## ⌄ 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-packages (from fmpy) (25.1.0)
   Requirement already satisfied: Jinja2 in /usr/local/lib/python3.11/dist-packages (from fmpy) (3.1.5)
   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 (from fmpy) (5.3.1)
   Requirement already satisfied: msgpack in /usr/local/lib/python3.11/dist-packages (from fmpy) (1.1.0)
   Requirement already satisfied: numpy in /usr/local/lib/python3.11/dist-packages (from fmpy) (1.26.4)
   Requirement already satisfied: MarkupSafe>=2.0 in /usr/local/lib/python3.11/dist-packages (from Jinja2->fm
   Downloading FMPy-0.3.22-py3-none-any.whl (4.9 MB)
   ──────────────────────────────────────── 4.9/4.9 MB 34.7 MB/s eta 0:00:00
   Downloading lark-1.2.2-py3-none-any.whl (111 kB)
   ──────────────────────────────────────── 111.0/111.0 kB 6.6 MB/s eta 0:00:00
   Installing collected packages: lark, fmpy
   Successfully installed fmpy-0.3.22 lark-1.2.2
```

```
!conda update -n base -c defaults conda --yes
```

```
⇥  /bin/bash: line 1: conda: command not found
```

## ⌄ 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/CONF_2023_10_MODELICA15
```

```
⇥  Cloning into 'CONF_2023_10_MODELICA15'...
```

```
%cd CONF_2023_10_MODELICA15
```

```
⇥  /content/CONF_2023_10_MODELICA15
```

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

```
⇥  Linux - run FMU pre-comiled OpenModelica 1.21.0

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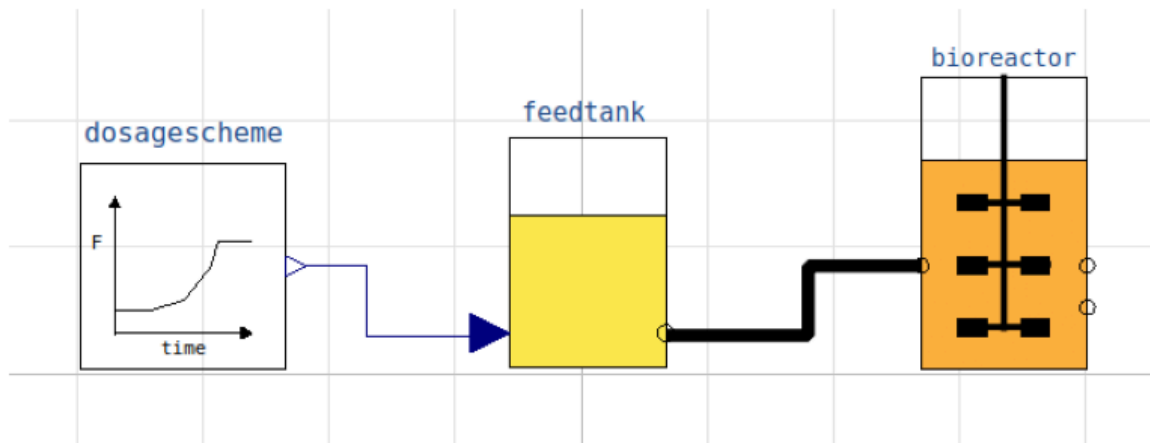
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

## ∨  BPL_TEST2_Fedbatch - demo

```
process_diagram()
```
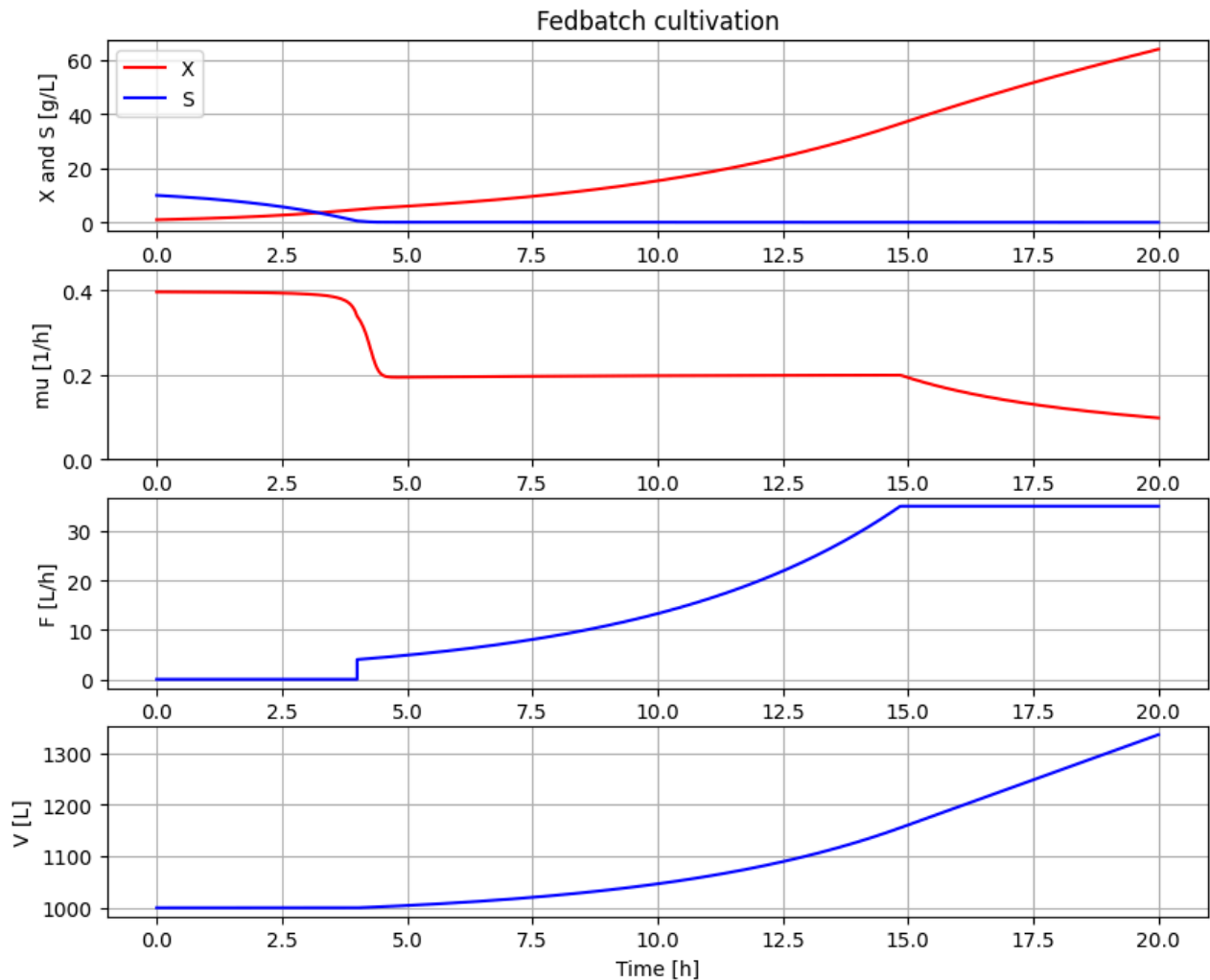


```
describe('culture'); print(); #describe('liquidphase')                              # Pump schedule param
```

Simplified text book model – only substrate S and cell concentration X

```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
ax2.set_ylim([0, 0.45])
init(V_0=1000, VX_0=1*1e3, VS_0=10*1e3)
par(feedtank_S_in=600, Ks=0.1, Y=0.40)
par(t_start=4, F_start=4.0, mu_feed=0.2, F_max=35)
simu(20)
```

Fedbatch cultivation

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

```
bioreactor.V_0 : V_0 : 1000
bioreactor.m_0[1] : VX_0 : 1000.0
bioreactor.m_0[2] : VS_0 : 10000.0
bioreactor.culture.Y : Y : 0.4
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1
feedtank.c_in[2] : feedtank_S_in : 600
feedtank.V_0 : feedtank_V_0 : 10.0
dosagescheme.mu_feed : mu_feed : 0.2
dosagescheme.t_start : t_start : 4
dosagescheme.F_start : F_start : 4.0
dosagescheme.F_max : F_max : 35
```

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

Cell specific growth rate variable : 0.098 [ 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 1.21.0
–FMI: 2.0
–Type: ME
–Name: BPL_TEST2.Fedbatch
–Generated: 2023–04–20T12:24:29Z
–MSL: 3.2.3
–Description: Bioprocess Library version 2.1.1
–Interaction: FMU–explore for FMPy version 0.9.8
```

Start coding or generate with AI.