

✓ BPL_TEST2_Fedbatch script with PyFMI

The key library PyFMI 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 22.04.3 LTS
Release:        22.04
Codename:       jammy

```

```
%env PYTHONPATH=
```

```
env: PYTHONPATH=
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-Linux-x86_64.sh
```

```
!chmod +x Miniconda3-py310_23.1.0-1-Linux-x86_64.sh
```

```
!bash ./Miniconda3-py310_23.1.0-1-Linux-x86_64.sh -b -f -p /usr/local
```

```
import sys
```

```
sys.path.append('/usr/local/lib/python3.10/site-packages/')
```

```

--2025-01-14 09:19:06--  https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.191.158, 104.16.32.241, 2606:4700::6810:20f1,
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.191.158|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 74403966 (71M) [application/x-sh]
Saving to: 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh'

```

```
Miniconda3-py310_23 100%[=====>] 70.96M 154MB/s in 0.5s
```

```
2025-01-14 09:19:07 (154 MB/s) - 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh' saved [74403966/74403966]
```

```

PREFIX=/usr/local
Unpacking payload ...

```

```
Installing base environment...
```

```
Downloading and Extracting Packages
```

```
Downloading and Extracting Packages
```

```

Preparing transaction: done
Executing transaction: done
installation finished.

```

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

```


```

```
Preparing transaction: done  
Verifying transaction: done  
Executing transaction: done
```

```
!conda --version  
!python --version
```

```
🔄 conda 23.1.0  
Python 3.10.16
```

```
!conda install -c conda-forge pyfmi --yes # Install the key package
```

```
🔄
```

```

Preparing transaction: done
Verifying transaction: done
Executing transaction: done

```

✓ 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_explore.me.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_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 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]

```

```

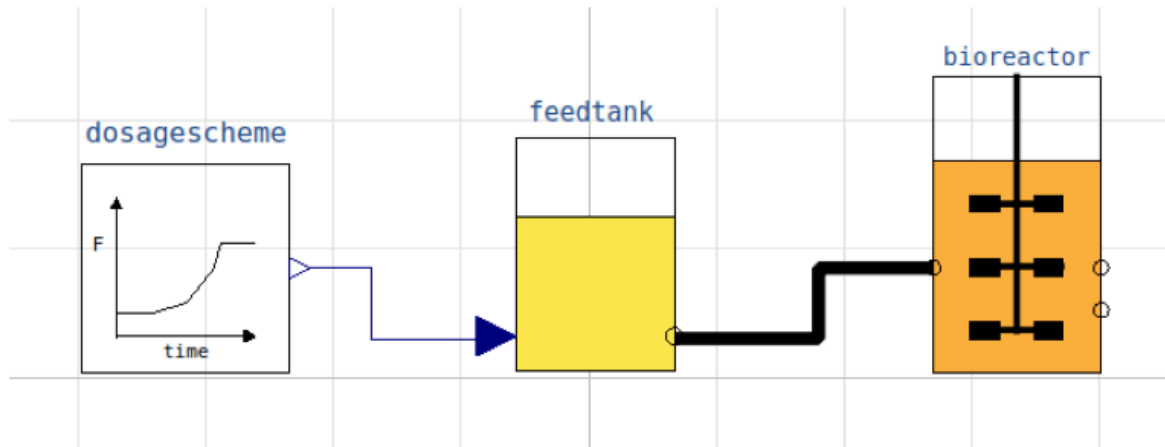
import warnings
warnings.filterwarnings("ignore")

```

✓ BPL_TEST2_Fedbatch - demo

```
process_diagram()
```

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



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

```
# Pump schedule para
```

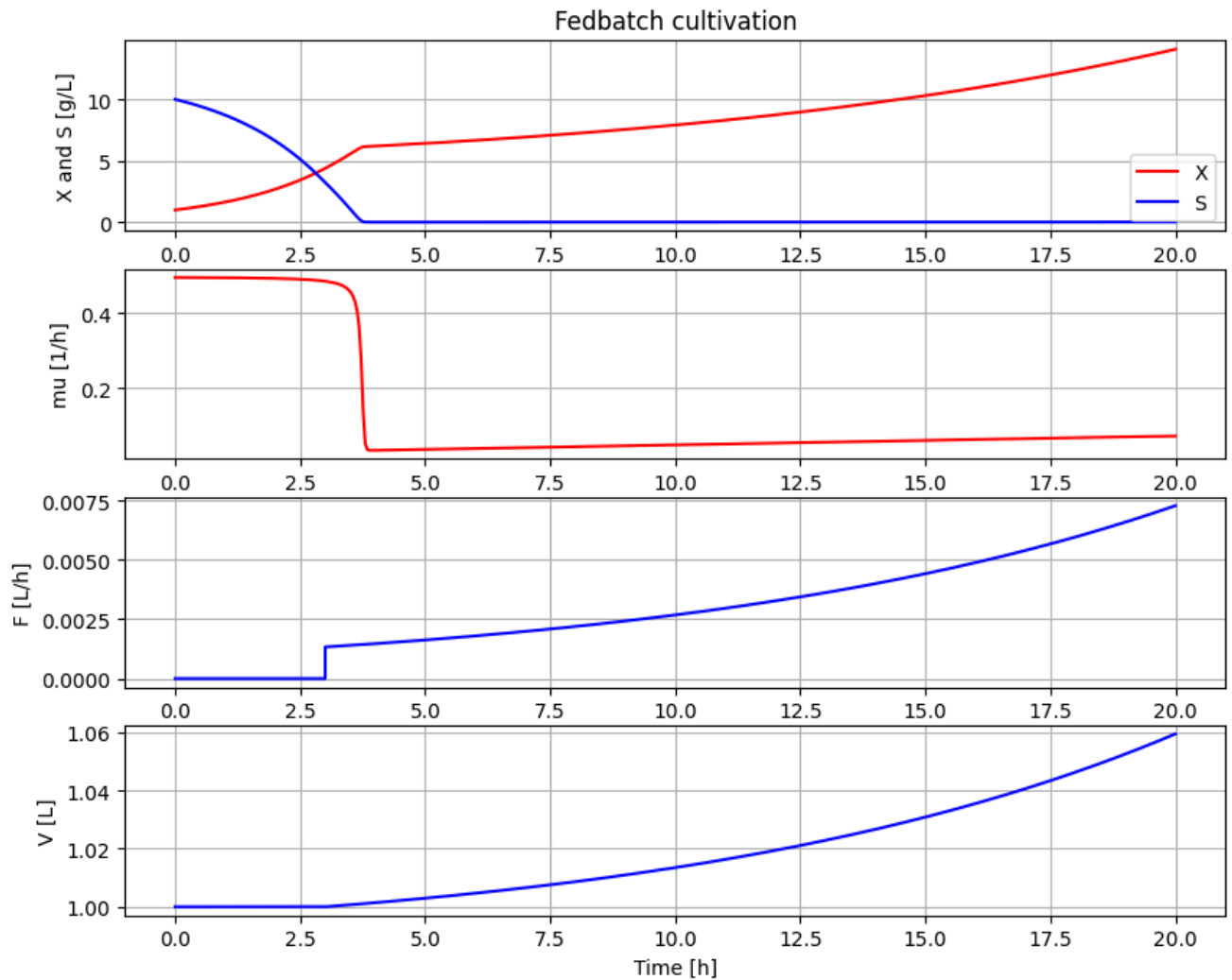
📁 Simplified text book model – only substrate S and cell concentration X

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

```

↳ Could not find cannot import name 'dopri5' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/
Could not find cannot import name 'rodas' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/a
Could not find cannot import name 'odassl' from 'assimulo.lib' (/usr/local/lib/python3.10/site-packages/
Could not find ODEPACK functions.
Could not find RADAR5
Could not find GLIMDA.

```



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

```

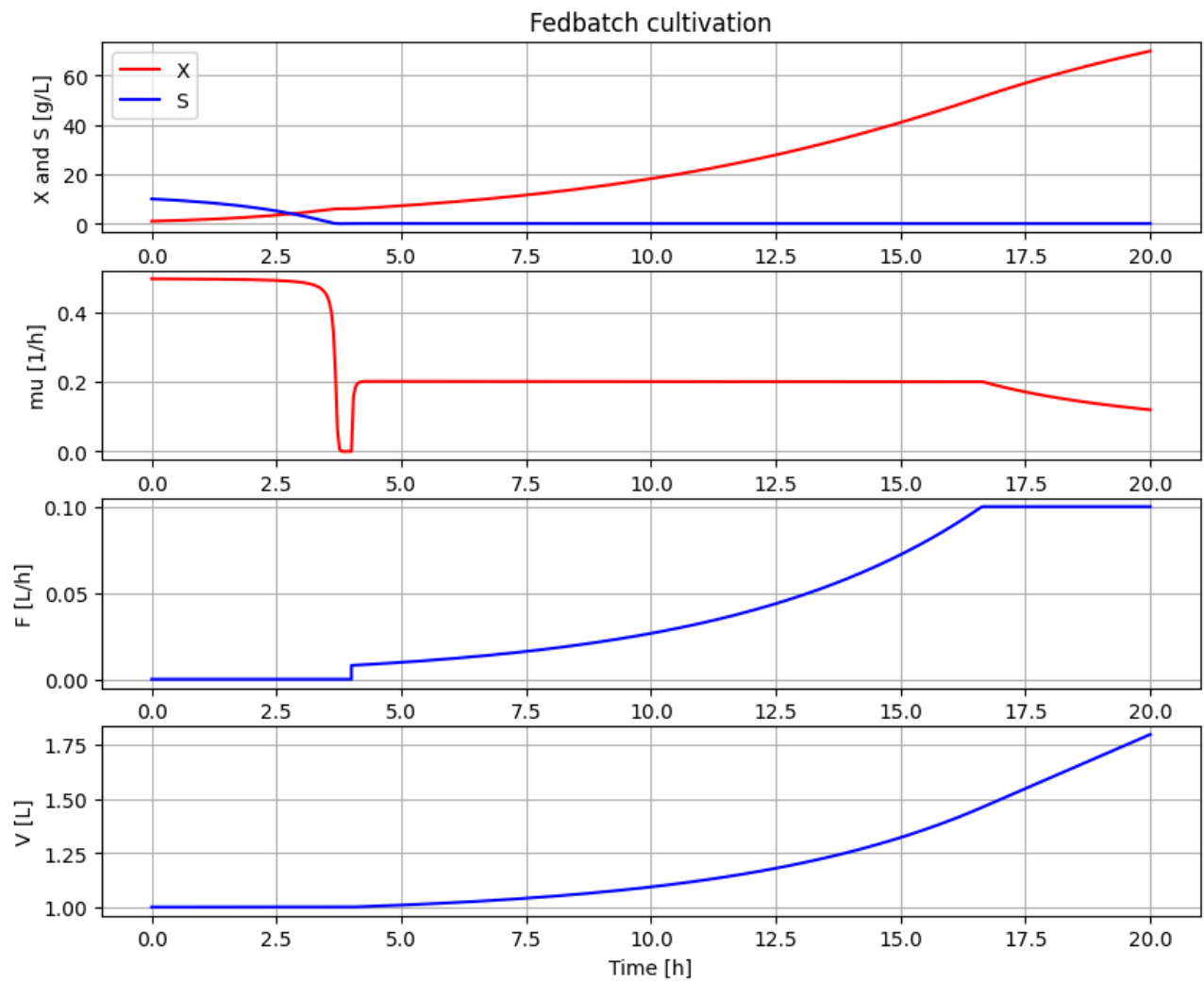
↳ bioreactor.V_start : V_start : 1.0
bioreactor.m_start[1] : VX_start : 1.0
bioreactor.m_start[2] : VS_start : 10.0
bioreactor.culture.Y : Y : 0.5
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1
feedtank.c_in[2] : feedtank.S_in : 300.0
feedtank.V_start : feedtank.V_start : 10.0
dosagescheme.F_start : F_start : 0.0
dosagescheme.mu_feed : mu_feed : 0.1
dosagescheme.t_startExp : t_startExp : 3.0
dosagescheme.F_startExp : F_startExp : 0.001
dosagescheme.F_max : F_max : 0.3

```

```

# 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)

```



```
# Test function simu(mode='cont')
newplot()
simu(15)
simu(5, 'cont')
```



Fedbatch cultivation



```
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')
```