BPL_TEST2_Fedbatch - demo

In [1]:
```
run -i BPL_TEST2_Fedbatch_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()
```
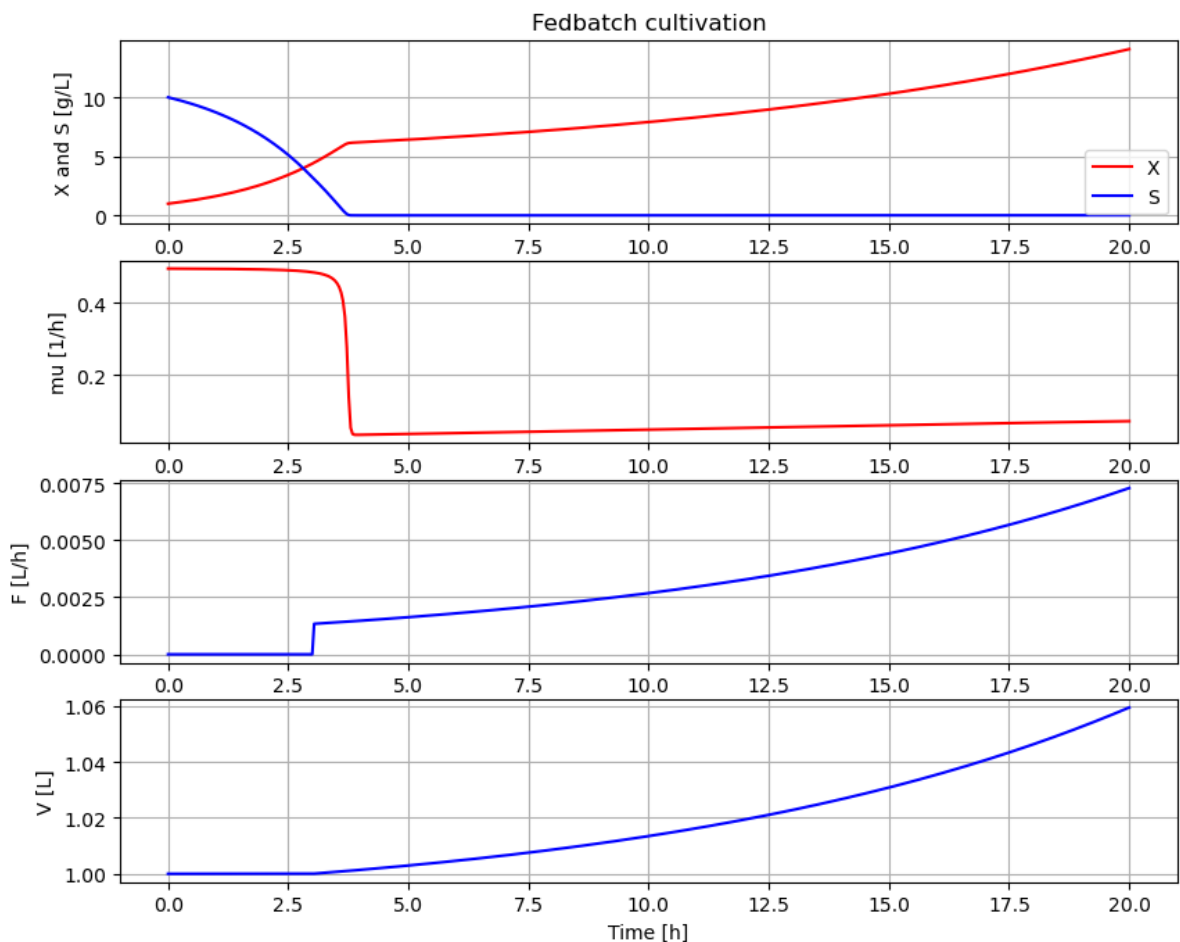
In [2]:
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

In [3]:
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)
```

```
In [4]: disp(mode='long')

        bioreactor.V_0 : V_0 : 1.0
        bioreactor.m_0[1] : VX_0 : 1.0
        bioreactor.m_0[2] : VS_0 : 10.0
        bioreactor.culture.Y : Y : 0.5
        bioreactor.culture.qSmax : qSmax : 1.0
        bioreactor.culture.Ks : Ks : 0.1
        feedtank.c_in[2] : feedtank.S_in : 300.0
        feedtank.V_0 : feedtank.V_0 : 10.0
        dosagescheme.mu_feed : mu_feed : 0.1
        dosagescheme.t_start : t_start : 3.0
        dosagescheme.F_start : F_start : 0.001
        dosagescheme.F_max : F_max : 0.3
```

```
In [5]: # A more typical feed scheme for the culture at hand
        newplot(plotType='TimeSeries')
        par(t_start=4, F_start=0.008, mu_feed=0.2, F_max=0.1)
        simu(20)
```


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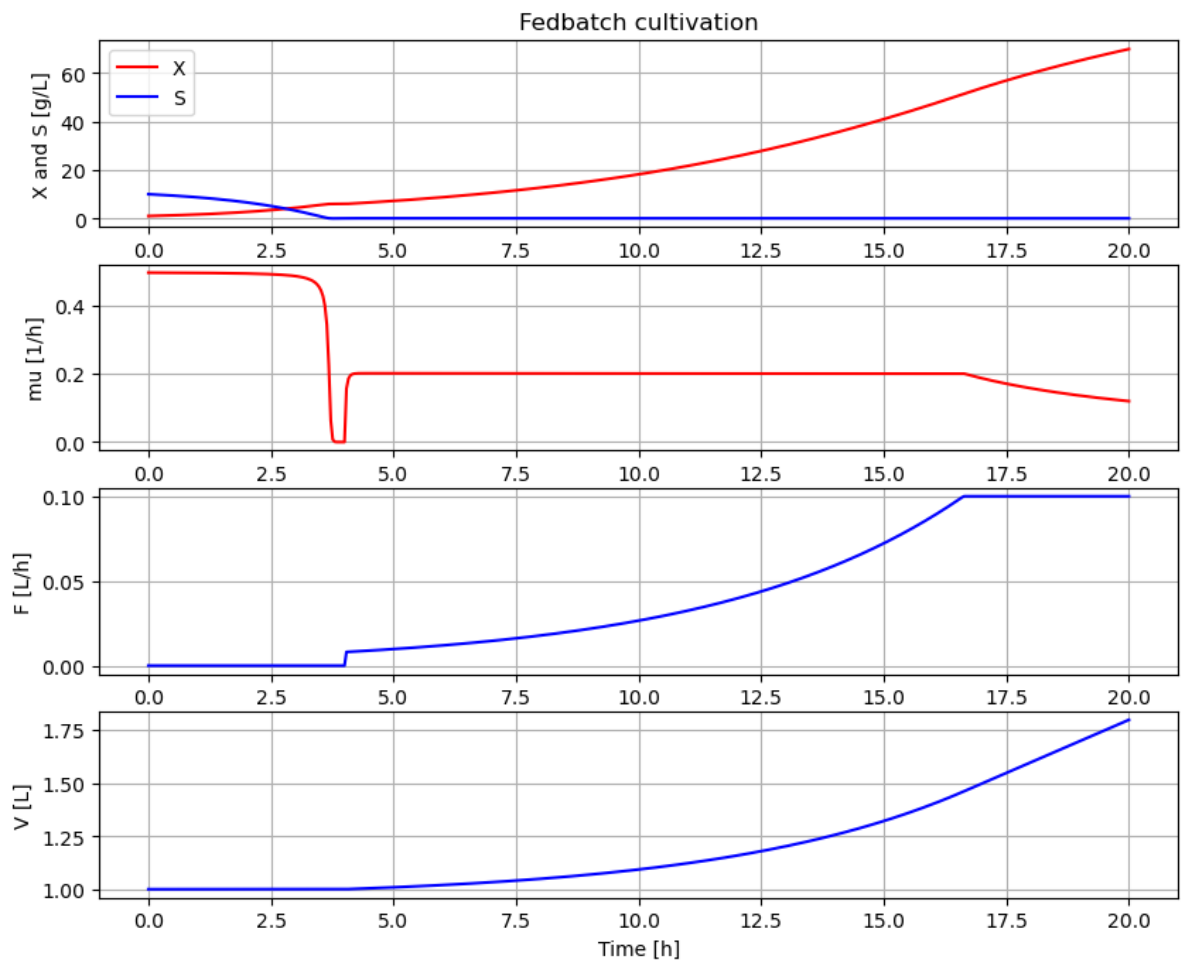
```
In [6]: disp('culture')

        Y : 0.5
        qSmax : 1.0
        Ks : 0.1
```

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

        Cell specific growth rate variable : 0.12 [ 1/h ]
```

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

```
['bioreactor', 'bioreactor.culture', 'dosagescheme', 'feedtank', 'liquidphase', 'M
SL']
```

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

```
MSL: RealInput, RealOutput
```

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.Fedbatch
 -Generated: 2022-10-17T13:04:04
 -MSL: 3.2.2 build 3
 -Description: Bioprocess Library version 2.1.0
 -Interaction: FMU-explore version 0.9.6
```

In [ ]: