

BPL_TEST2_Fedbatch - demo

In [1]: `run -i BPL_TEST2_Fedbatch_explore.py`

Windows - run FMU pre-compiled JModelica 2.14

Model for the process 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 and the command `process_diagram()` brings up the main configuration

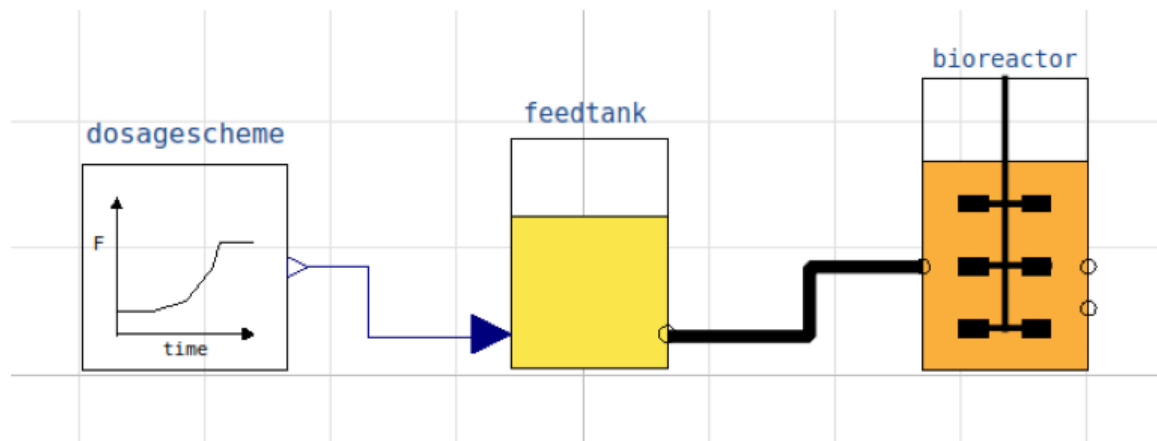
Brief information about a command by `help()`, eg `help(simu)`

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()`

No processDiagram.png file in the FMU, but try the file on disk.

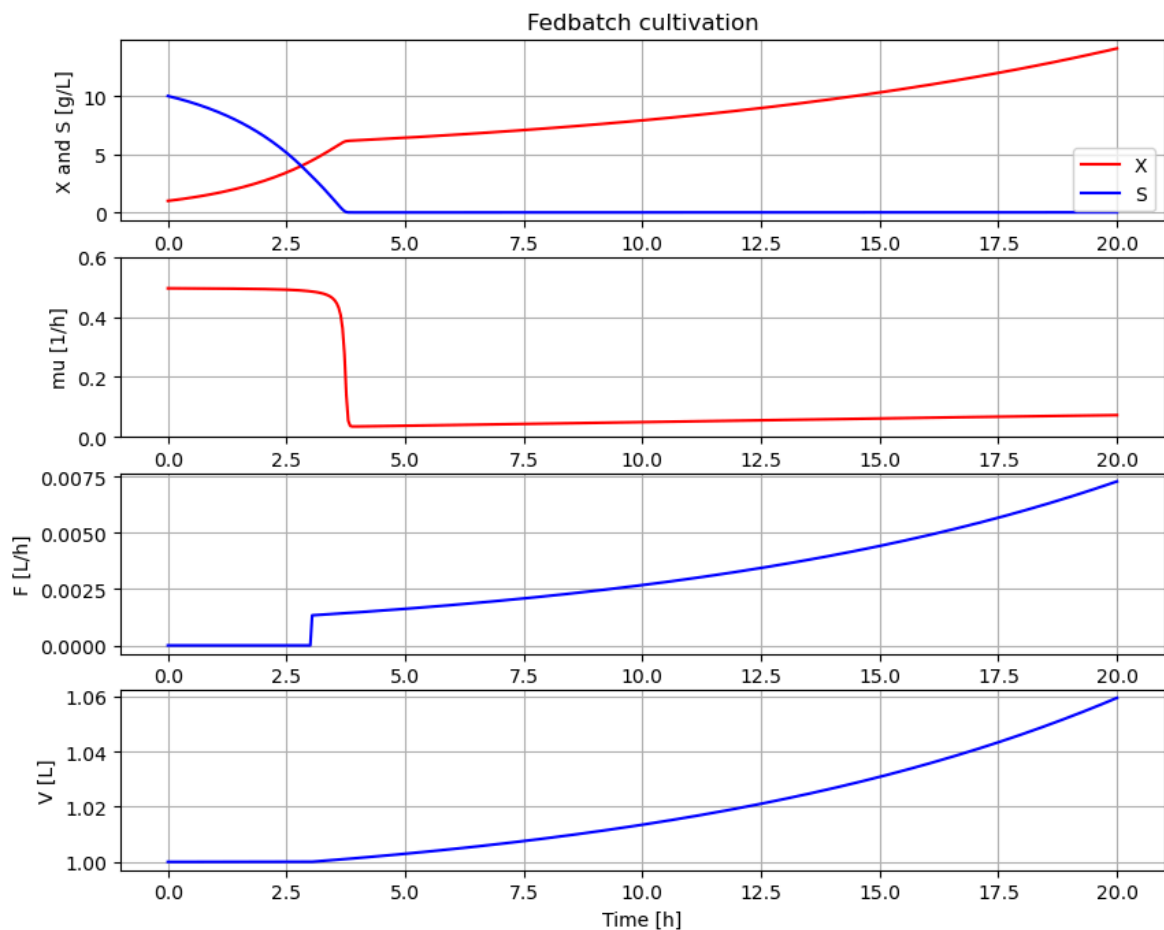


`disp('dosagescheme')`

In [4]: `#disp('feedtank')`

In [5]: `#disp('bioreactor', mode='Long')`

In [6]: `# Simulation with default values of the process`
`newplot(plotType='TimeSeries'); ax2.set_ylim(0,0.6)`
`simu(20)`



```
In [7]: # Let us display and then save the feedprofile
        disp('dosagescheme')
```

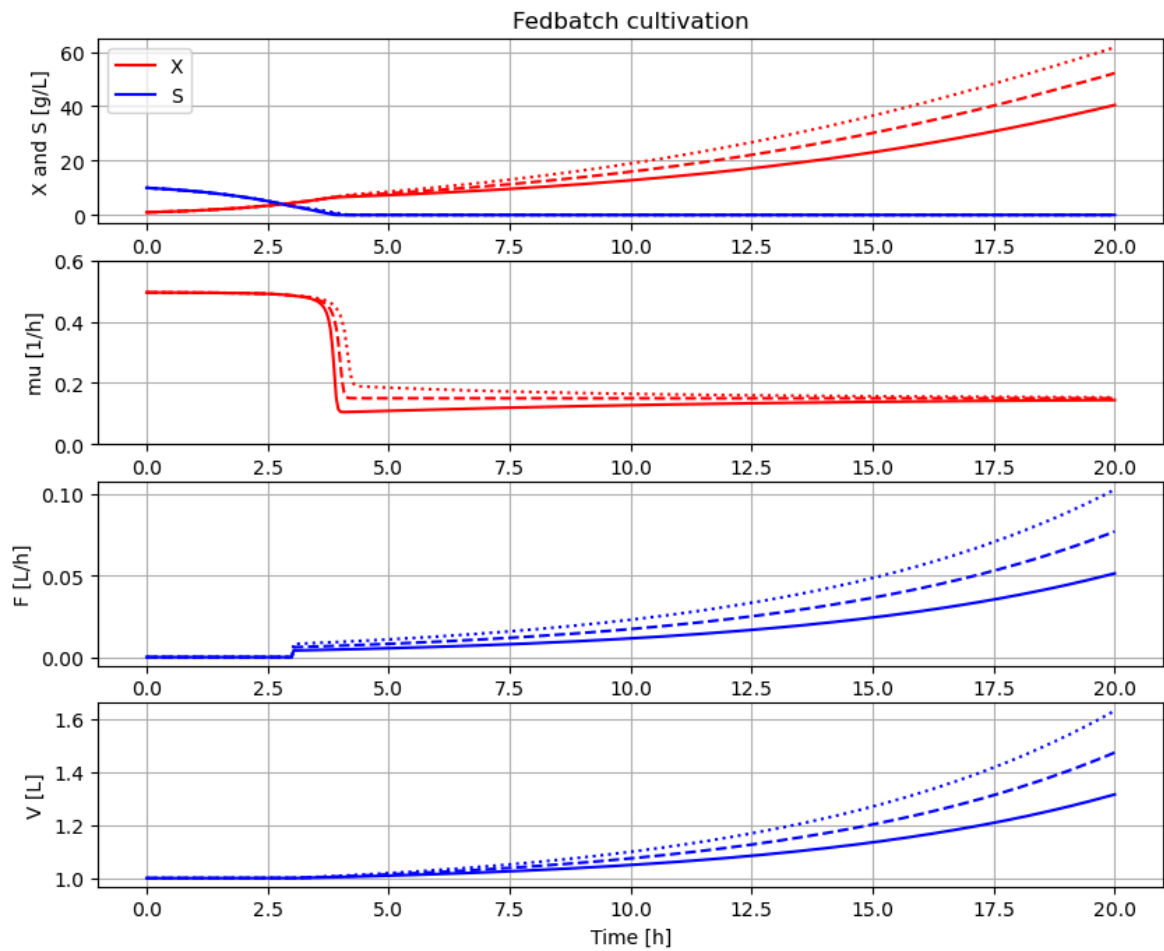
```
F_start : 0.0
mu_feed : 0.1
t_startExp : 3.0
F_startExp : 0.001
F_max : 0.3
```

```
In [8]: feedprofile_1={'F_start':0, 'mu_feed':0.1, 't_startExp':3, 'F_startExp':0.001, '
```

```
In [9]: # Let us develop a feedprofile with mu_feed=0.15 1/h instead
        newplot(plotType='TimeSeries'); ax2.set_ylim(0,0.6)

        # Choose mu_feed
        par(mu_feed=0.15)

        # Tune F_startExp value to get a stable culture growth rate at mu 0.15 1/h
        for value in [0.004, 0.006, 0.008]:
            par(F_startExp=value)
            simu(20)
```

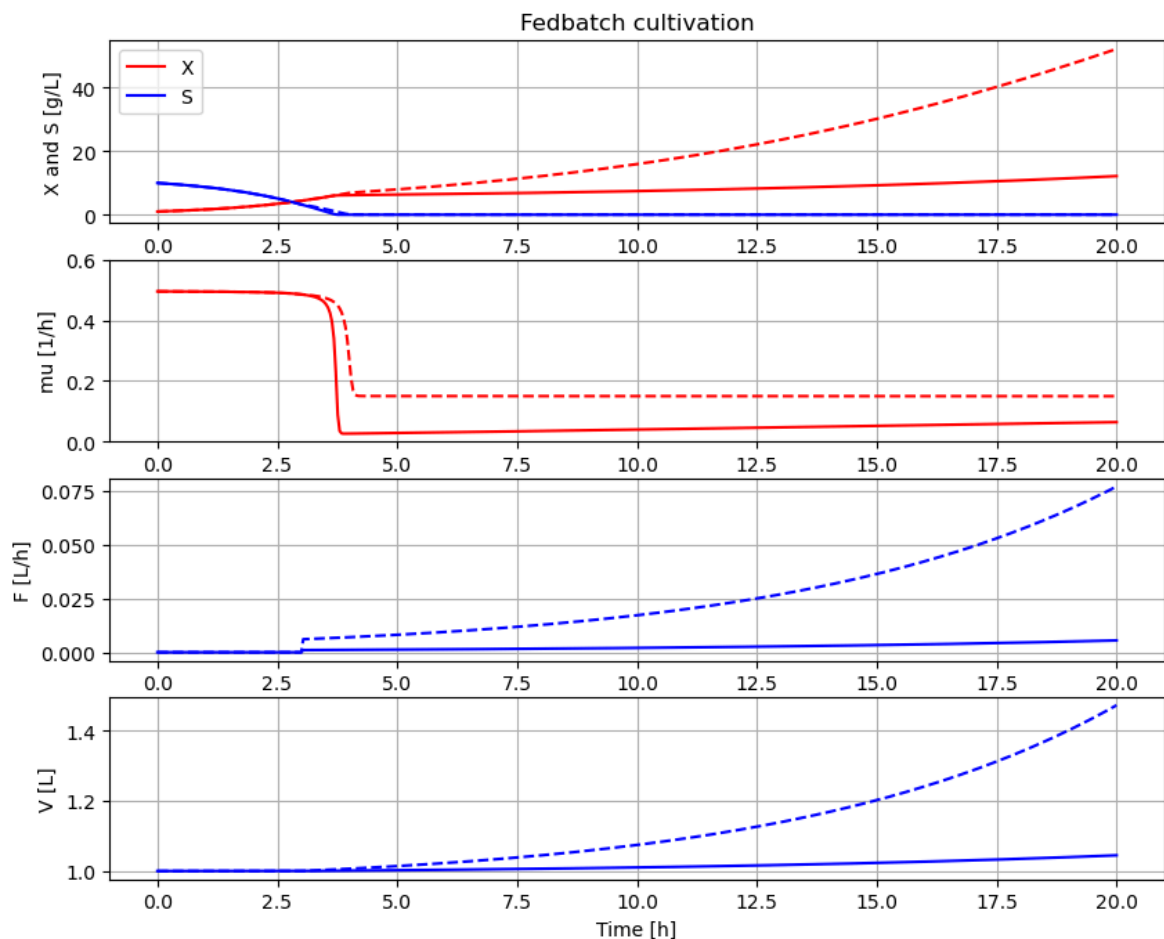


```
In [10]: # We choose F_startExp = 0.008 and save the new feedprofile
feedprofile_2={'F_start':0, 'mu_feed':0.15, 't_startExp':3, 'F_startExp':0.006,
```

```
In [11]: # Compare the result of ot the two
newplot(plotType='TimeSeries'); ax2.set_ylim(0,0.6)

for feedprofile in [feedprofile_1, feedprofile_2]:
    par(feedprofile)
    simu(20)

# Restore the original feedprofile
par(feedprofile_2)
```



```
In [12]: describe('mu')
```

Cell specific growth rate variable : 0.15 [1/h]

```
In [13]: describe('parts')
```

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

```
In [14]: describe('MSL')
```

MSL: RealInput, RealOutput

```
In [15]: system_info()
```

System information

- OS: Windows
- Python: 3.12.11
- Scipy: not installed in the notebook
- PyFMI: 2.20.0
- FMU by: JModelica.org
- FMI: 2.0
- Type: FMUModelCS2
- Name: BPL.Examples_TEST2.Fedbatch
- Generated: 2025-07-26T09:38:43
- MSL: 3.2.2 build 3
- Description: Bioprocess Library version 2.3.1
- Interaction: FMU-explore version 1.0.2

```
In [16]: !lsb_release -a
```

'lsb_release' is not recognized as an internal or external command, operable program or batch file.

In []: