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.

```
!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
```

```
%env PYTHONPATH=
```

```
env: PYTHONPATH=
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py38_22.11.1-1-Linux-x86_64.sh
!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 10:22:32--  https://repo.anaconda.com/miniconda/Miniconda3-py38_22.11.1-1-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.130.3, 104.16.131.3, 2606:4700::6810:8303, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.130.3|: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   261MB/s    in 0.2s

2023-01-25 10:22:33 (261 MB/s) - ‘Miniconda3-py38_22.11.1-1-Linux-x86_64.sh’ saved [64630241/64630241]

PREFIX=/usr/local
Unpacking payload ...

Installing base environment...


Downloading and Extracting Packages


Downloading and Extracting Packages

Preparing transaction: done
Executing transaction: done
installation finished.
```

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

```
Package six conflicts for:
numpy -> mkl-service[version='>=2.3.0,<3.0a0'] -> six
suitesparse -> mkl-service[version='>=2.3.0,<3.0a0'] -> six
conda -> conda-package-handling[version='>=1.3.0'] -> six[version='>=1.5.2']
scipy -> mkl-service[version='>=2.3.0,<3.0a0'] -> six
conda[version='>=22.11.1'] -> conda-package-handling[version='>=1.3.0'] -> six[version='>=1.5.2']
conda-content-trust -> cryptography -> six[version='>=1.4.1']
conda-content-trust -> six

Package libgfortran-ng conflicts for:
assimulo -> scipy -> libgfortran-ng[version='>=7,<8.0a0|>=7.2.0,<8.0a0']
assimulo -> libgfortran-ngThe following specifications were found to be incompatible with your system:

  - feature:/linux-64::__glibc==2.31=0
  - feature:|@/linux-64::__glibc==2.31=0
  - assimulo -> libgfortran-ng -> __glibc[version='>=2.17']
  - libopenblas -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
  - numpy -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
  - openssl -> libgcc-ng[version='>=7.5.0'] -> __glibc[version='>=2.17']
  - python=3.8 -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
  - scipy -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
  - suitesparse -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
  - tbb -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']

Your installed version is: 2.31
```

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

```
conda 22.11.1
Python 3.8.15
```

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

```
  - conda-forge/linux-64::liblapack==3.9.0=16_linux64_openbladone


==> WARNING: A newer version of conda exists. <==
  current version: 22.11.1
  latest version: 23.1.0

Please update conda by running

    $ conda update -n base -c defaults conda

Or to minimize the number of packages updated during conda update use

     conda install conda=23.1.0



## Package Plan ##

  environment location: /usr/local

  added / updated specs:
    - pyfmi


The following packages will be downloaded:

    package                    |            build
    ---------------------------|-----------------
    conda-22.11.1              |   py38h578d9bd_1         905 KB  conda-forge
    ------------------------------------------------------------
                                           Total:         905 KB

The following packages will be REMOVED:
Downloading and Extracting Packages

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

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

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

    Cloning into 'BPL_TEST2_Perfusion'...
```

```
%cd BPL_TEST2_Perfusion

    /content/BPL_TEST2_Perfusion/BPL_TEST2_Perfusion
```

```
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 simula
     - 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()
    <Figure size 708.661x566.929 with 0 Axes>
```

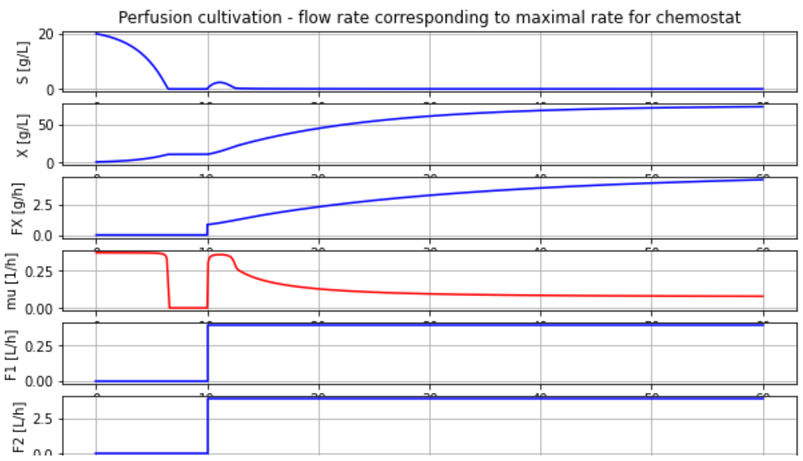
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

```
# 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 substrate conc
init(V_0=1.0, VX_0=1.0)                                             # Process initial conditions that are common
eps = parDict['filter_eps']                                         # Pump schedule parameter
```

```
# 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 flow 10 times perfusion flow
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=960)

newplot(title='Perfusion cultivation - flow rate corresponding to maximal rate for chemostat')
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 = 1.089
```

```
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[151:]),3))
```

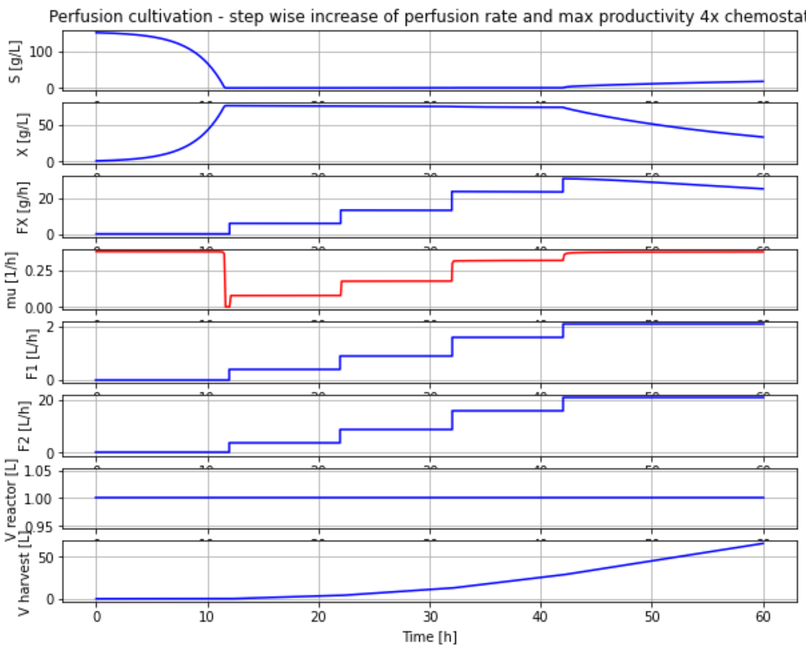
```
    Conc factor variation 1.089 1.089
    <ipython-input-40-0b550512bc49>:1: RuntimeWarning: invalid value encountered in true_divide
      c_data=sim_res['filter.retentate.c[1]']/sim_res['filter.inlet.c[1]']
```

```
# 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 flow 10 times perfusion flow
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 productivity 4x chemostat')
simu(60)
```



```
# Simulation without a plot and just to check typical values at high production rate
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_data[190:]),3))
```

```
Conc factor variation 1.089 to 1.089
<ipython-input-42-e9e4b9ad2684>:3: RuntimeWarning: invalid value encountered in true_divide
  c_data=sim_res['filter.retentate.c[1]']/sim_res['filter.inlet.c[1]']
```

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

```
# 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],1)
```

```
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 for outlfow
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 liquidphase and D
describe('parts')
```

```
['bioreactor', 'bioreactor.culture', 'D', 'feedtank', 'filter', 'harvesttank', 'schemePump1', 'schemePump2']
```

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

```
MSL: 3.2.3 - used components: RealInput, RealOutput, CombiTimeTable, Types
```

```
system_info()
```

```
System information
 -OS: Linux
 -Python: 3.8.10
 -Scipy: not installed in the notebook
 -PyFMI: 2.9.8
 -FMU by: OpenModelica Compiler OpenModelica 1.21.0~dev-185-g9d983b8
 -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 0.9.6e
```

✓ 0s completed at 11:27