

# BPL\_TEST2\_Chemostat - demo

In [1]: `run -i BPL_TEST2_Chemostat_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

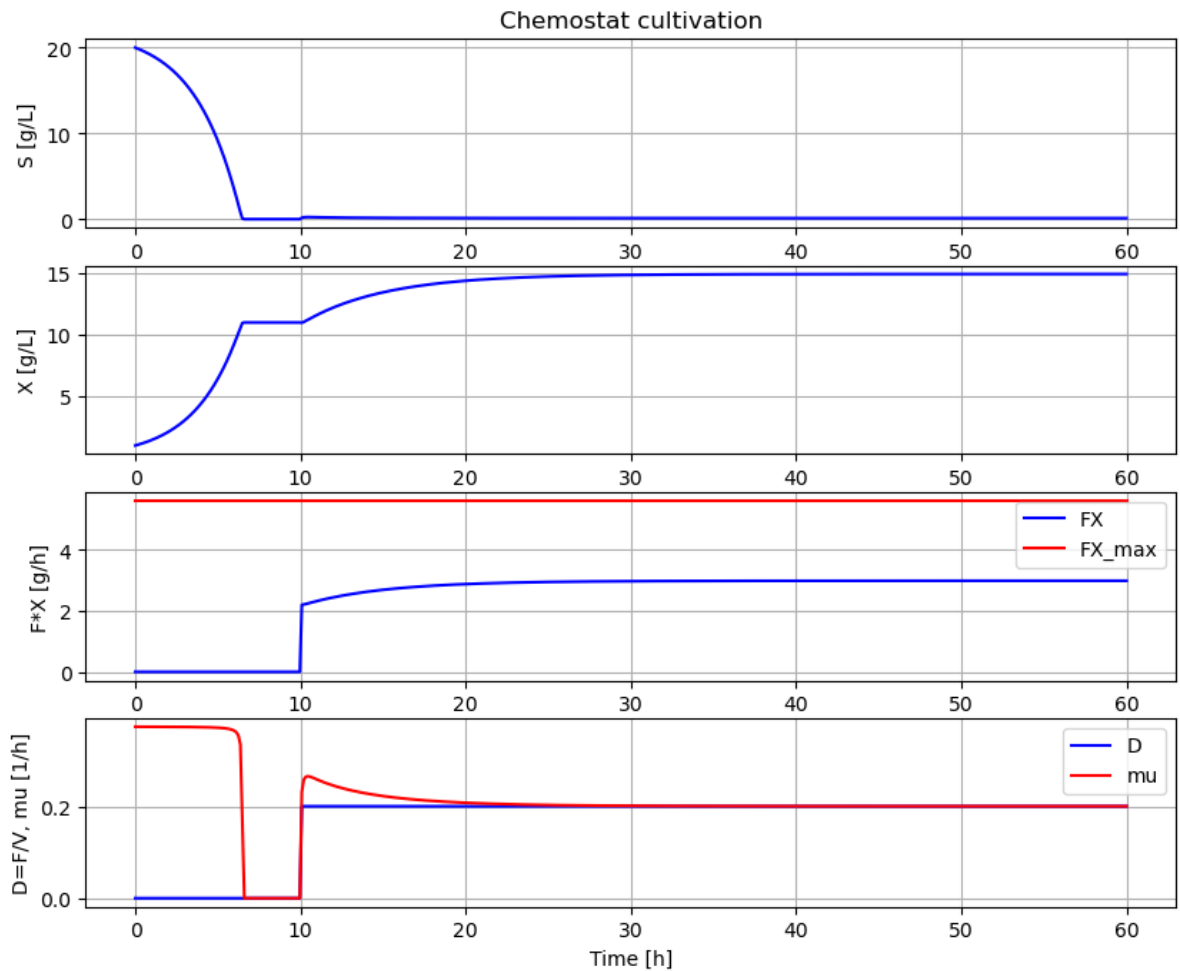
Note that both `disp()` and `describe()` takes values from the last simulation

Brief information about a command by `help()`, eg `help(simu)`

Key system information is listed with the command `system_info()`

In [2]: `%matplotlib inline`  
`plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]`

In [3]: `newplot()`  
`par(Y=0.50, qSmax=0.75, Ks=0.1) # Culture parameters`  
`init(V_0=1.0, VX_0=1.0, VS_0=20) # Bioreactor startup`  
`par(S_in=30, t0=0, F0=0, t1=10, F1=0.2) # Substrate feeding`  
`simu(60)`



```
In [4]: # The maximal biomass productivity FX_max [g/h] marked red in the diagram above
# can be calculated for CSTR from the FMU and is
cstrProdMax(model)
```

```
Out[4]: 5.625
```

```
In [5]: describe('cstrProdMax')
```

Calculate from the model maximal chemostat productivity  $FX_{max}$  : 5.625 [ g/h ]

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

```
Y : 0.5
qSmax : 0.75
Ks : 0.1
```

```
In [7]: describe('mu')
```

Cell specific growth rate variable : 0.2 [ 1/h ]

```
In [8]: describe('parts')
```

```
['bioreactor', 'bioreactor.culture', 'D', 'dosagescheme', 'feedtank', 'harvesttan
k', 'liquidphase', 'MSL']
```

```
In [9]: describe('MSL')
```

MSL: RealInput, RealOutput, CombiTimeTable, Types

```
In [10]: system_info()
```

## System information

- OS: Windows
- Python: 3.10.6
- Scipy: not installed in the notebook
- PyFMI: 2.9.8
- FMU by: JModelica.org
- FMI: 2.0
- Type: FMUModelCS2
- Name: BPL\_TEST2.Chemostat
- Generated: 2022-10-17T19:59:47
- MSL: 3.2.2 build 3
- Description: Bioprocess Library version 2.1.0
- Interaction: FMU-explore version 0.9.6e

In [ ]: