

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 / unit
- s

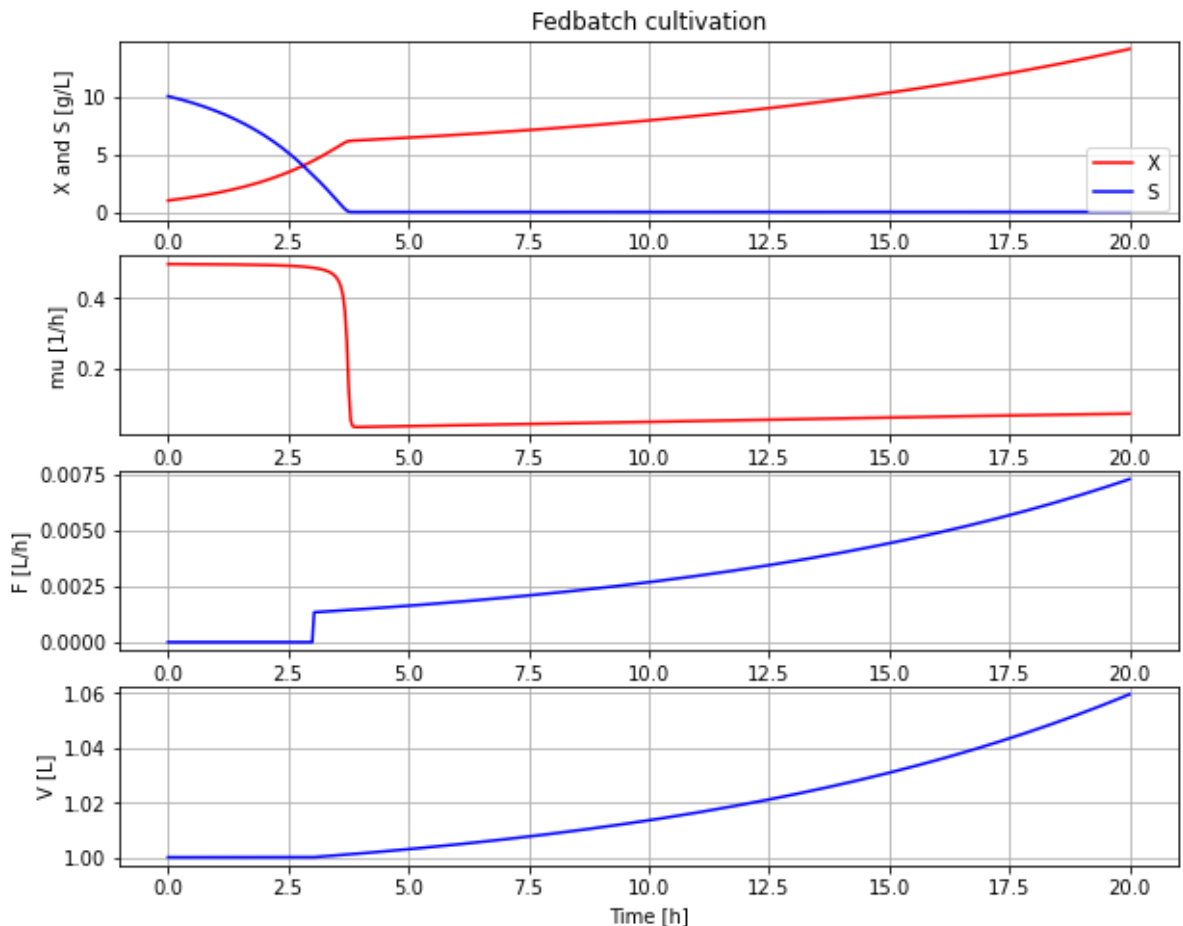
Note that both `disp()` and `describe()` takes values from the last simulation

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')`

```

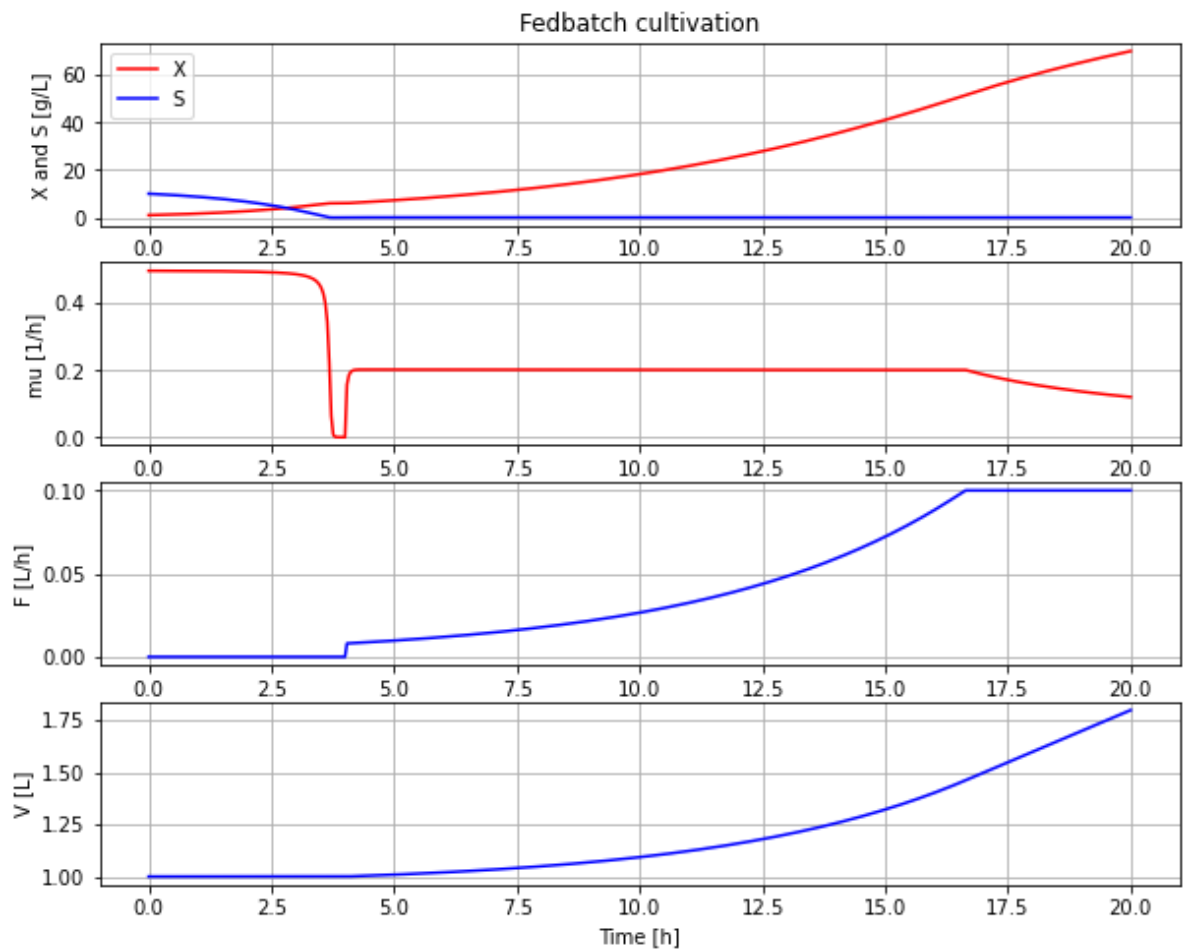
bioreactor.V_0 : V_0 : 1.0
bioreactor.m_0[1] : VX_0 : 1.0
bioreactor.m_0[2] : VS_0 : 10.0
bioreactor.culture.Y : Y : 0.5
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1
feedtank.c_in[2] : feedtank.S_in : 300.0
feedtank.V_0 : feedtank.V_0 : 10.0
dosagescheme.mu_feed : mu_feed : 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)

```



```

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: 3.2.2 build 3 - used components: RealInput, RealOutput

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

System information

- OS: Windows
- Python: 3.9.2
- 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 ver 0.9.5

```
In [ ]:
```