BPL_STEM_AIR_Perfusion script with PyFMI

The key library PyFMI is installed.

After the installation a small application BPL_STEM_AIR_Pefusion 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-py310_23.1.0-1-Linux-x86_64.
!chmod +x Miniconda3-py310_23.1.0-1-Linux-x86_64.sh
!bash ./Miniconda3-py310_23.1.0-1-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.10/site-packages/')
```

```
--2024-09-11 12:32:03--  https://repo.anaconda.com/miniconda/Miniconda3-py310
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.191.158, 104.16.32.
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.191.158|:443... co
HTTP request sent, awaiting response... 200 OK
Length: 74403966 (71M) [application/x-sh]
Saving to: ‘Miniconda3-py310_23.1.0-1-Linux-x86_64.sh’

Miniconda3-py310_23 100%[===================>]  70.96M   141MB/s    in 0.5s

2024-09-11 12:32:04 (141 MB/s) - ‘Miniconda3-py310_23.1.0-1-Linux-x86_64.sh’

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
```

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

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

```
conda 23.1.0
Python 3.10.14
```

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

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

BPL_STEM_AIR_Perfusion setup

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

- FMU - BPL_STEM_AIR_Perfusion_linux_om_me.fmu
- Setup-file - BPL_STEM_AIR_Perfusion_explore

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

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

```
Cloning into 'BPL_STEM_AIR_Perfusion'...
```

```
%cd BPL_STEM_AIR_Perfusion
```

```
/content/BPL_STEM_AIR_Perfusion
```

BPL_STEM_AIR_Perfusion - test

Author: Jan Peter Axelsson

Here we show simulations of stem cell cultivation in an aerated hollow fiber reactor. The reactor volume is kept constant and cells recycled, thus the setup is similar to perfusion cultivation.

The model combines rudimentary cell growth and metabolism combined with times series data of of the metabolic rates: qNmax, qLc, and qO2, marked with red in the comprehensive plot.

Ref Greuel et al: "Online measurement of oxygen enables continuous noninvasive evalation of human-induced pluripotent stem cell (hiPSC) culture in a perfused 3D hollow-fober bioreactor", Biotech. Bioeng., 2019.

Setup of the simulation model

```
run -i BPL_STEM_AIR_Perfusion_explore.py
```

```
Linux - run FMU pre-compiled OpenModelica

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

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'] = [30/2.54, 24/2.54]
```

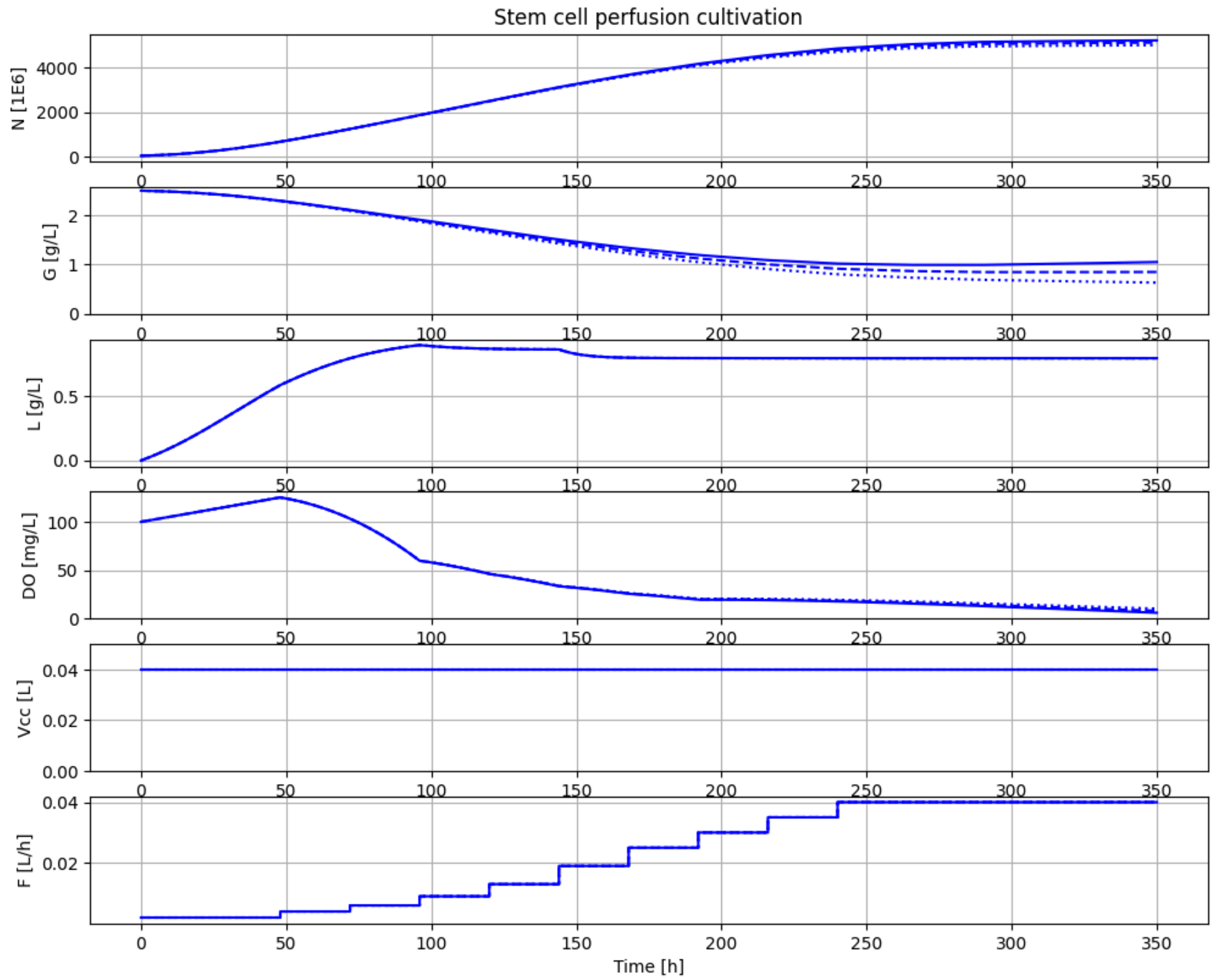
About the process model

Here a process diagram is shown of the process. Further information about the culutre stored in the model code is extracted.

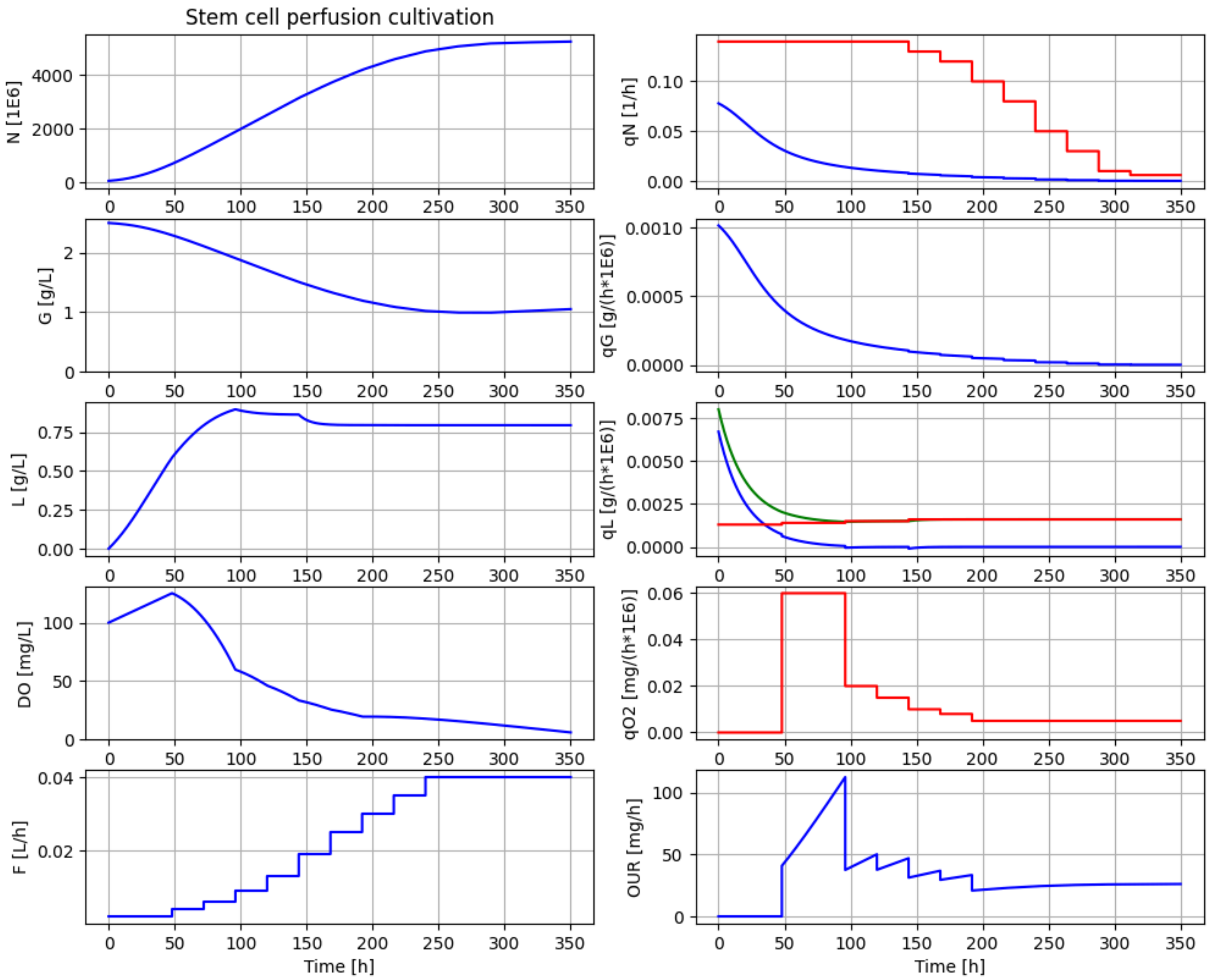
```
#process_diagram()
```

Simulations

```
# Process parameters to mimic stem cell example
# - study impact of different values maintenatnce qm

newplot(plotType='Basic')
for value in [1.0e-6, 10.0e-6, 20e-6]:
    par(qm=value)
    simu(350)
```



```
# Process parameters to mimic stem cell example
# . comprehensvie plot including metabolic rates

par(qm=1e-6)

newplot(plotType='Comprehensive')
simu(350)
```



```
describe('culture')
```

```
Reactor culture human-induced pluripotent stem cells - hiPSCs
```

```
describe('Vcc')
```

```
Volume of the reactor : 0.04 [ L ]
```

```
describe('N_start')
```

```
Number of cells at start : 50.0 [ 1E6 ]
```

```
describe('N')
```

```
Number of cells : 5223.752 [ 1E6 ]
```

```
describe('G_start')
```

```
Glucose conc at start : 2.5 [ g/L ]
```

```
describe('G_in')
```

```
Glucose feed conc : 2.5 [ g/L ]
```

```
describe('L')
```

```
Lactate conc : 0.796 [ g/L ]
```

```
describe('DO')
```

```
Dissolved oxygen conc : 6.044 [ mg/L ]
```

Appendix

+ Code + Text

```
system_info()
```

```

System information
 -OS: Linux
 -Python: 3.10.12
 -Scipy: not installed in the notebook
 -PyFMI: 2.14.0
 -FMU by: OpenModelica Compiler OpenModelica 1.23.1
 -FMI: 2.0
 -Type: FMUModelME2
 -Name: BPL_STEM.Reactor
 -Generated: 2024-09-06T19:04:53Z
 -MSL: 3.2.3
 -Description: BPL - not used
 -Interaction: FMU-explore version 1.0.0
```

Start coding or generate with AI.