BPL_YEAST_AIR_Fedbatch script with FMPy

The key library FMPy is installed.

After the installation a small application BPL_YEAST_AIR_Fedbatch 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 22.04.4 LTS
Release:        22.04
Codename:       jammy
```

```
%env PYTHONPATH=
```

```
env: PYTHONPATH=
```

```
!python --version
```

```
Python 3.11.11
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py311_24.11.1-0-Linux-x86_64
!chmod +x Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
!bash ./Miniconda3-py311_24.11.1-0-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.11/site-packages/')
```

```
--2025-02-14 15:44:45--  https://repo.anaconda.com/miniconda/Miniconda3-py311
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... con
HTTP request sent, awaiting response... 200 OK
Length: 145900576 (139M) [application/octet-stream]
Saving to: ‘Miniconda3-py311_24.11.1-0-Linux-x86_64.sh’

Miniconda3-py311_24 100%[===================>] 139.14M   124MB/s    in 1.1s

2025-02-14 15:44:46 (124 MB/s) - ‘Miniconda3-py311_24.11.1-0-Linux-x86_64.sh’

PREFIX=/usr/local
Unpacking payload ...

Installing base environment...

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

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

```
Channels:
 - defaults
Platform: linux-64
Collecting package metadata (repodata.json): done
Solving environment: done

## Package Plan ##

  environment location: /usr/local

  added / updated specs:
    - conda


The following packages will be downloaded:

    package                    |            build
    ---------------------------|-----------------
    ca-certificates-2024.12.31 |       h06a4308_0         128 KB
    certifi-2025.1.31          |  py311h06a4308_0         163 KB
    ------------------------------------------------------------
                                           Total:         291 KB

The following packages will be UPDATED:

  ca-certificates                    2024.11.26-h06a4308_0 --> 2024.12.31-h0
  certifi                          2024.8.30-py311h06a4308_0 --> 2025.1.31-py3



Downloading and Extracting Packages:
certifi-2025.1.31    | 163 KB    | :   0% 0/1 [00:00<?, ?it/s]
certifi-2025.1.31    | 163 KB    | : 100% 1.0/1 [00:00<00:00, 23.23it/s]
ca-certificates-2024 | 128 KB    | : 100% 1.0/1 [00:00<00:00, 19.51it/s]


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

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

```
conda 24.11.1
Python 3.11.11
```

```
!conda config --set channel_priority strict
```

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

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

```
#!conda install matplotlib --yes
```

```
#!conda install scipy --yes
```

```
#!conda install xlrd --yes
```

```
#!conda install openpyxl --yes
```

Notes of BPL_YEAST_AIR_Fedbatch

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

- FMU - BPL_YEAST_AIR_Fedbatch_linux_jm_cs.fmu
- Setup-file - BPL_YEAST_AIR_Fedbatch_fmpy_explore

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

```
Cloning into 'BPL_YEAST_AIR_Fedbatch'...
```

```
%cd BPL_YEAST_AIR_Fedbatch
```

```
/content/BPL_YEAST_AIR_Fedbatch
```

BPL_YEAST_AIR_Fedbatch - demo

Author: Jan Peter Axelsson

This notebook demonstrate yeast fedbatch cultivation. We look at impact of changes in the glucose feeding. We also take a look at tuning of the DO-control system. Both liquid- and gasphase are included in the model. The culture growth and metabolism are formulated in relation to to the respiratory capacity [1] and the model is exapanded to describe also the gas phase as well as the culture heat production [2]. The model was derived mainly from continuous culture data but proved to capture dynamic aspects well of ethanol production and consumption [3]. Several cultivations where donw with ethnol control that facilatated high cell density cultivations [4].

Interaction with the compiled model as FMU is mainly through the simplified commands: par(), init(), newplot(), simu() etc. The last simulation is always available in the workspace and called 'sim_res'. The command describe() brings mainly up description infomration from the actual Modelica code from the FMU but is complemented with information given in the dedicated Python setup-file.

The idea is to demonstrate how simulations and varyiing conditions can provide some process insight that can support the experimetnal work. I hope that at the end of this session you are ready to formulate your own questions you want to address with simulations - and you can just go on in this notebook! Just press the field "+Code" in the upper left part of notebook interface

and you get a new "cell" where you write your own code. You can copy and paste from cells above using ctrol-c and ctrl-p as usual and edit the cell. When your are ready to execute the cell just press the "play button" to the left in the cell or press shift-enter as in "ordinary" Jupyter notebooks.

After a session you may want to save your own notebook. That you can do on your Google Drive account and I refer to Colab instructions for how to do this. It is easy.

Enjoy!

```
run -i BPL_YEAST_AIR_Fedbatch_DOcontrol_fmpy_explore.py
```

```
Linux - run FMU pre-comiled 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'] = [36/2.54, 30/2.54]
```

About the process model

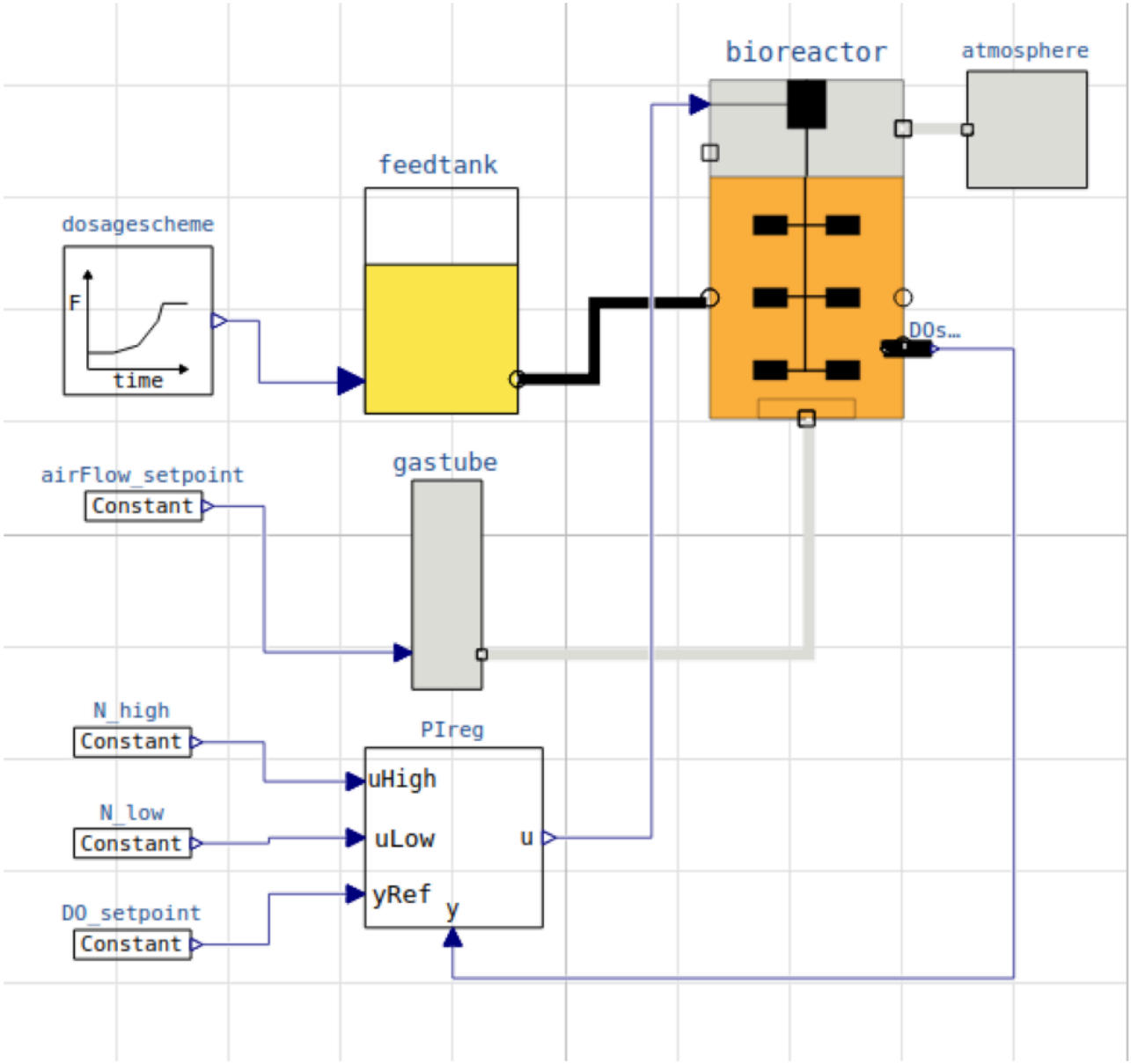
We can get information about the process, liquid- and gas-phase by the command describe(). This command can also be used to bring up information about a specific variable or parameter. However, you should use describe() after a simulation to get the valued used during the simulation.

```
describe('culture'); print(); #describe('liquidphase'); print(); describe('gaspha
```

```
Saccharomyces cerevisae - default parameters for strain H1022
```

```
process_diagram()
```

```
No processDiagram.png file in the FMU, but try the file on disk.
```



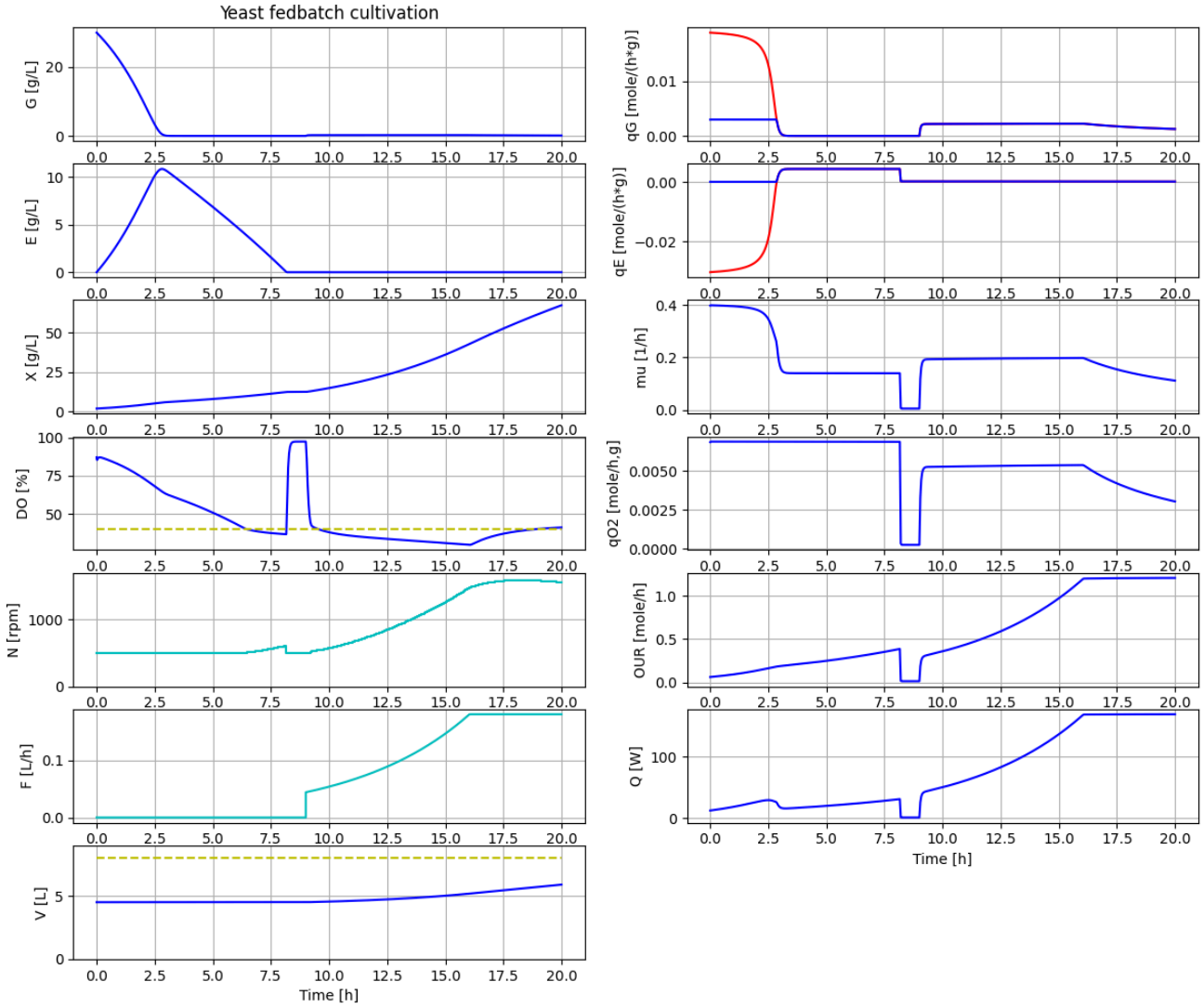
The model of the process has parameters both for culture, gas_liquid_transfer, as well as feeding procedure. The paramters that are available for changes you find by the command

disp() and you get a long list and you change by them by command par(). The model has even more parameters in the background but not made available for interaction.

First simulations - adjusting start of substrate feeding

```
# Culture parameters and others at default values
par(qO2lim=0.0069)

# Process initial conditions
init(V_start=4.5, VG_start=4.5*30, VX_start=4.5*2, VE_start=4.5*0)

# Feed profile
par(t_startExp=9, F_startExp=0.044, mu_feed=0.20, F_max=0.18)

# DO-control parameters
par(K=10, Ti=0.5)

# Simulate and plot
newplot(title='Yeast fedbatch cultivation', plotType='Overview')
simu(20)
```

```
Error: qO2lim - seems not an accessible parameter - check the spelling
```



Now we can get value of broth volume as well as the headspace and values are the last ones in the simulation

```
describe('bioreactor.V')
```

```
Reactor broth volume : 5.892 [ L ]
```

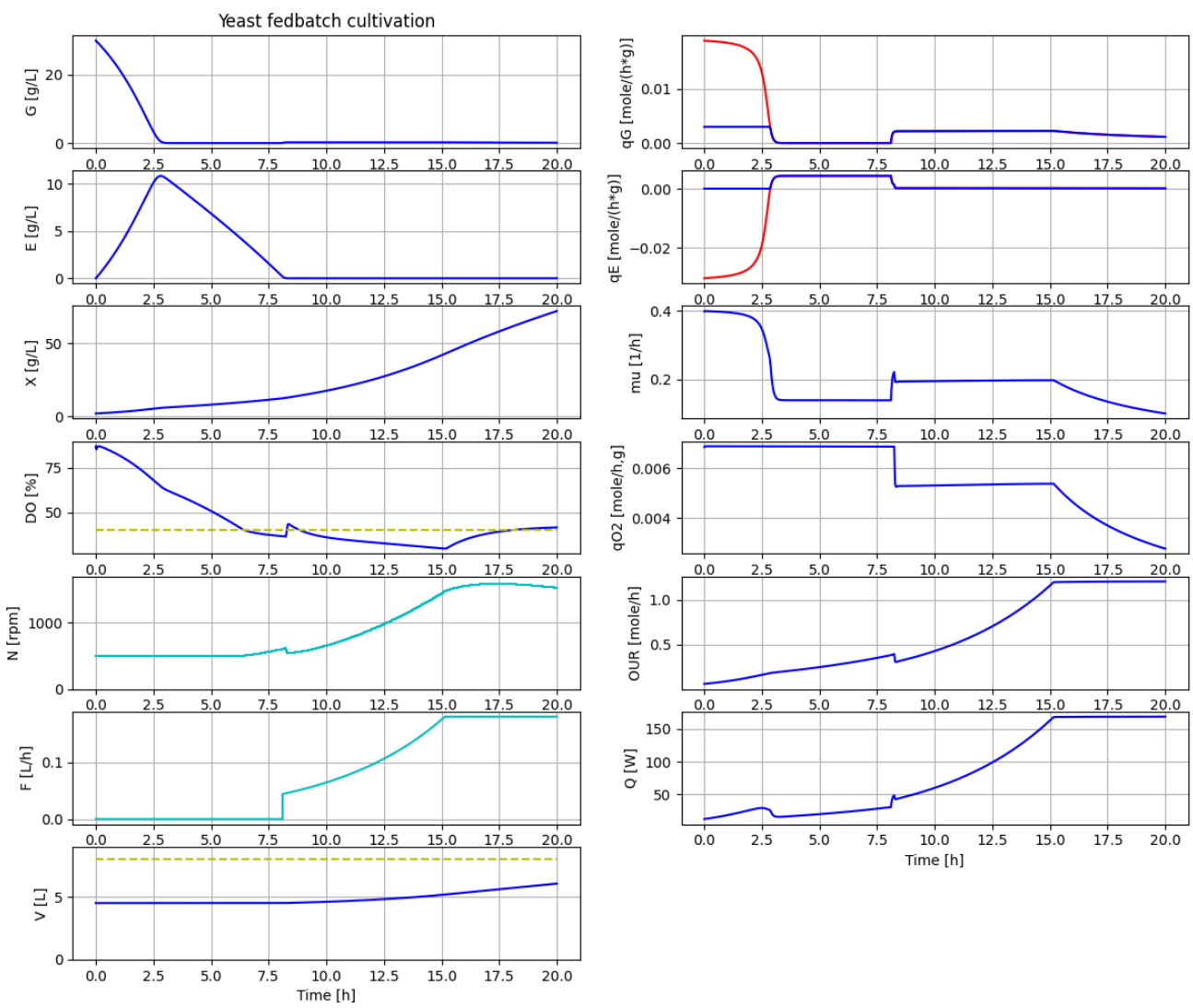
```
describe('bioreactor.V_gasphase')
```

```
Volume of the gas phase : 2.108 [ L ]
```

```
# Take a look at the parameters available to adjust the dosage scheme
disp('dosage', decimals=4)
```

```
F_start : 0.0
mu_feed : 0.2
t_startExp : 2.0
F_startExp : 0.12
F_max : 3.0
```

```
# Let us start the feeding just after the batch phase has ended and keep other pa
par(t_startExp=8.1)

# Simulate and plot
newplot(title='Yeast fedbatch cultivation', plotType='Overview')
simu(20)
```



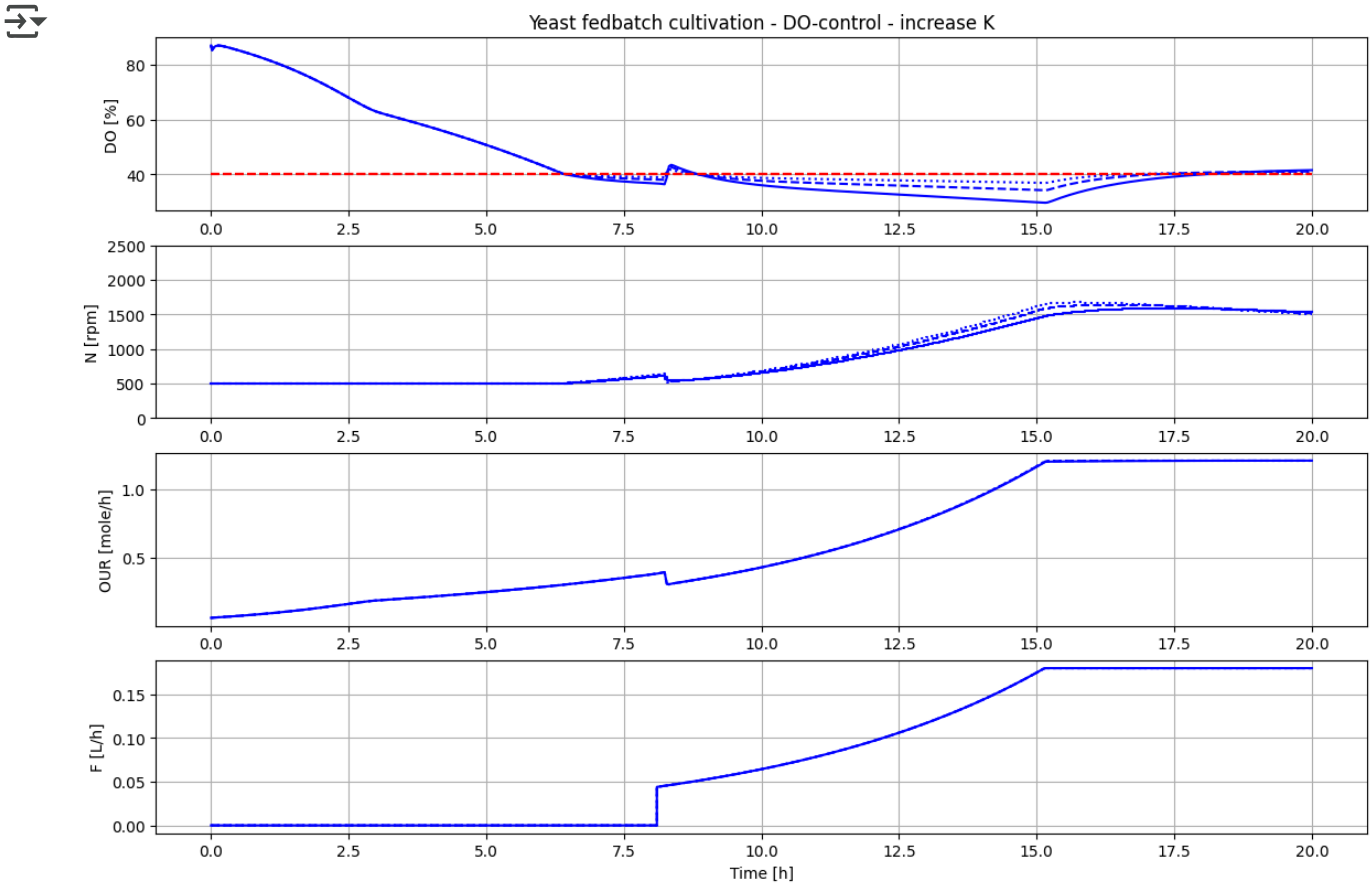
The increase of DO to about 50 % at end of batch phase should be possible to detect easily. This simulation is more realistic and we use these settings from now on.

DO-control - tuning of PI-regulator parameters

Let us focus on the DO-control system and choose a more limited plotType. We study the impact of PI control parameters and see if we can decrease the control error without looing

stability.

```
# Let us take a closer look at the DO-control system and try to make control erro
newplot(title='Yeast fedbatch cultivation - DO-control - increase K', plotType='F
for value in [10, 20, 40]: par(K=value); simu(20)

# Reset K to the original value
par(K=10)
```



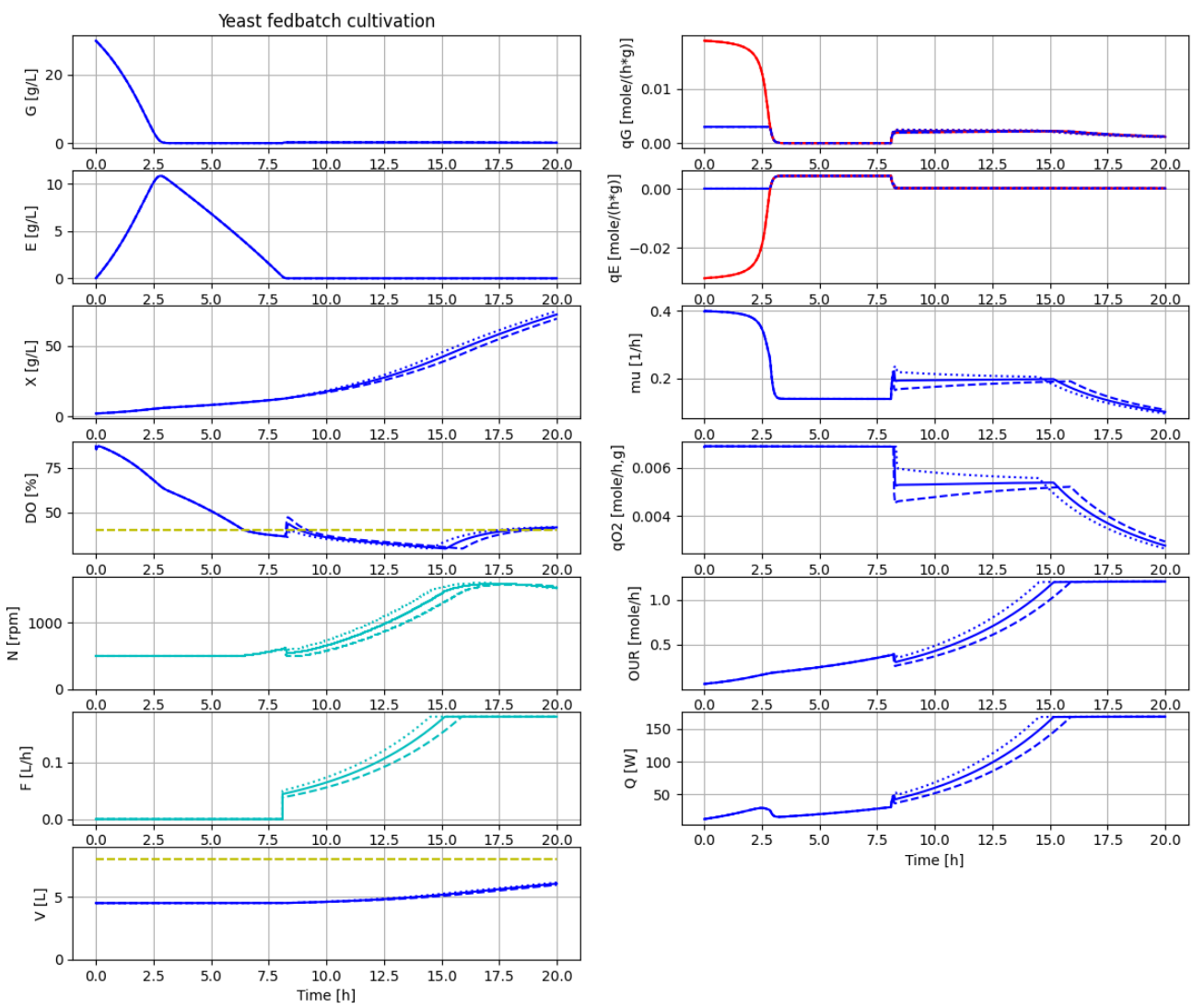
We see that by a higher control gain K the DO-control error get smaller and the stability of the control system is maintained.

Exercise I leave for you to study the impact variation of the Ti-parameter. Just make a new cell below. Then copy and paste the cell above and change parameter to Ti.

Sensitivity to changes in feed-profile

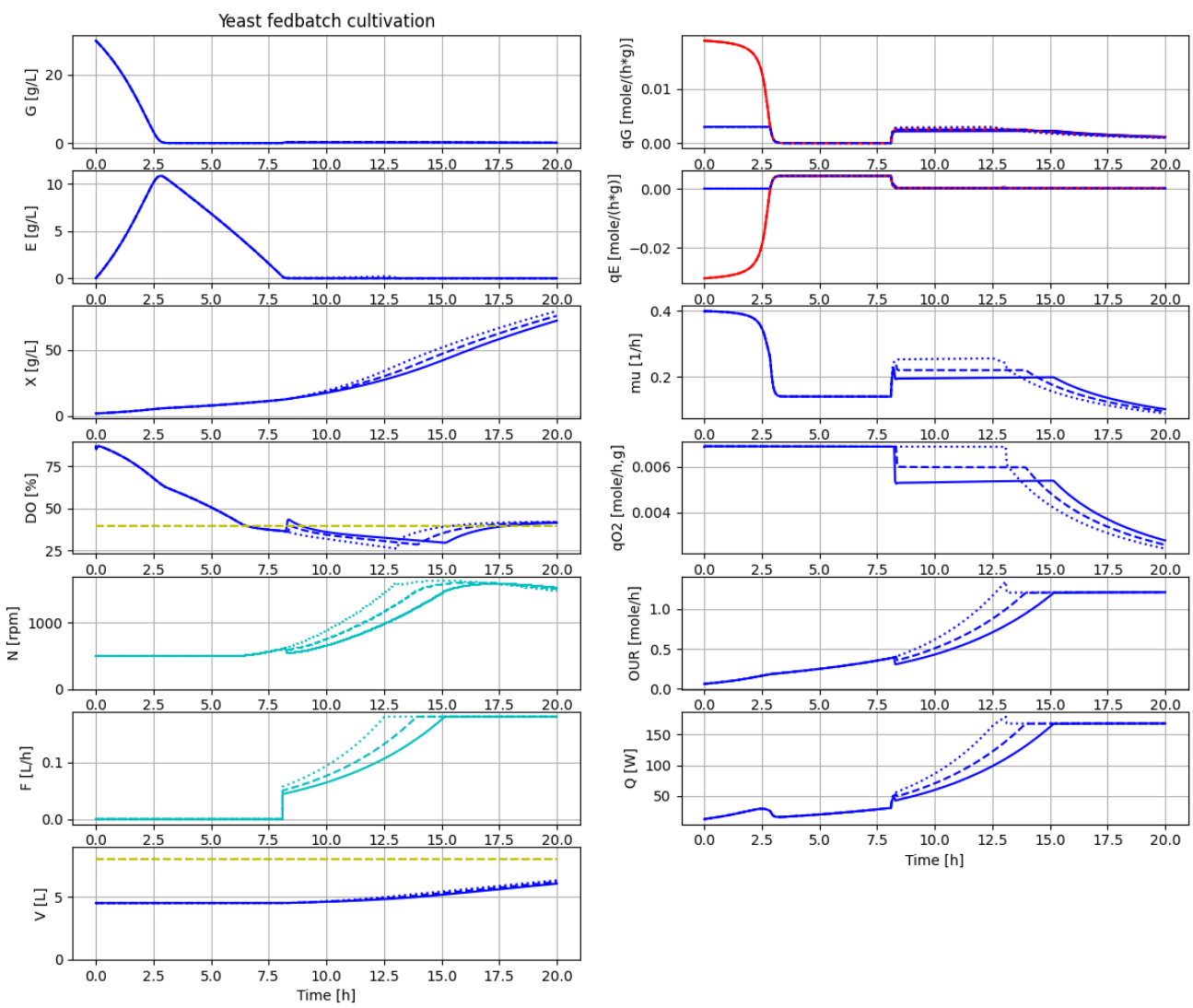
Now, let us focus on investigating impact of changes in the feed-profile. The goal is to increase the produced cell mass without accumulation of by-product ethanol. Simulation can bring some insight into how behaviour of the differen variables change when by-product is formed. This insight can help to interpret experimental results.

```
# Let us check the sensitivity to changes in the feed profile design
newplot(title='Yeast fedbatch cultivation', plotType='Overview')
for value in [0.044, 0.038, 0.050]: par(F_startExp=value); simu(20)
```

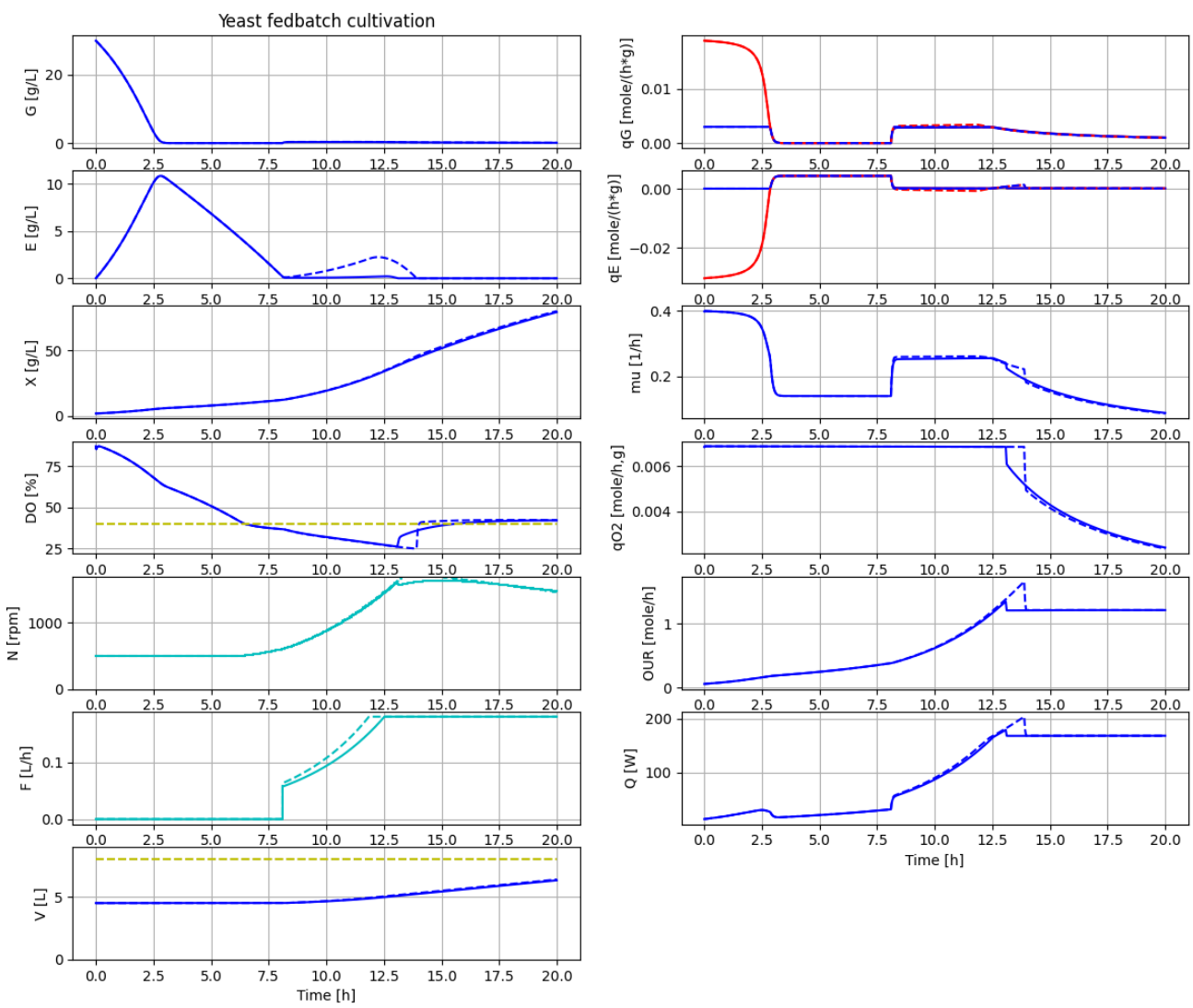


The variation in F_start has an impact and we see that the actual growth rate during fedbatch phase do converge to the set growth rate of the feed, but i takes more than 5 hours.

```
# Let us investigate a feedprofile that is closer to the maximal capacity
newplot(title='Yeast fedbatch cultivation', plotType='Overview')
par(F_startExp=0.044, mu_feed=0.20); simu(20)
par(F_startExp=0.050, mu_feed=0.22); simu(20)
par(F_startExp=0.057, mu_feed=0.26); simu(20)
```




```
# And let us see what happens if the feedprofile exceed the culture capacity
newplot(title='Yeast fedbatch cultivation', plotType='Overview')
par(F_startExp=0.057, mu_feed=0.26); simu(20)
par(F_startExp=0.063, mu_feed=0.28); simu(20)
par(F_startExp=0.044, mu_feed=0.20)
```



Note that with the feedprofile that exceed culture respiratory capacity, ethanol is accumulated during time 8-12.5 hours. When the feedprofile then is constant from time 12.5 hours and on, then the accumulated ethanol is consumed over about an hour. This leads to a higher oxygen demand and heat production during this time. The specific cell growth rate is also slightly higher during this period.

Exercise You can investiate the impact of changing the maximal feedrate F_max. Make sure that the DO level do not get too low.

Sensitivity to low dissolved oxygen levels

```
# Let us instead see what happens when the aeration read a limit in terms of stir
newplot(title='Yeast fedbatch cultivation', plotType='Overview'); ax22.set_ylim([
par(F_startExp=0.057, mu_feed=0.26); simu(20)
par(F_startExp=0.057, mu_feed=0.26, N_high=900); simu(20)
par(F_startExp=0.044, mu_feed=0.20, N_high=2000)
```