BPL_STEM_AIR_Perfusion - test

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.

```
In [1]:  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 simul
ation
 - describe()  - describe culture, broth, parameters, variables with value
s/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()
```
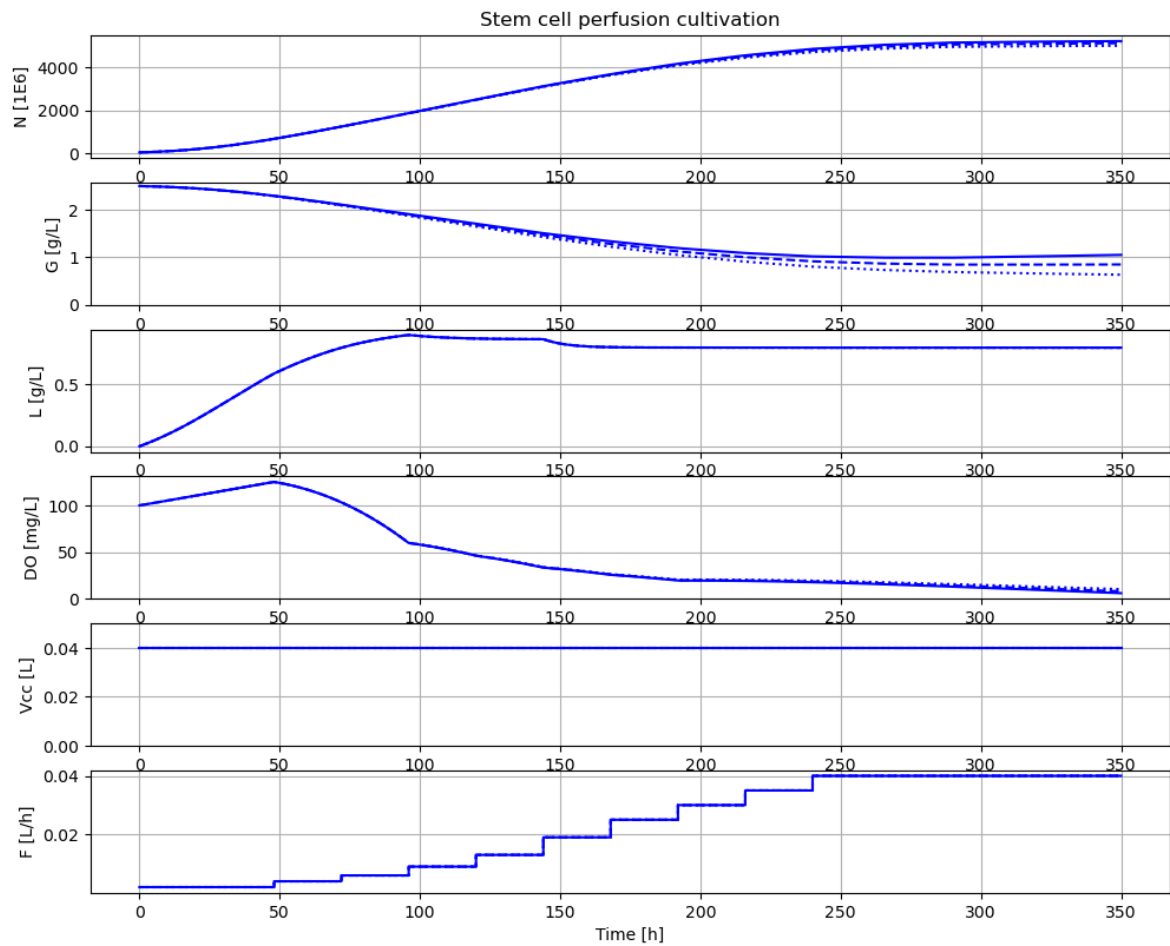
```
In [2]:  plt.rcParams['figure.figsize'] = [30/2.54, 24/2.54]
```

```
In [3]:  #process_diagram()
```

```
In [4]:  # 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)
```
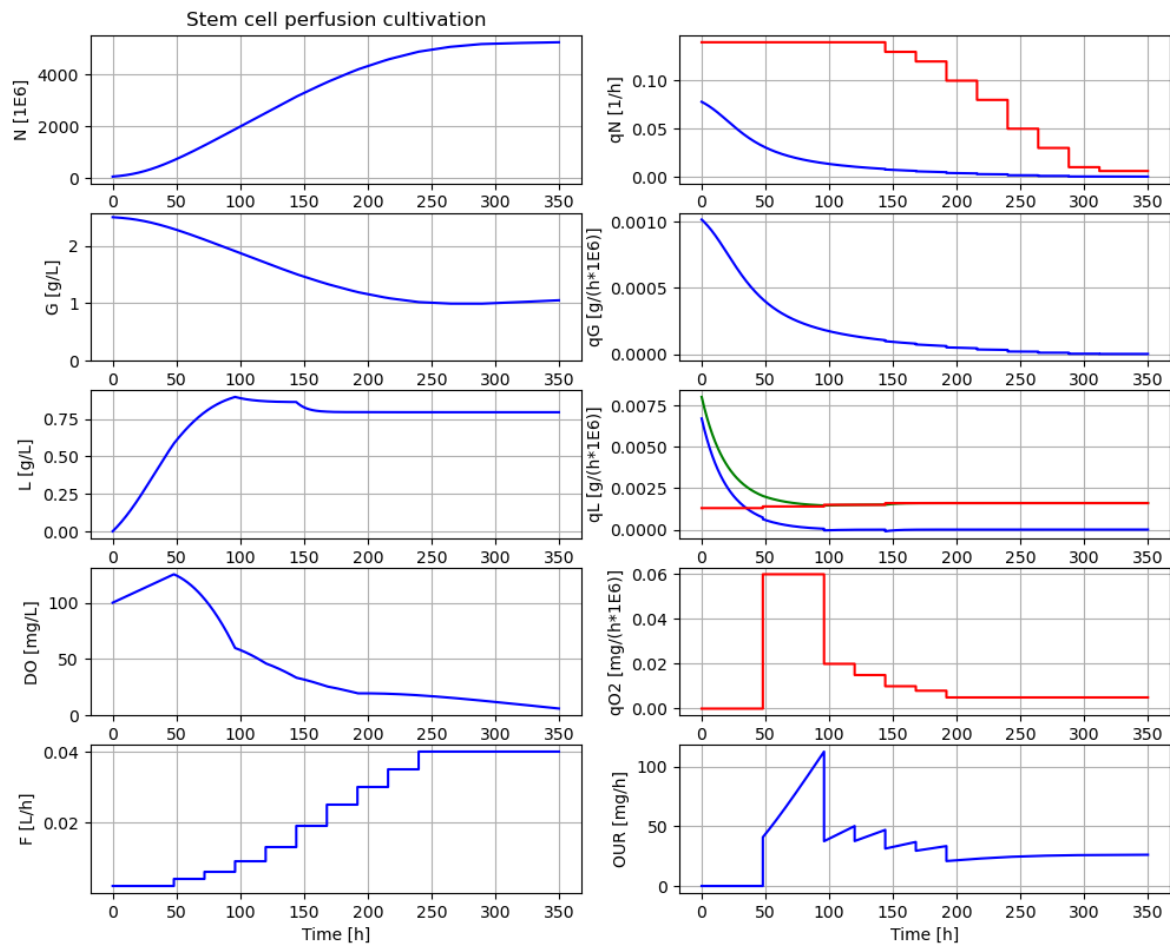
Stem cell perfusion cultivation

In [5]:
```
# Process parameters to mimic stem cell example
# . comprehensvie plot including metabolic rates

par(qm=1e-6)

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

Stem cell perfusion cultivation

```
In [6]:  describe('culture')

         Reactor culture human-induced pluripotent stem cells - hiPSCs

In [7]:  describe('Vcc')

         Volume of the reactor : 0.04 [ L ]

In [8]:  describe('N_start')

         Number of cells at start : 50.0 [ 1E6 ]

In [9]:  describe('N')

         Number of cells : 5223.752 [ 1E6 ]

In [10]: describe('G_start')

         Glucose conc at start : 2.5 [ g/L ]

In [11]: describe('G_in')

         Glucose feed conc : 2.5 [ g/L ]

In [12]: describe('L')

         Lactate conc : 0.796 [ g/L ]

In [13]: describe('DO')

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

Appendix

In [14]: `system_info()`

```
System information
 -OS: Linux
 -Python: 3.10.14
 -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
```

In [ ]: