BPL_YEAST_AIR_Fedbatch demo

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

```
Windows - run FMU pre-compiled JModelica 2.14

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 [9]:
```
describe('culture'); print(); describe('liquidphase'); print(); describe('gasphase')
```

```
Saccharomyces cerevisae - 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 [5]:
```python
# Culture parameters and others at default values
par(qO2lim=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)
```
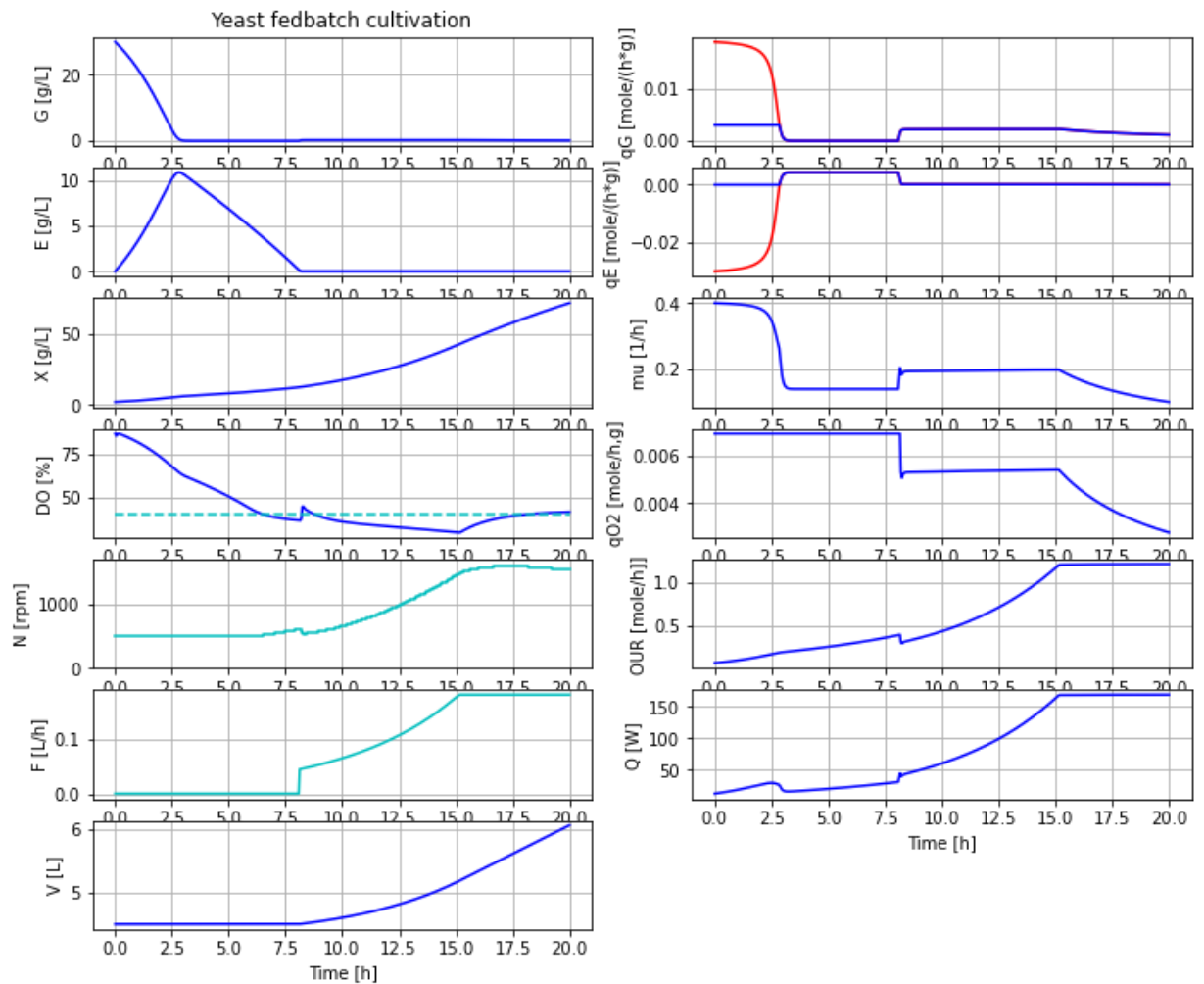
Yeast fedbatch cultivation
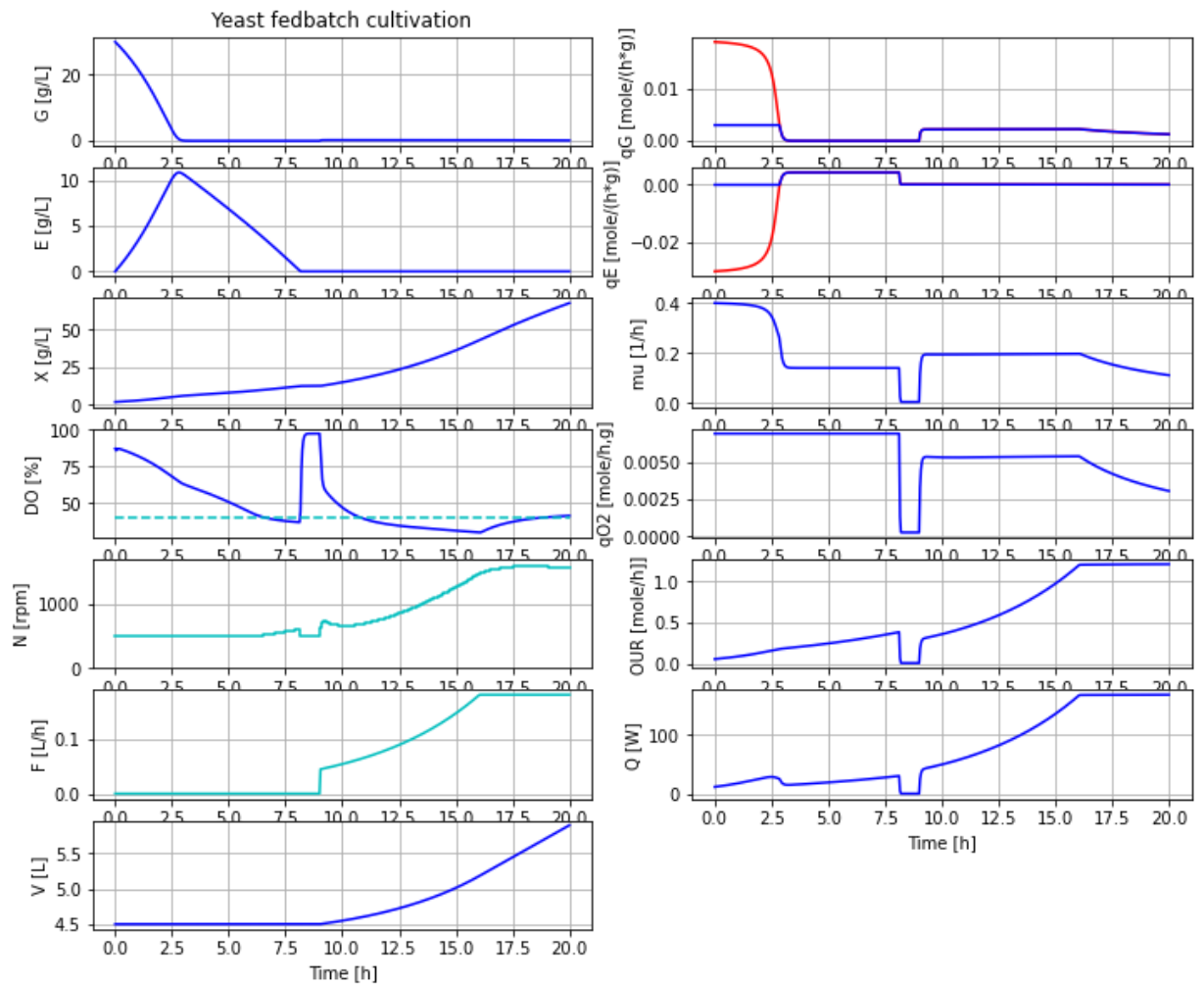
In [13]:
```
disp('culture', decimals=4)
```

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

In [17]:
```
# Let us start the feeding just after the batch phase has ended and keep other param
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 [20]:
```python
# 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)
```
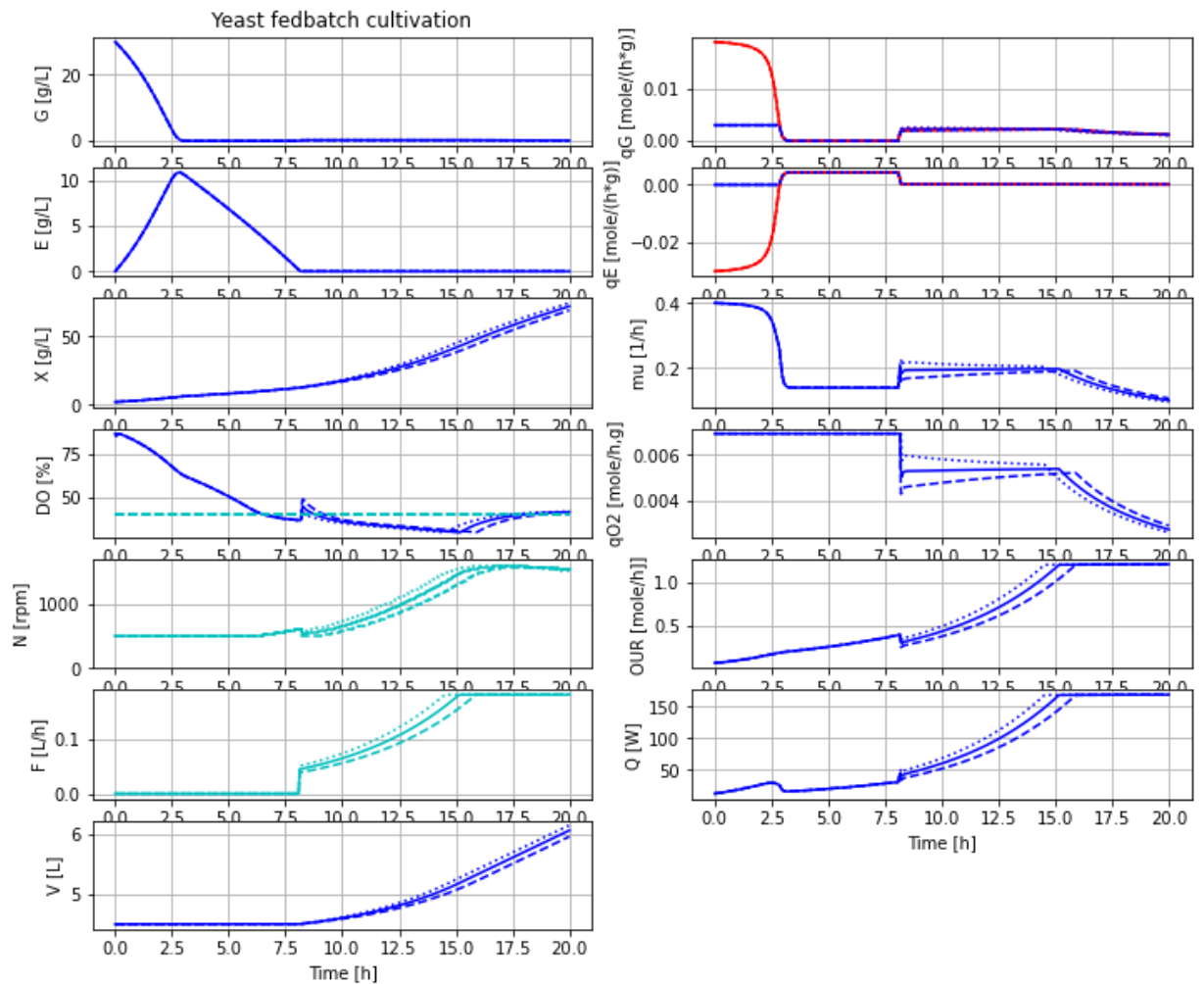
The variation in F_start has an impact and we see that the actual growth rate during fedbatch phase do converge to the set growth rate of the feed, but i takes more than 5 hours.

In [30]:
```python
# 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)
```

Yeast fedbatch cultivation
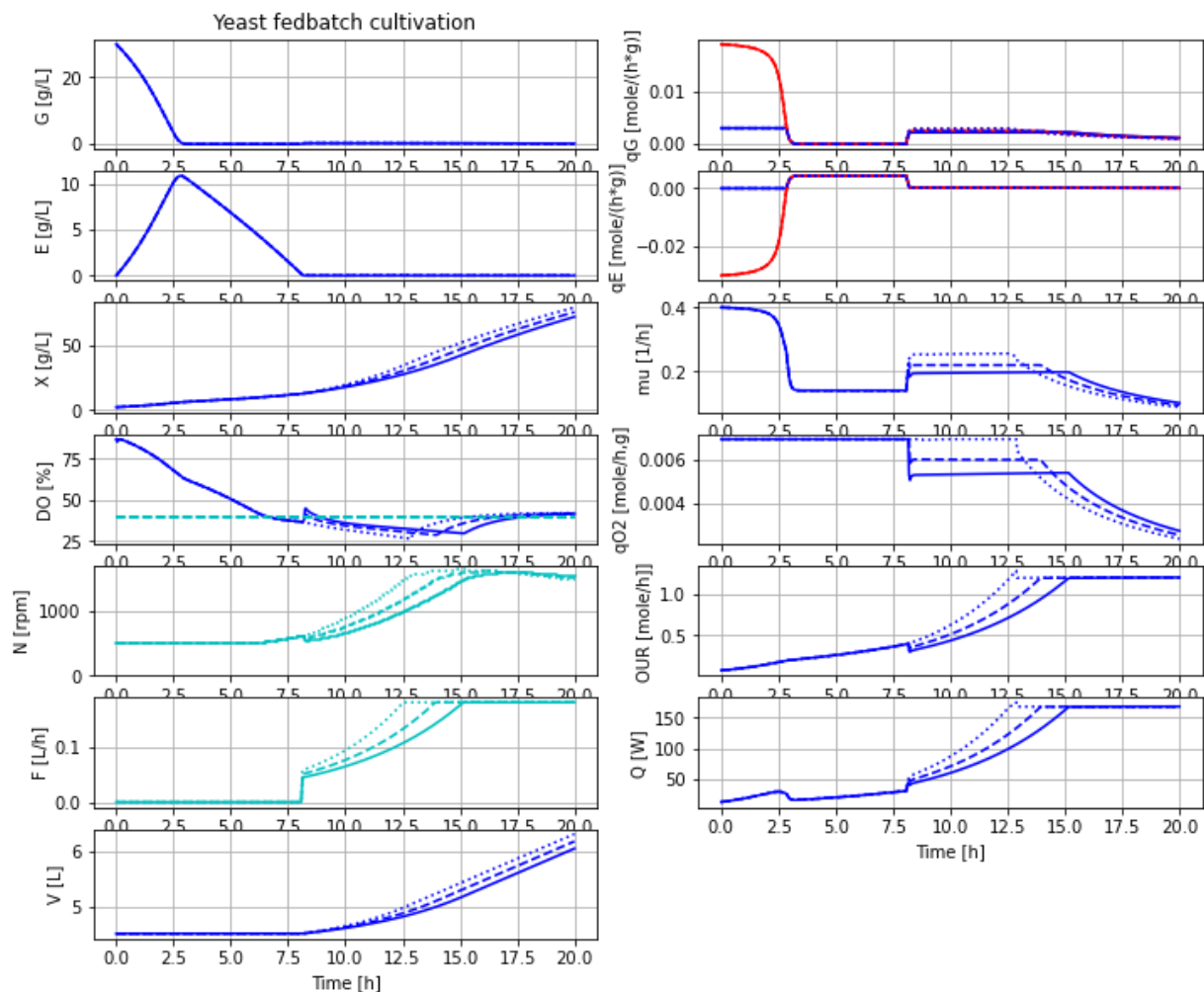
```
In [31]:    # And let us see what happens if the feedprofile exceed the culture capacity
            newplot(title='Yeast fedbatch cultivation', plotType='Extended_2')
            par(F_start=0.057, mu_feed=0.26); simu(20)
            par(F_start=0.063, mu_feed=0.28); simu(20)
```

Yeast fedbatch cultivation
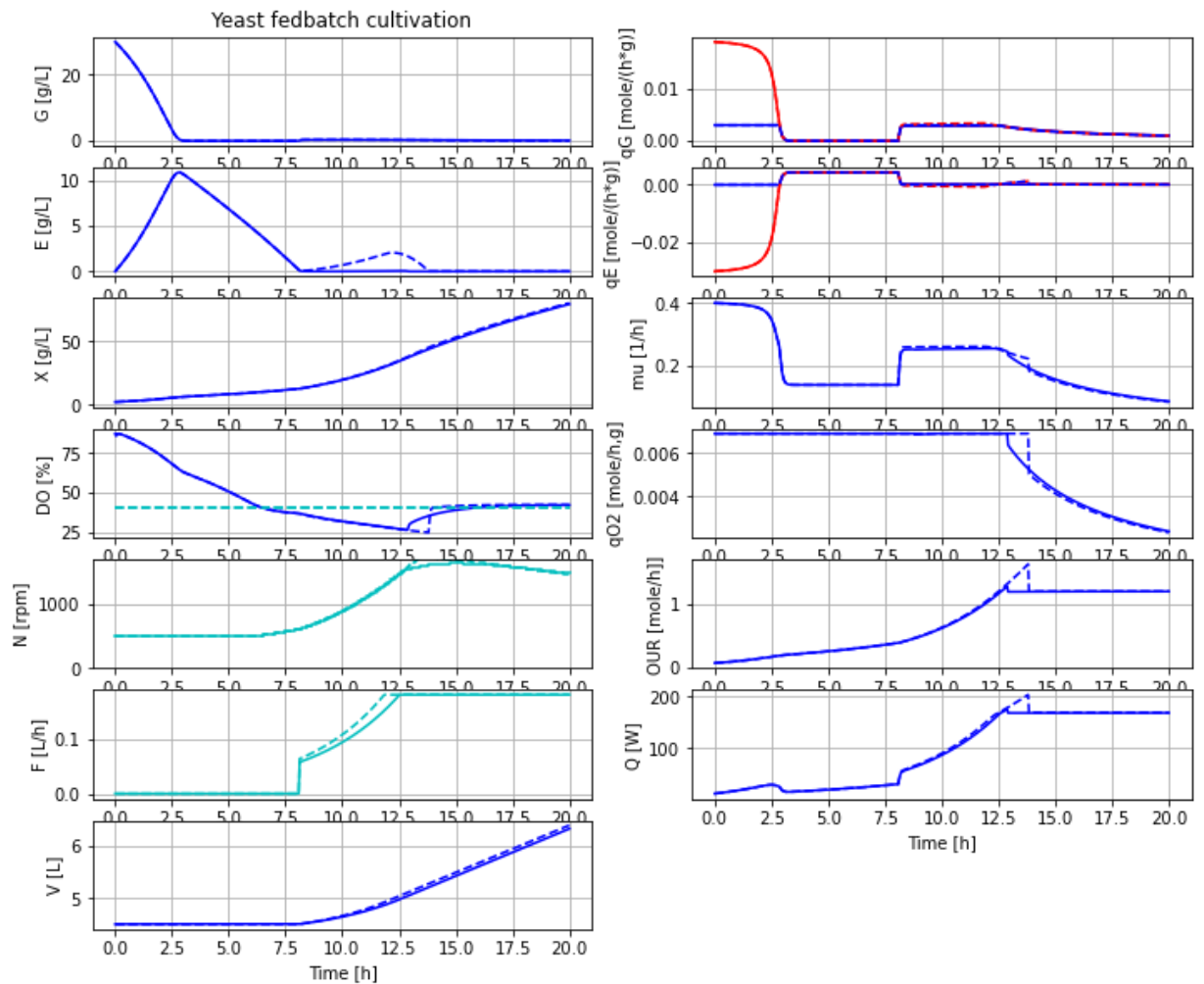
In [32]:

```
system_info()
```

```
System information
 -OS: Windows
 -Python: 3.9.5
 -PyFMI: 2.9.5
 -FMU by: JModelica.org
 -FMI: 2.0
 -Type: FMUModelCS2
 -Name: BPL_YEAST_AIR.Fedbatch_DOcontrol
 -Generated: 2022-08-19T11:13:22
 -MSL: 3.2.2 build 3
 -Description: Bioprocess Library version 2.1.0 beta
 -Interaction: FMU-explore ver 0.9.2
```

In [ ]: