BPL_TEST2_Fedbatch - demo

```
In [1]:  run -i BPL_TEST2_Fedbatch_fmpy_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/uni
ts

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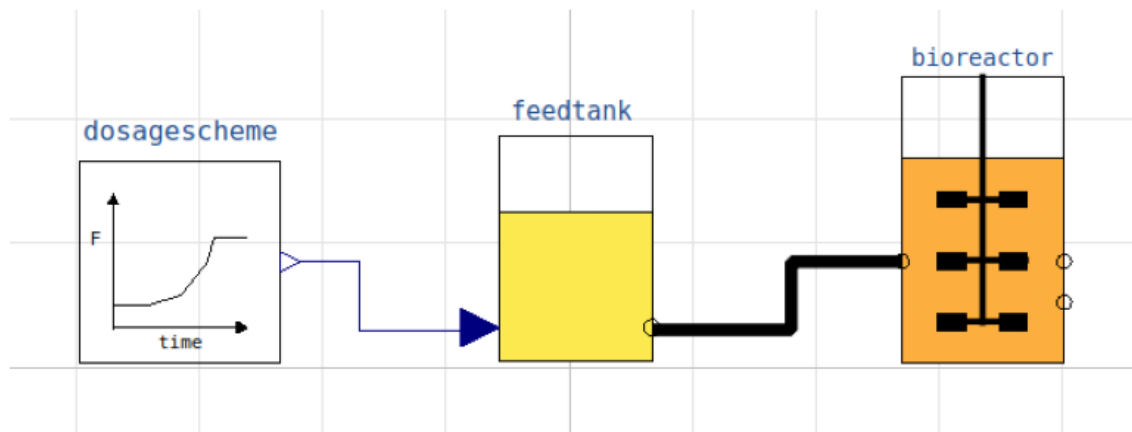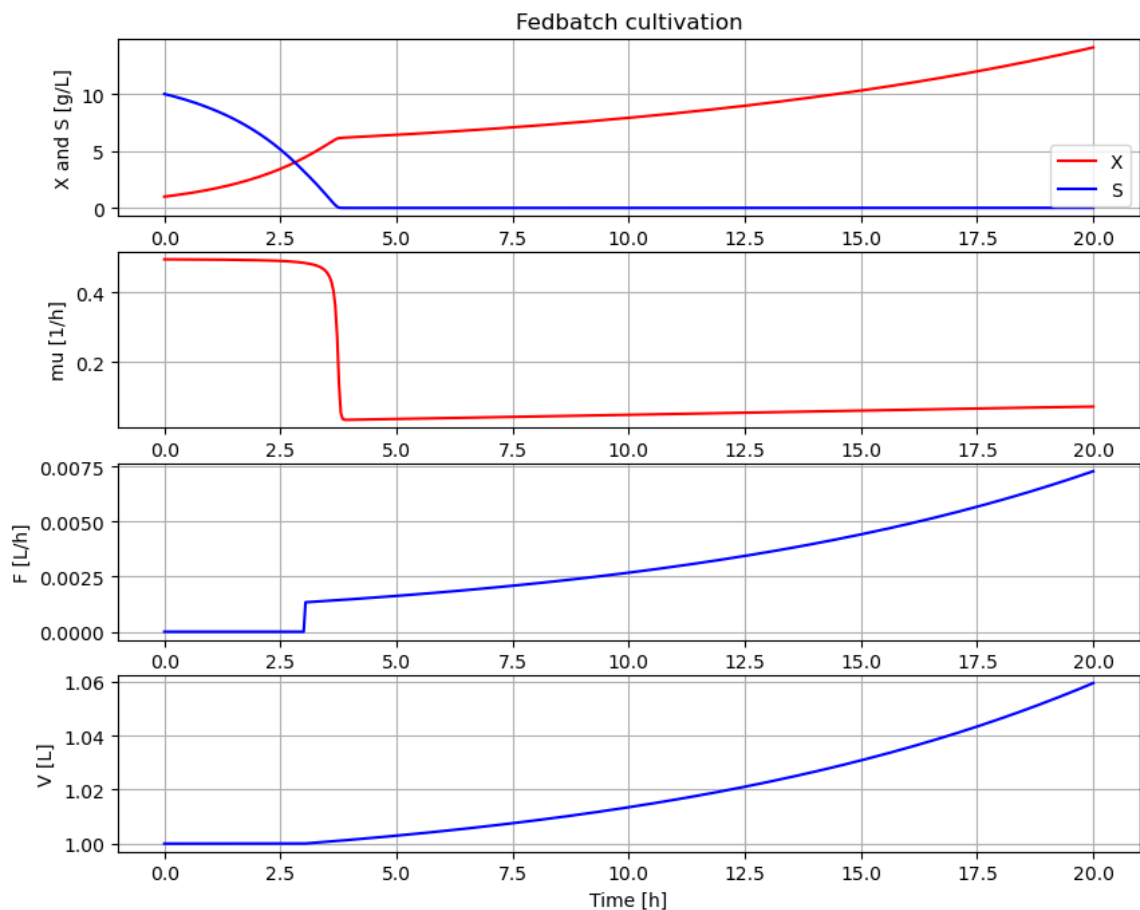
```
In [2]:  %matplotlib inline
         plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

```
In [3]:  process_diagram()
```



```
In [4]:  # Simulation with default values of the process
         newplot(plotType='TimeSeries')
         simu(20)
```

Fedbatch cultivation

```
In [5]:  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
```
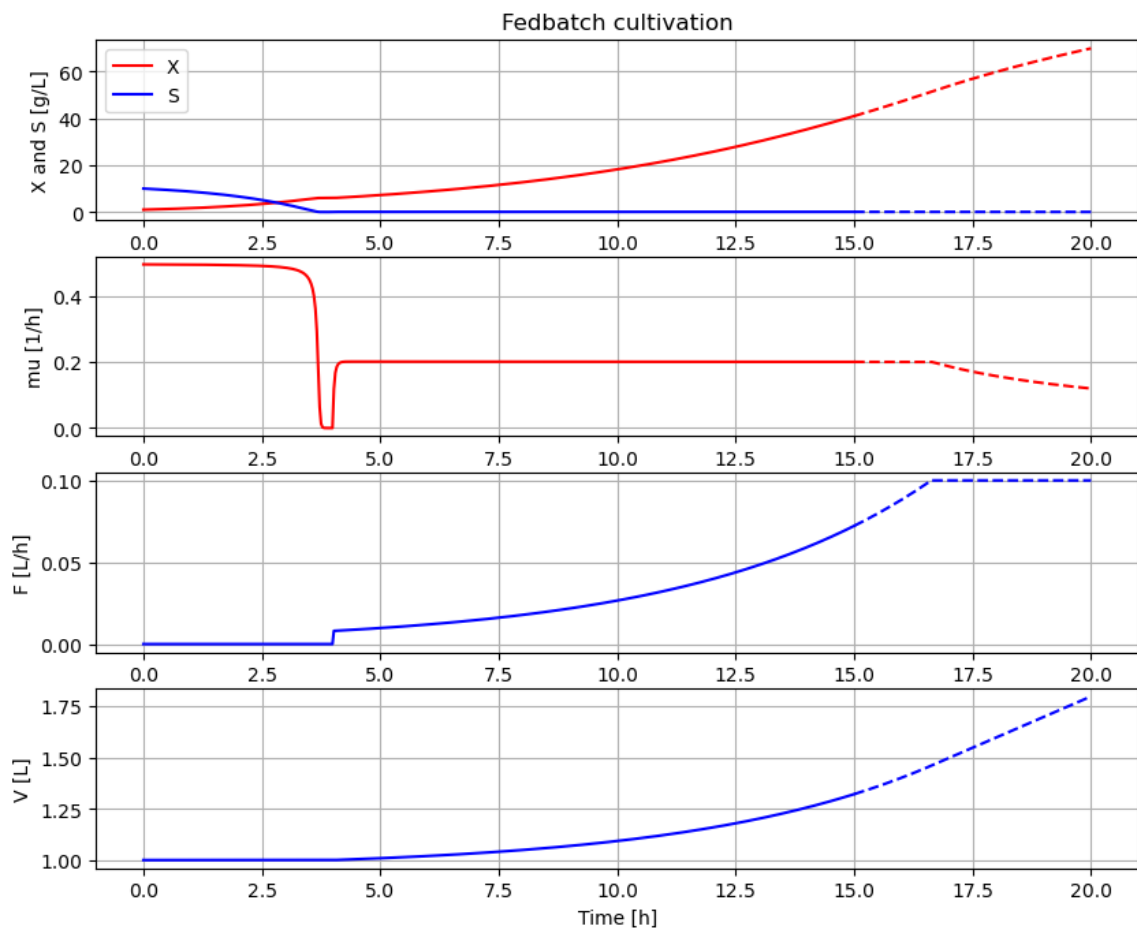
```
In [6]:  # A more typical feed scheme for the culture at hand
         newplot(plotType='TimeSeries')
         par(t_start=4, F_start=0.008, mu_feed=0.2, F_max=0.1)
         simu(20)
```

Fedbatch cultivation
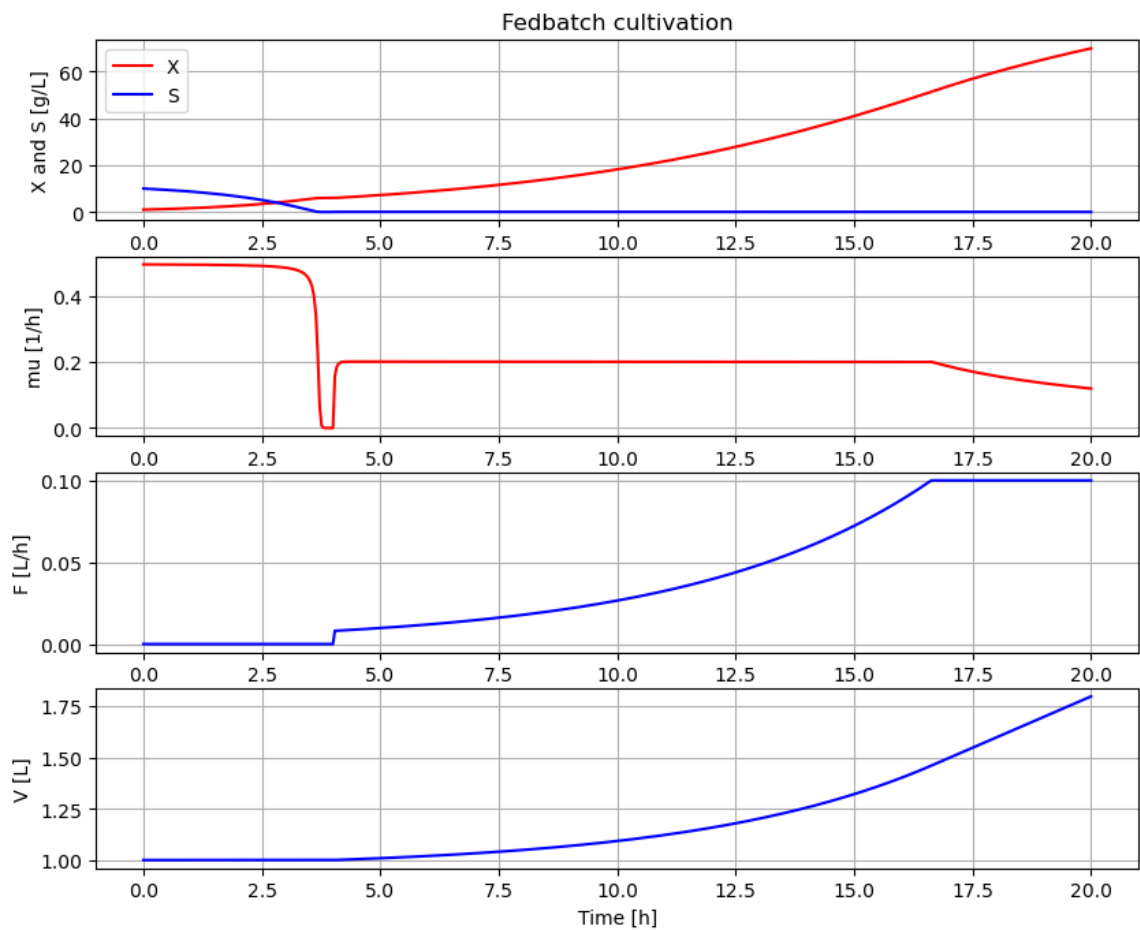
In [7]:
```
# Test function simu(mode='cont')
newplot()
simu(15)
simu(5,'cont')
```

Fedbatch cultivation

```
In [8]:  disp('culture')

         Y : 0.5
         qSmax : 1.0
         Ks : 0.1

In [9]:  disp('Y', mode='long')

         bioreactor.culture.Y : Y : 0.5

In [10]: describe('mu')

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

In [11]: describe('parts')

         ['bioreactor', 'bioreactor.culture', 'dosagescheme', 'feedtank', 'liquidphase',
         'MSL']

In [12]: describe('MSL')

         MSL: RealInput, RealOutput

In [13]: system_info()
```

```
System information
 -OS: Windows
 -Python: 3.9.16
 -Scipy: not installed in the notebook
 -FMPy: 0.3.15
 -FMU by: JModelica.org
 -FMI: 2.0
 -Type: CS
 -Name: BPL_TEST2.Fedbatch
 -Generated: 2023-03-30T09:13:00
 -MSL: 3.2.2 build 3
 -Description: Bioprocess Library version 2.1.1
 -Interaction: FMU-explore for FMPy version 0.9.8
```

In [ ]: