substra
init(V_0=1.0, VX_0=1.0)                                                 # Process initi
eps = parDict['filter_eps']                                             # Pump schedule
```

```
# Simulation of process with flow rate clot to wash-out for chemostat

init(VS_0=20)                                               # Process initial
par(pump1_t1=10, pump2_t1=10)                               # Pump schedule - recycle
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, pump2_t4=
```

```
newplot(title='Perfusion cultivation - flow rate corresponding to maximal rate for
simu(60)
```




```
# Concentration factor of the filter
c=model.get('filter.retentate.c[1]')[0]/model.get('filter.inlet.c[1]')[0]
print('Conc factor of perfusion filter =', np.round(c,3))
```

```
    Conc factor of perfusion filter = 1.369
```

```
c_data=sim_res['filter.retentate.c[1]']/sim_res['filter.inlet.c[1]']
print('Conc factor variation', np.round(min(c_data[151:]), 3), np.round(max(c_data[
```

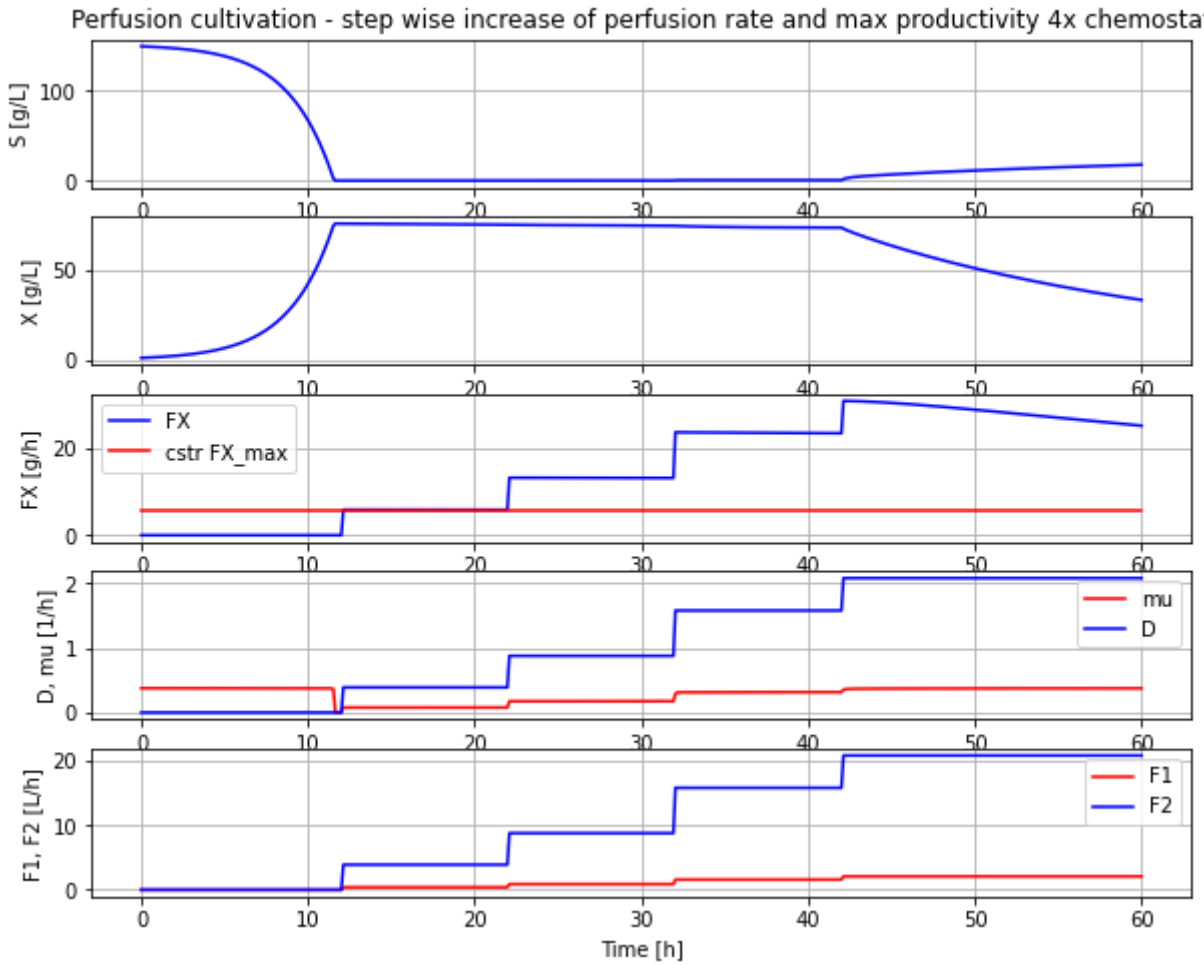
```
    Conc factor variation 1.369 1.649
```

```
# Simulation of process with step-wise increase of pefusion rate until wash-out.
# This means that re-circulation rate change at the same time as the perfusion rate

init(VS_0=150)                                          # Process initial varied

par(pump1_t1=12, pump2_t1=12)                           # Pump schedule - recycle
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 rate and max
simu(60)
```




```
# Simulation without a plot and just to check typical values at high production rat
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.round(max(c
```

```
Conc factor variation 1.075 to 1.087
```

```
describe('cstrProdMax')
```

```
Calculate from the model maximal chemostat productivity FX_max : 5.625 [ g/h ]
```

```
# The maximal biomass productivity before washout is obtained aroudn 40 hours
np.round(model.get('harvesttank.inlet.F')[0]*model.get('harvesttank.inlet.c[1]')[0]
```

```
23.5
```

```
# Thus perfusion (with this filter) brings a productivity improvement of about
np.round(23.5/5.6,1)
```

```
4.2
```

```
# Finally we check the filter flow rates at time 40 hour - note the negative sign f
model.get('filter.inlet.F')[0]
```

```
15.749999999999998
```

```
model.get('filter.filtrate.F')[0]
```

```
-1.575
```

```
model.get('filter.retentate.F')[0]
```

```
-14.174999999999999
```

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 simplifed 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 things like li
describe('parts')
```

```
['bioreactor', 'bioreactor.culture', 'D', 'feedtank', 'filter', 'harvesttank',
```

```
system_info()
```

```
System information
 -OS: Linux
```

```
-Python: 3.7.15
-Scipy: not installed in the notebook
-PyFMI: 2.7.4
-FMU by: JModelica.org
-FMI: 2.0
-Type: FMUModelCS2
-Name: BPL_TEST2.Perfusion
-Generated: 2022-10-17T11:47:04
-MSL: 3.2.2 build 3
-Description: Bioprocess Library version 2.1.0
-Interaction: FMU-explore version 0.9.5
```