BPL_TEST2_Fedbatch script with FMPy

The key library FMPy is installed.

After the installation a small application BPL_TEST2_Fedbatch is loaded and run. You can continue with this example if you like.

```
!lsb_release -a # Actual VM Ubuntu version used by Google
```

```
No LSB modules are available.
Distributor ID: Ubuntu
Description:    Ubuntu 22.04.4 LTS
Release:        22.04
Codename:       jammy
```

```
!python --version
```

```
Python 3.11.11
```

```
!pip install fmpy
```

```
Collecting fmpy
  Downloading FMPy-0.3.22-py3-none-any.whl.metadata (1.9 kB)
Requirement already satisfied: attrs in /usr/local/lib/python3.11/dist-packag
Requirement already satisfied: Jinja2 in /usr/local/lib/python3.11/dist-packa
Collecting lark (from fmpy)
  Downloading lark-1.2.2-py3-none-any.whl.metadata (1.8 kB)
Requirement already satisfied: lxml in /usr/local/lib/python3.11/dist-packages
Requirement already satisfied: msgpack in /usr/local/lib/python3.11/dist-packa
Requirement already satisfied: numpy in /usr/local/lib/python3.11/dist-packag
Requirement already satisfied: MarkupSafe>=2.0 in /usr/local/lib/python3.11/d
Downloading FMPy-0.3.22-py3-none-any.whl (4.9 MB)
   ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 4.9/4.9 MB 40.0 MB/s eta 0:00:00
Downloading lark-1.2.2-py3-none-any.whl (111 kB)
   ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 111.0/111.0 kB 7.5 MB/s eta 0:00:0
Installing collected packages: lark, fmpy
Successfully installed fmpy-0.3.22 lark-1.2.2
```

BPL_TEST2_Fedbatch setup

Now specific installation and the run simulations. Start with connecting to Github. Then upload the two files:

- FMU - BPL_TEST2_Fedbatch_linux_om_me.fmu
- Setup-file - BPL_TEST2_Fedbatch_fmpy_explore.py

```
%%bash
git clone https://github.com/janpeter19/BPL_TEST2_Fedbatch
```

```
Cloning into 'BPL_TEST2_Fedbatch'...
```

```
%cd BPL_TEST2_Fedbatch
```

```
/content/BPL_TEST2_Fedbatch
```

```
run -i BPL_TEST2_Fedbatch_fmpy_explore.py
```

```
Linux - run FMU pre-comiled OpenModelica

    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 simulati
     - describe()  - describe culture, broth, parameters, variables with values/u

    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()
```

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

```
import warnings
warnings.filterwarnings("ignore")
```

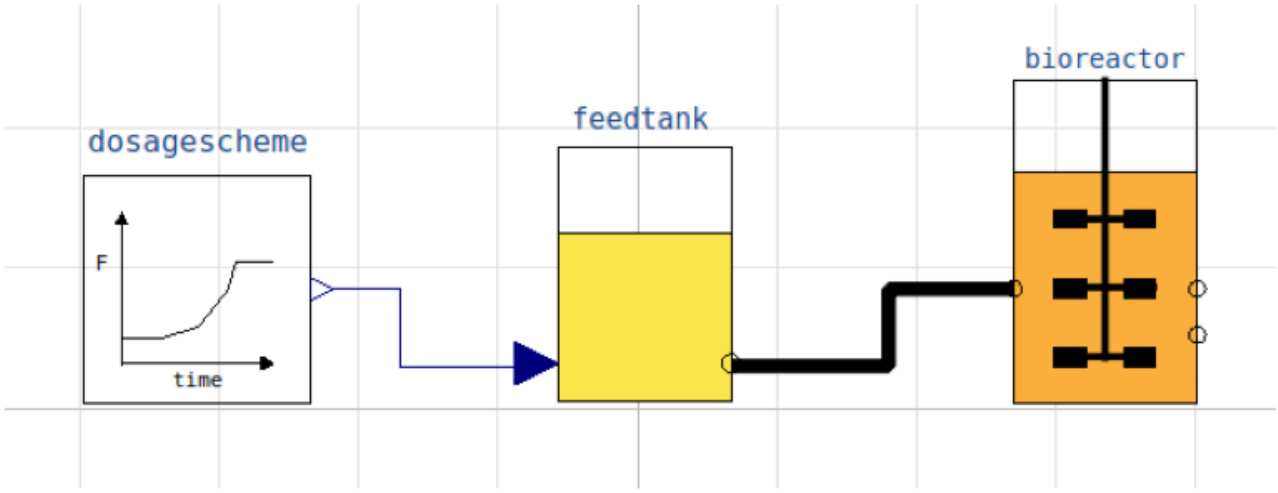
BPL_TEST2_Fedbatch - demo

```
describe('culture'); print(); #describe('liquidphase')
```

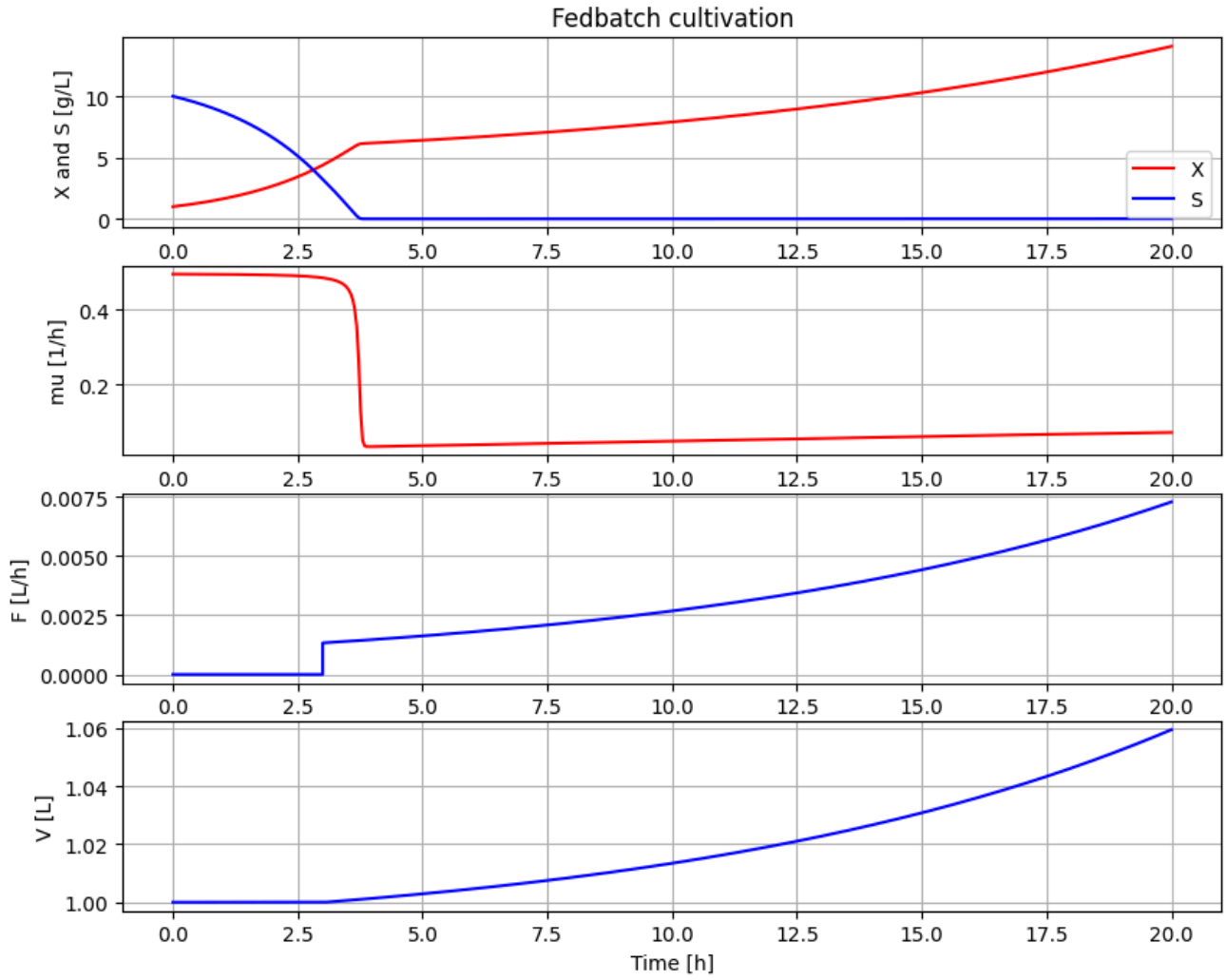
```
Simplified text book model - only substrate S and cell concentration X
```

```
process_diagram()
```

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




```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)
```

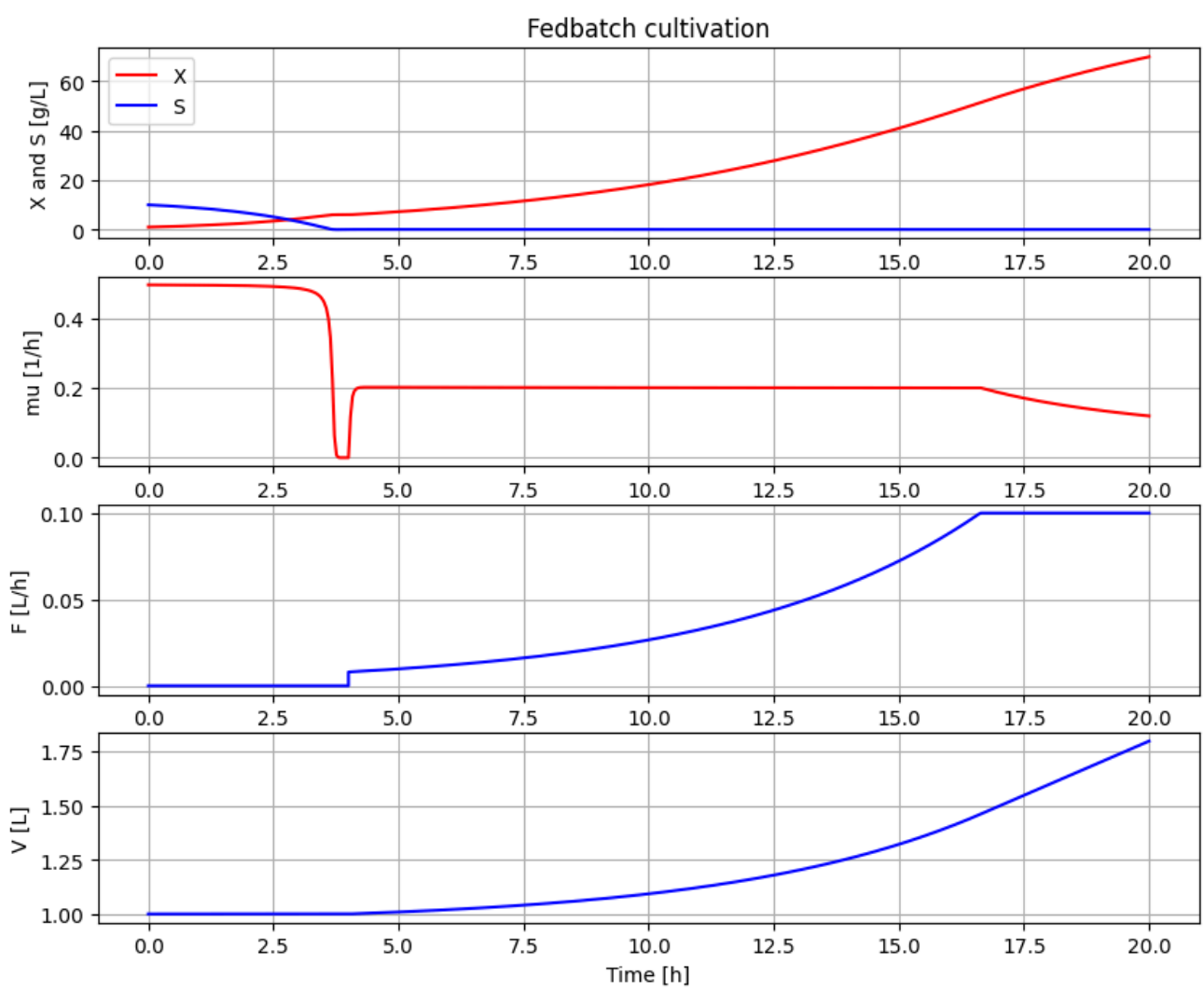



```
disp(mode='long')
```

```
bioreactor.V_start : V_start : 1.0
bioreactor.m_start[1] : VX_start : 0.0
bioreactor.m_start[2] : VS_start : 0.0
```

```
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 : 0.0
feedtank.V_start : feedtank.V_start : 100.0
dosagescheme.mu_feed : mu_feed : 0.2
dosagescheme.t_startExp : t_startExp : 2.0
dosagescheme.F_startExp : F_startExp : 0.12
dosagescheme.F_max : F_max : 3.0
```

```
# A more typical feed scheme for the culture at hand
newplot(plotType='TimeSeries')
par(t_startExp=4, F_startExp=0.008, mu_feed=0.2, F_max=0.1)
simu(20)
```




```
disp('culture')
```

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

```
describe('mu')
```

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

```
describe('parts')
```

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

```
describe('MSL')
```

```
MSL: 3.2.3 - used components: RealInput, RealOutput
```

```
system_info()
```

```
System information
 -OS: Linux
 -Python: 3.11.11
 -Scipy: not installed in the notebook
 -FMPy: 0.3.22
 -FMU by: OpenModelica Compiler OpenModelica 1.25.0~dev-133-ga5470be
 -FMI: 2.0
 -Type: ME
 -Name: BPL.Examples_TEST2.Fedbatch
 -Generated: 2024-11-06T21:37:05Z
 -MSL: 3.2.3
 -Description: Bioprocess Library version 2.3.0
 -Interaction: FMU-explore for FMPy version 1.0.1
```

Start coding or generate with AI.