

BPL_TEST2_Batch - demo

In [1]: `run -i BPL_TEST2_Batch_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

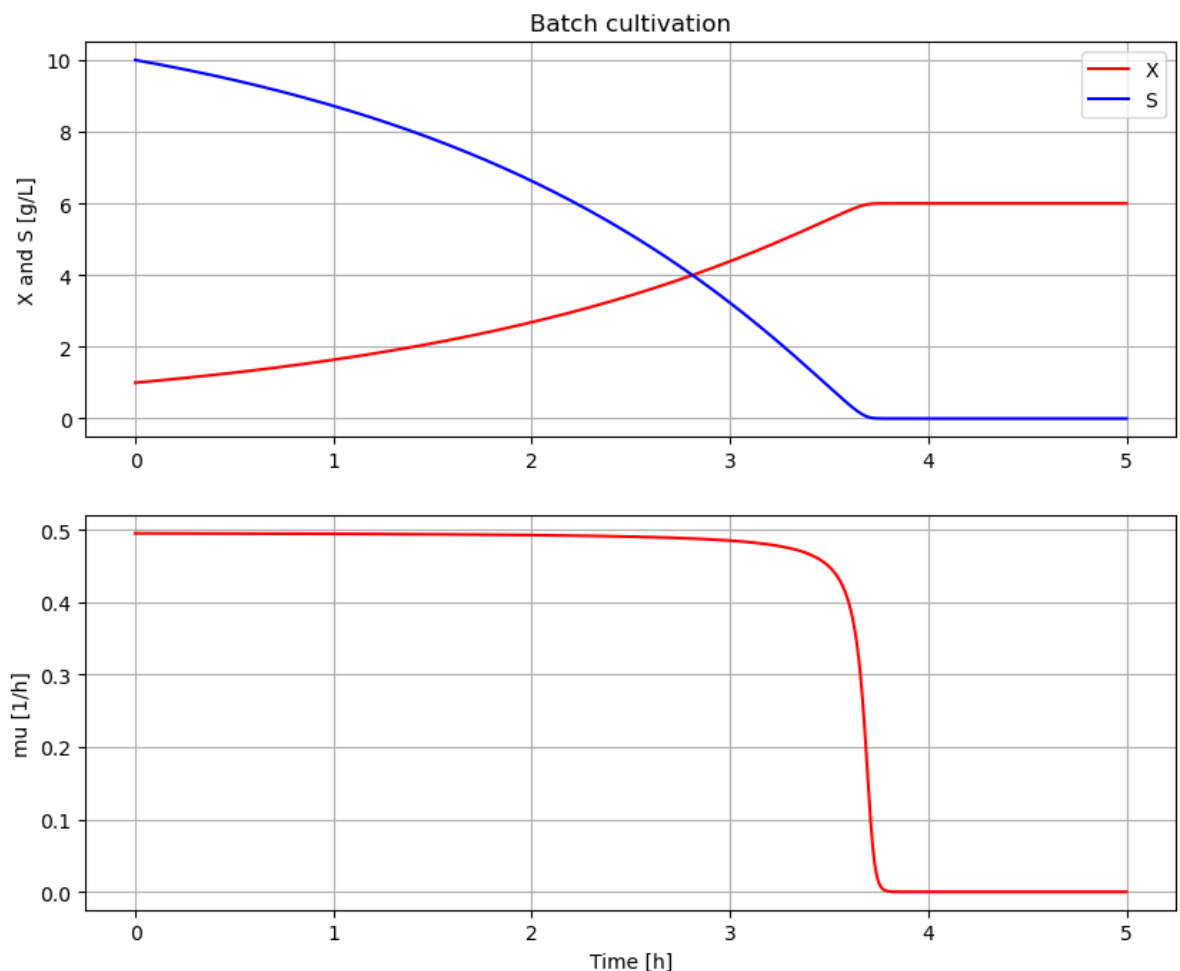
Note that both `disp()` and `describe()` takes values from the last simulation

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

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

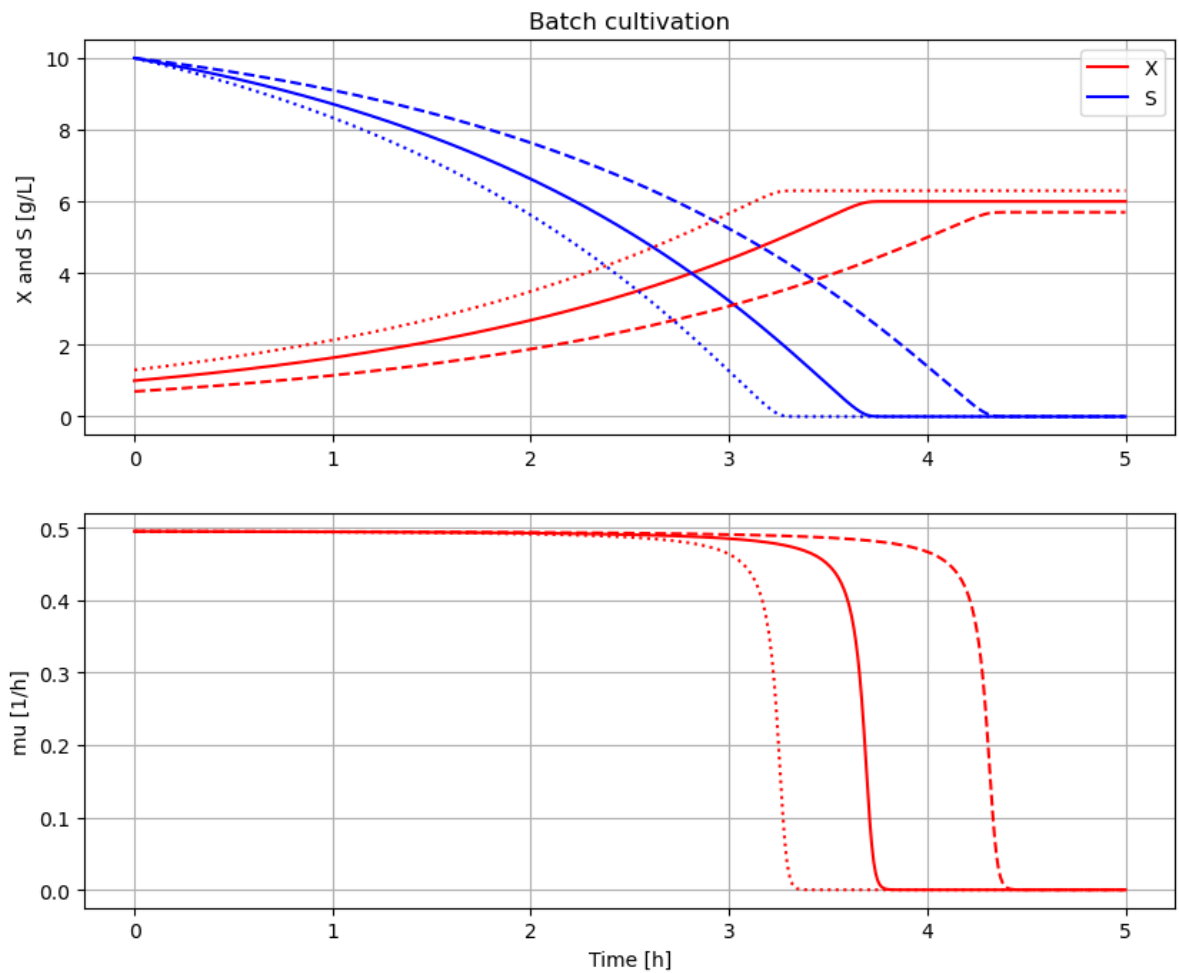
In [2]: `%matplotlib inline`
`plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]`

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



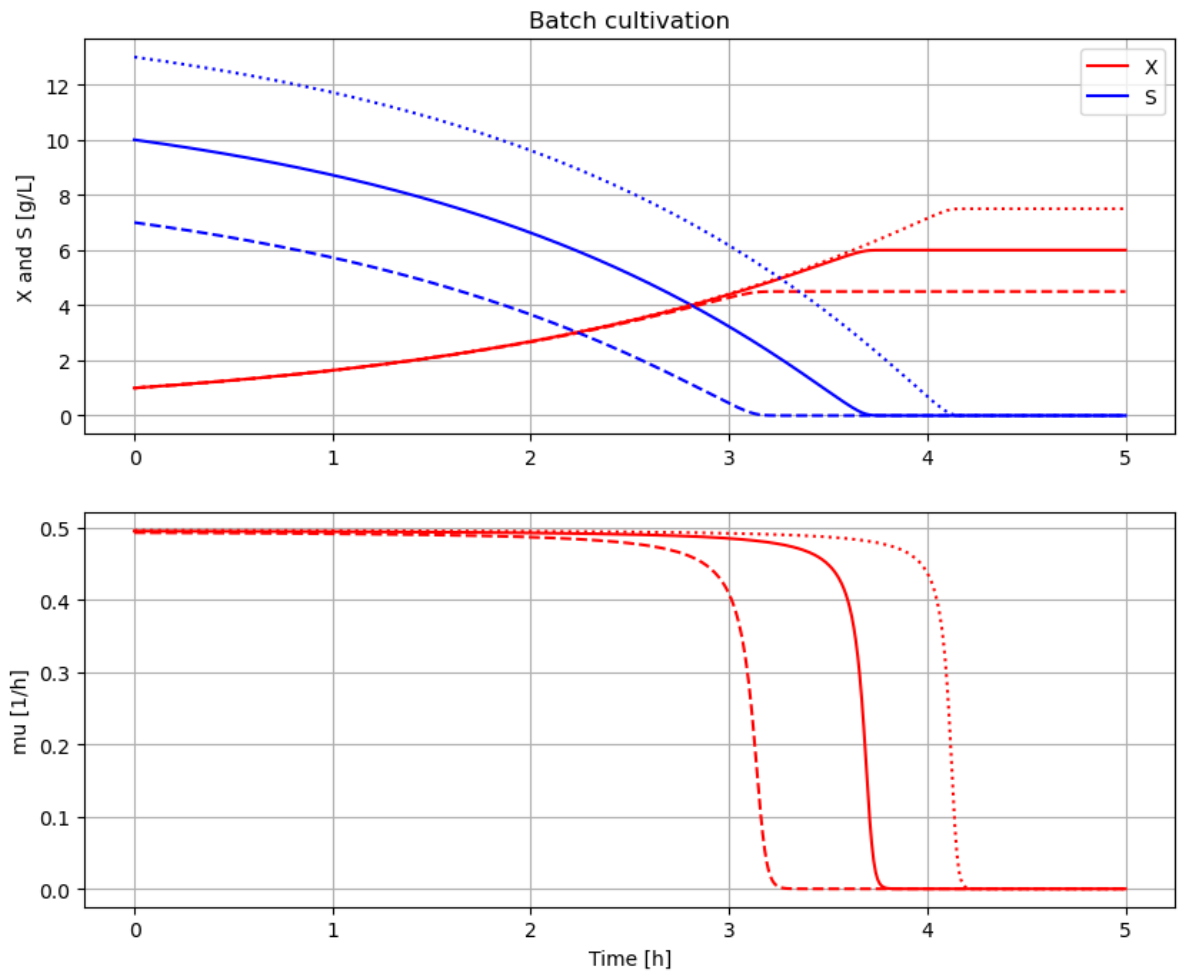
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In [4]: # Simulation were initial value of biomass VX_0 is varied
newplot(plotType='TimeSeries')
for value in [1.0, 0.7, 1.3]: init(VX_0=value); simu(5)

# Restore default value of VX_0
init(VX_0=1.0)
```



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In [5]: # Simulation were initial value of substrate VS_0 is varied
newplot(plotType='TimeSeries')
for value in [10, 7, 13]: init(VS_0=value); simu(5)

# Restore default value of VS_0
init(VS_0=10)
```



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In [ ]: # Simulation where metabolism is changed after 3 hours
newplot(plotType='TimeSeries')
simu(5)

simu(3)
par(Y=0.4, qSmax=1.0/(0.4/0.5)); simu(2, 'cont')

# Restore default value of Y and qSmax
par(Y=0.5, qSmax=1.0)
```

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In [ ]: disp('culture')
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In [ ]: describe('mu')
```

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

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

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In [ ]:
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