

BPL_YEAST_AIR_Fedbatch demo

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.

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 information 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 varying conditions can provide some process insight that can support the experimental 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 `ctrl-c` and `ctrl-p` as usual and edit the cell. When you 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!

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

- FNU - BPL_YEAST_AIR_Fedbatch_linux_jm_cs.fmu
- Setup-file - BPL_YEAST_AIR_Fedbatch_explore

Filter out DeprecationWarnings for 'np.float as alias' is needed - wish I could make filter more narrow

```
import warnings
warnings.filterwarnings("ignore")
```

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

```
%cd BPL_YEAST_AIR_Fedbatch
```

```
In [1]: run -i BPL_YEAST_AIR_Fedbatch_D0control_explore.py
```

```
Linux - run FMU pre-compiled 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 simulation
- describe() - describe culture, broth, parameters, variables with values / units
```

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()

```
In [2]: plt.rcParams['figure.figsize'] = [36/2.54, 30/2.54]
```

```
In [3]: describe('culture'); print(); describe('liquidphase'); print(); describe('gas
```

Saccharomyces cerevisiae - default parameters for strain H1022

Reactor broth substances included in the model

```
Cells index      = 1 - molecular weight = 24.6 Da
Glucose index    = 2 - molecular weight = 180.0 Da
Ethanol index    = 3 - molecular weight = 46.0 Da
Dissolved O2 index = 4 - molecular weight = 32.0 Da
Dissolved CO2 index = 5 - molecular weight = 44.0 Da
```

Reactor gasphase substances included in the model

```
N2 etc index = 1 - molecular weight = 28.0 Da
O2 index     = 2 - molecular weight = 32.0 Da
CO2 index    = 3 - molecular weight = 44.0 Da
Ethanol index = 4 - molecular weight = 46.0 Da
```

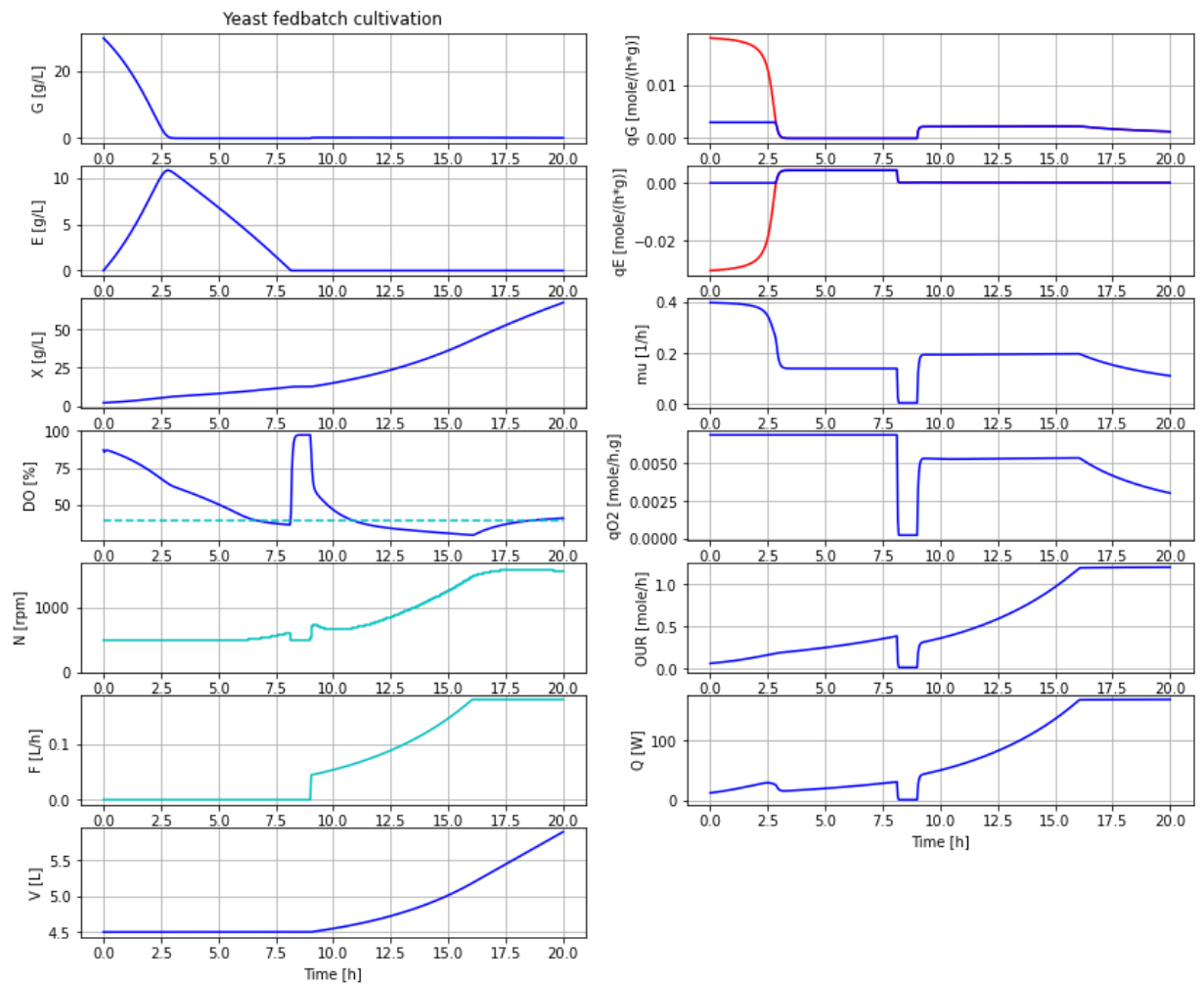
```
In [4]: # Culture parameters and others at default values
        par(q02lim=0.0069)

        # Process initial conditions
        init(V_0=4.5, VG_0=4.5*30, VX_0=4.5*2, VE_0=4.5*0)

        # Feed profile
        par(t_start=9, F_start=0.044, mu_feed=0.20, F_max=0.18)

        # DO-control parameters
        par(samplePeriod=1/60, K=10, Ti=0.5, I_0=500)

        # Simulate and plot
        newplot(title='Yeast fedbatch cultivation', plotType='Extended_2')
        simu(20)
```

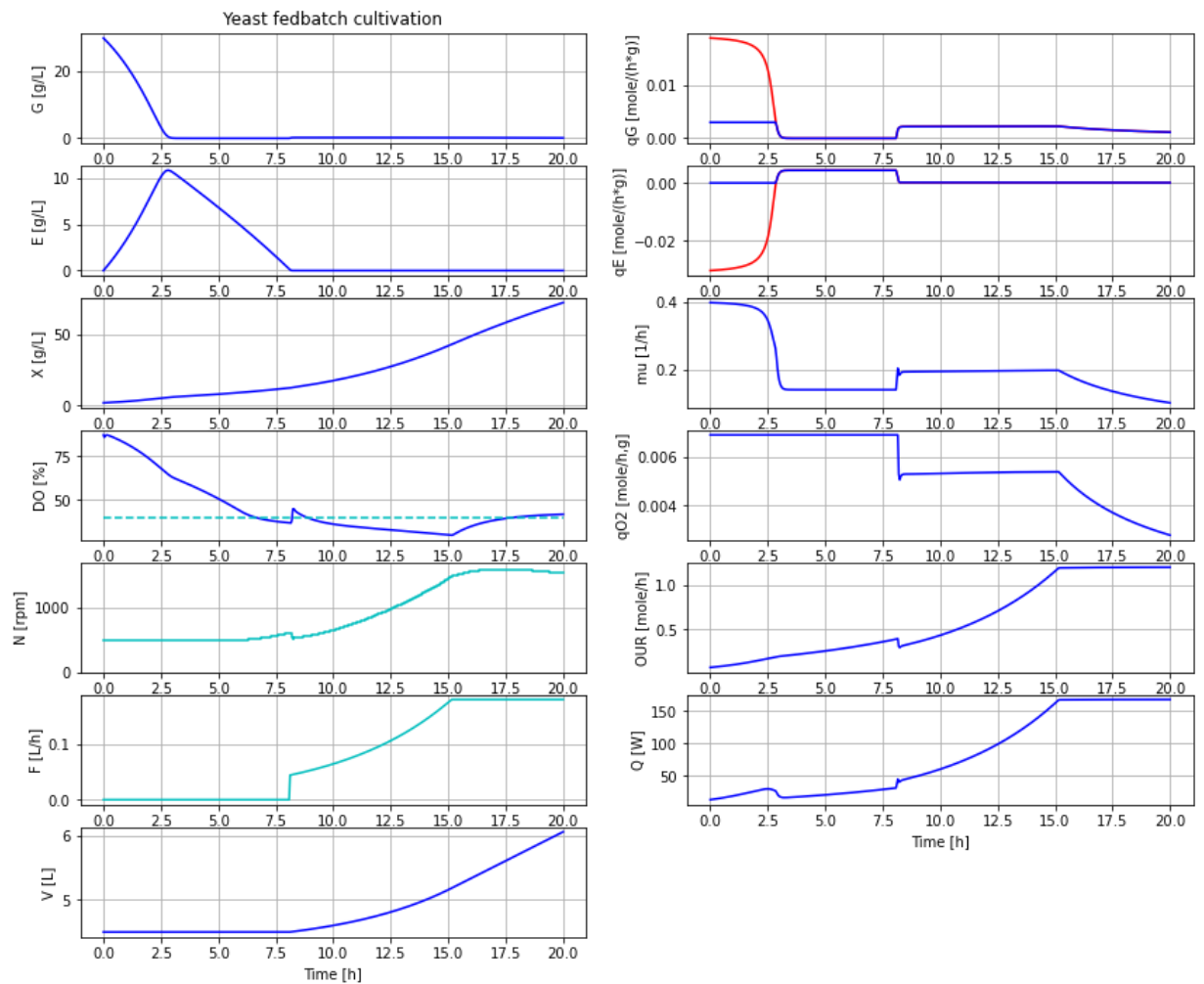


```
In [5]: disp('culture', decimals=4)
```

```
qGmax : 0.02
Ks : 0.01
qO2lim : 0.0069
```

```
In [6]: # Let us start the feeding just after the batch phase has ended and keep other
        par(t_start=8.1)

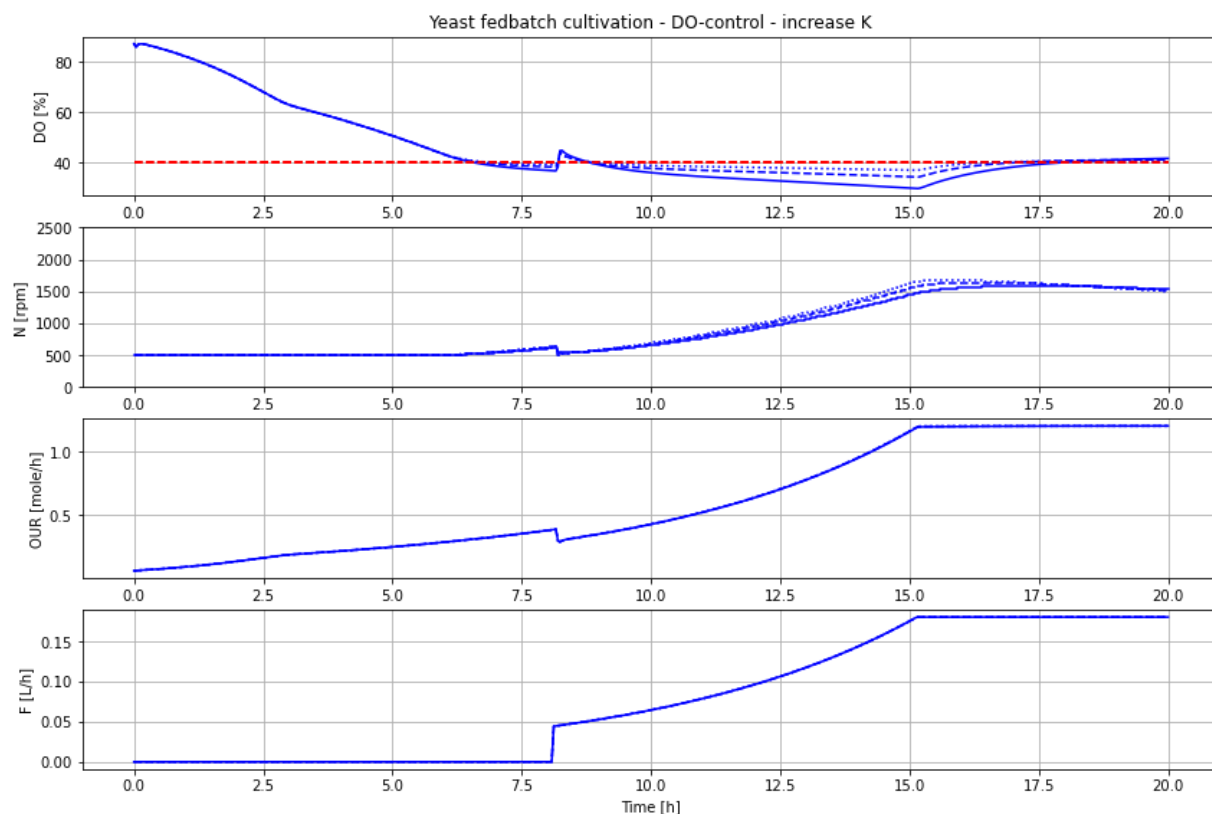
        # Simulate and plot
        newplot(title='Yeast fedbatch cultivation', plotType='Extended_2')
        simu(20)
```



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.

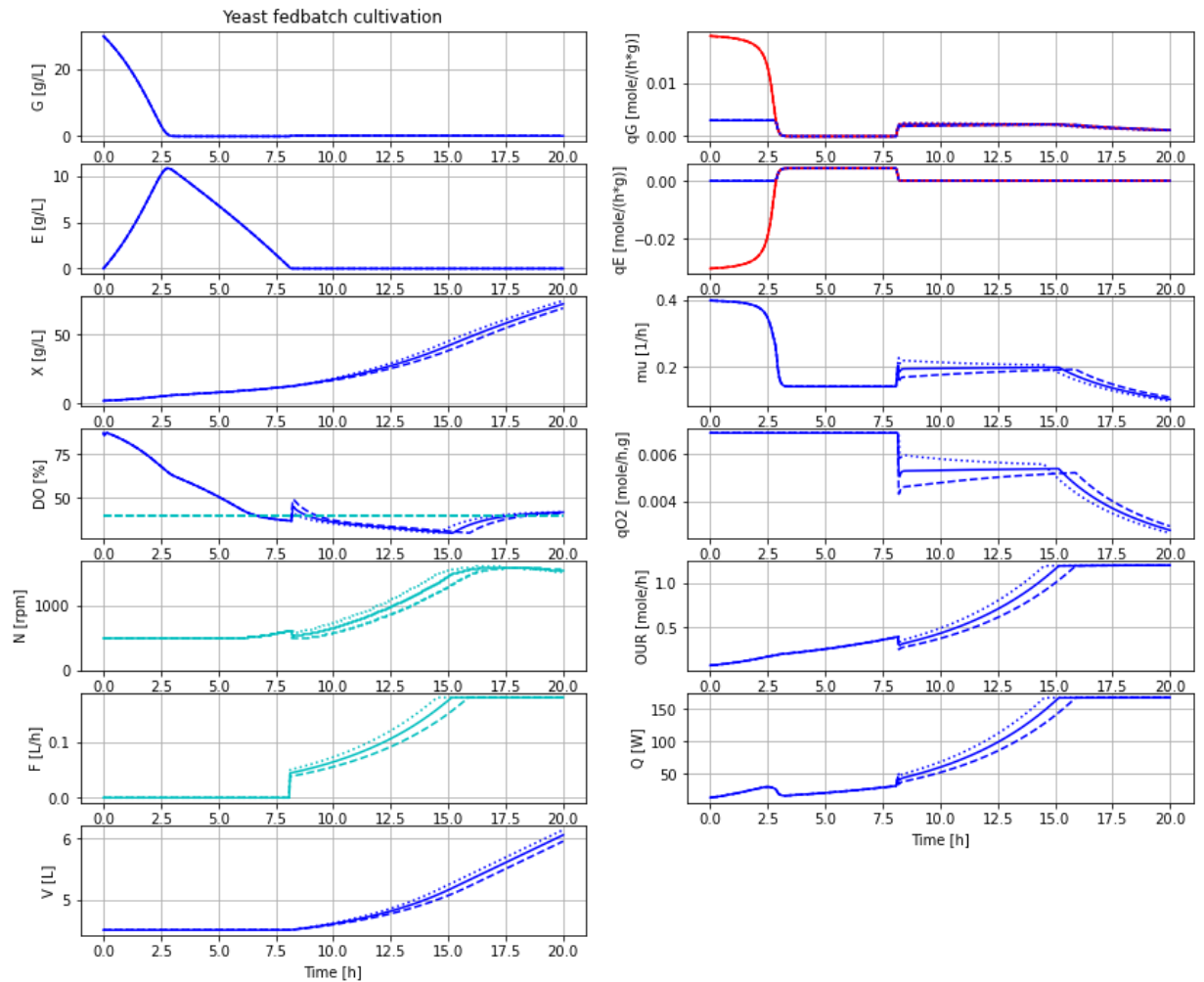
```
In [7]: # Let us take a closer look at the DO-control system and try to make control
newplot(title='Yeast fedbatch cultivation - DO-control - increase K', plotType='line')
for value in [10, 20, 40]: par(K=value); simu(20)

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



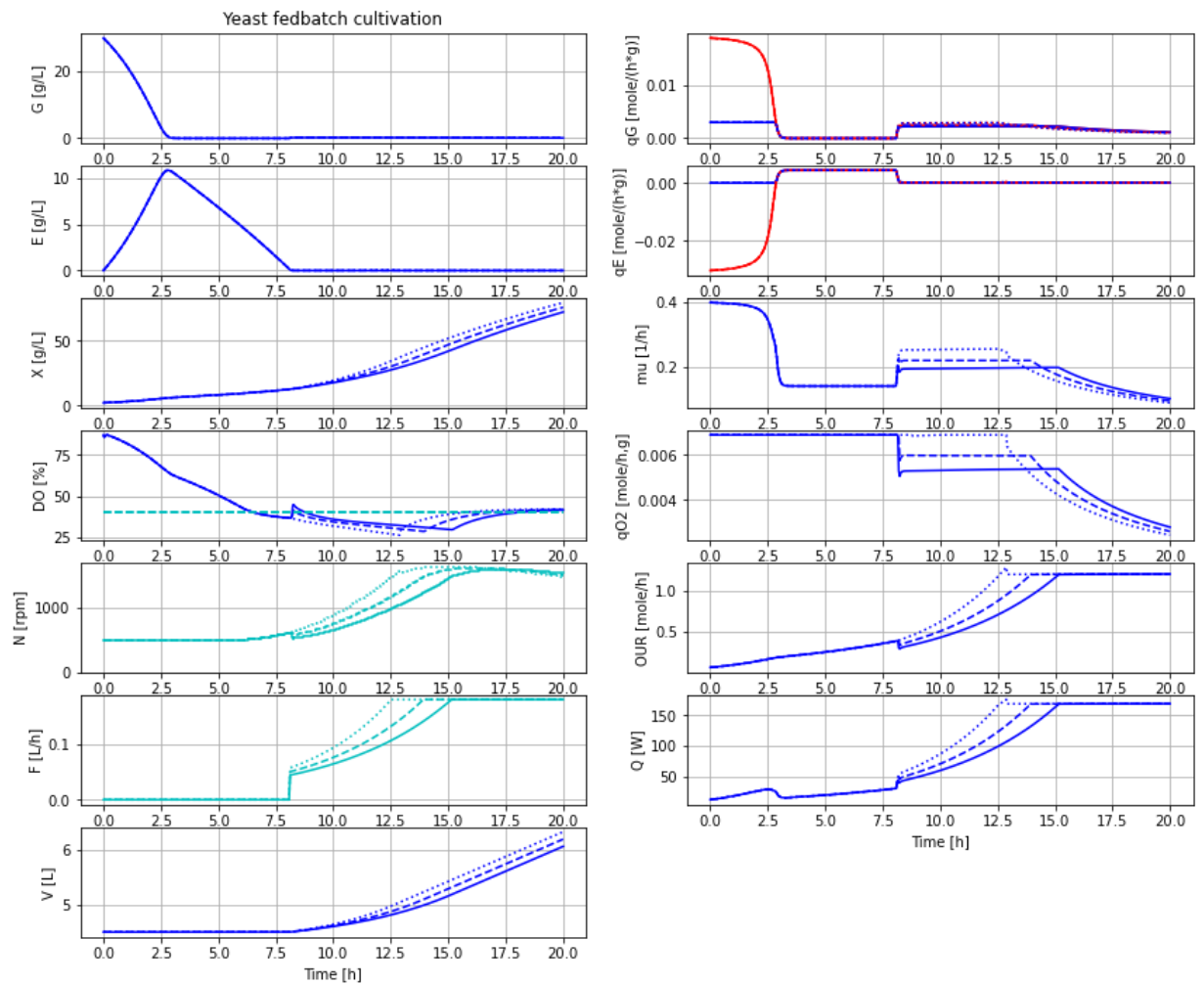
We see that by a higher control gain K the DO-control error get smaller and the stability of the control system is maintained.

```
In [8]: # Let us check the sensitivity to changes in the feed profile design
newplot(title='Yeast fedbatch cultivation', plotType='Extended_2')
for value in [0.044, 0.038, 0.050]: par(F_start=value); simu(20)
```

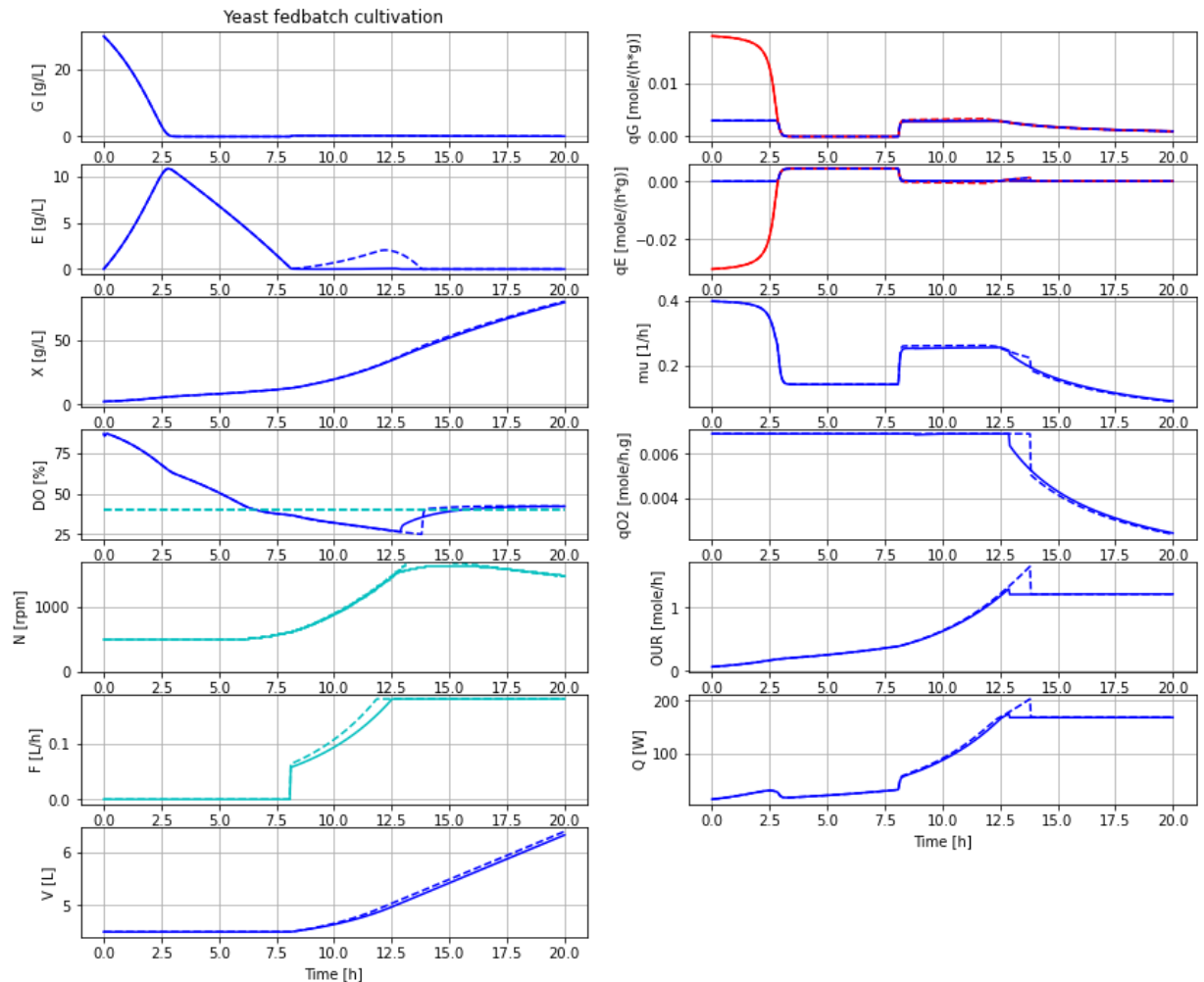


The variation in F_{start} has an impact and we see that the actual growth rate during fedbatch phase do converge to the set growth rate of the feed, but it takes more than 5 hours.

```
In [9]: # Let us investigate a feedprofile that is closer to the maximal capacity
newplot(title='Yeast fedbatch cultivation', plotType='Extended_2')
par(F_start=0.044, mu_feed=0.20); simu(20)
par(F_start=0.050, mu_feed=0.22); simu(20)
par(F_start=0.057, mu_feed=0.26); simu(20)
```



```
In [10]: # And let us see what happens if the feedprofile exceed the culture capacity
newplot(title='Yeast fedbatch cultivation', plotType='Extended_2')
par(F_start=0.057, mu_feed=0.26); simu(20)
par(F_start=0.063, mu_feed=0.28); simu(20)
par(F_start=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.

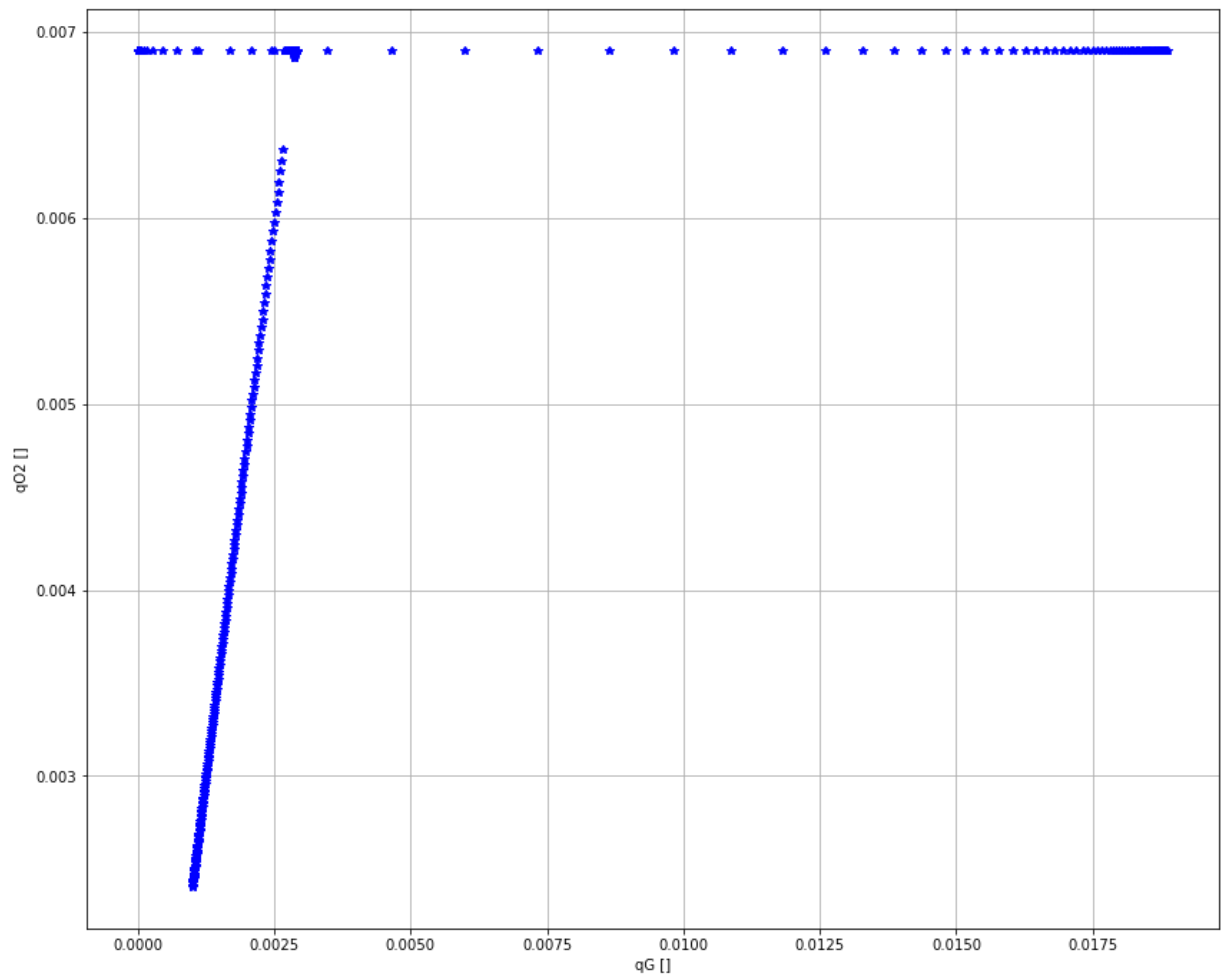
```
In [12]: # Improvise and make your own diagram - study the relation qO2 vs qG(G)

plt.figure()
ax1 = plt.subplot(1,1,1)
ax1.set_ylabel('qO2 [ ]')
ax1.set_xlabel('qG [ ]')
ax1.grid()

setLines()

diagrams.clear()
diagrams.append("ax1.plot(sim_res['bioreactor.culture.qGm'], sim_res['bioreac

par(F_start=0.057, mu_feed=0.26); simu(20)
simu(20)
```

In [14]: *# List of components in the process setup and also a couple of other things to describe('parts')*

```
['airFlow_setpoint', 'airtube', 'atmosphere', 'bioreactor', 'bioreactor.culture', 'bioreactor.gas_liquid_transfer', 'compressor', 'DO_setpoint', 'dosagescheme', 'DOSensor', 'feedtank', 'gasphase', 'liquidphase', 'MSL', 'N_high', 'N_low', 'PIreg', 'pump']
```

In [15]: `system_info()`

```
System information
-OS: Linux
-Python: 3.8.2
-PyFMI: 2.7.4
-FMU by: JModelica.org
-FMI: 2.0
-Type: FMUModelCS2
-Name: BPL_YEAST_AIR.Fedbatch_DOcontrol
-Generated: 2022-08-26T11:07:26
-MSL: 3.2.2 build 3
-Description: Bioprocess Library version 2.1.0 beta
-Interaction: FMU-explore ver 0.9.2
```

In []: