

✓ 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
```

```
%env PYTHONPATH=
```

```
⇒ env: PYTHONPATH=
```

```
!python --version
```

```
⇒ Python 3.11.11
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py311_24.11.1-0-Linux-x86_64
!chmod +x Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
!bash ./Miniconda3-py311_24.11.1-0-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.11/site-packages/')
```

```
⇒ --2025-02-07 20:03:23-- https://repo.anaconda.com/miniconda/Miniconda3-py311\_24.11.1-0-Linux-x86\_64.sh
   Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.1
   Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... con
   HTTP request sent, awaiting response... 200 OK
   Length: 145900576 (139M) [application/octet-stream]
   Saving to: 'Miniconda3-py311_24.11.1-0-Linux-x86_64.sh'
```

```
Miniconda3-py311_24 100%[=====>] 139.14M  146MB/s    in 1.0s
```

```
2025-02-07 20:03:24 (146 MB/s) - 'Miniconda3-py311_24.11.1-0-Linux-x86_64.sh'
```

```
PREFIX=/usr/local
Unpacking payload ...
```

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

```
Preparing transaction: ...working... done
Executing transaction: ...working... done
installation finished.
```

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



```
Channels:
- defaults
Platform: linux-64
Collecting package metadata (repodata.json): done
Solving environment: done
```

```
## Package Plan ##
```

```
environment location: /usr/local
```

```
added / updated specs:
- conda
```

```
The following packages will be downloaded:
```

package	build	
ca-certificates-2024.12.31	h06a4308_0	128 KB
certifi-2025.1.31	py311h06a4308_0	163 KB
Total:		291 KB

```
The following packages will be UPDATED:
```

```
ca-certificates          2024.11.26-h06a4308_0 --> 2024.12.31-h06a4308_0
certifi                  2024.8.30-py311h06a4308_0 --> 2025.1.31-py311h06a4308_0
```

```
Downloading and Extracting Packages:
```

```
certifi-2025.1.31      | 163 KB | : 0% 0/1 [00:00<?, ?it/s]
certifi-2025.1.31      | 163 KB | : 100% 1.0/1 [00:00<00:00, 25.63it/s]
ca-certificates-2024   | 128 KB | : 100% 1.0/1 [00:00<00:00, 20.61it/s]
```

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

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



```
conda 24.11.1
Python 3.11.11
```

```
!conda config --set channel_priority strict
```

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



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

```
#!conda install matplotlib --yes
```

```
#!conda install scipy --yes
```

```
#!conda install xlrd --yes
```

```
#!conda install openpyxl --yes
```

✓ 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 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")
```

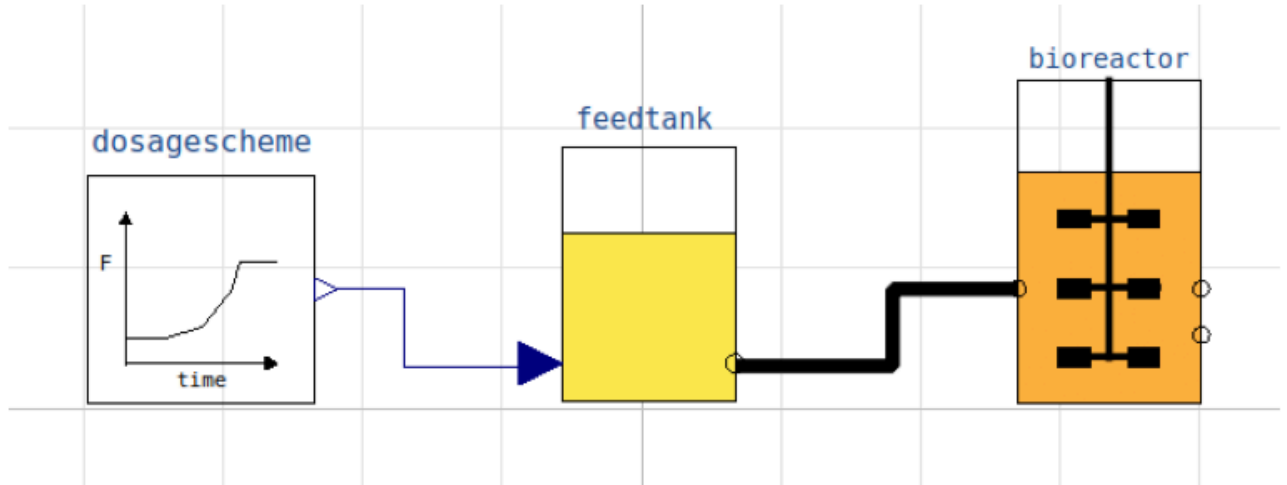
✓ BPL_TEST2_Fedbatch - demo

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

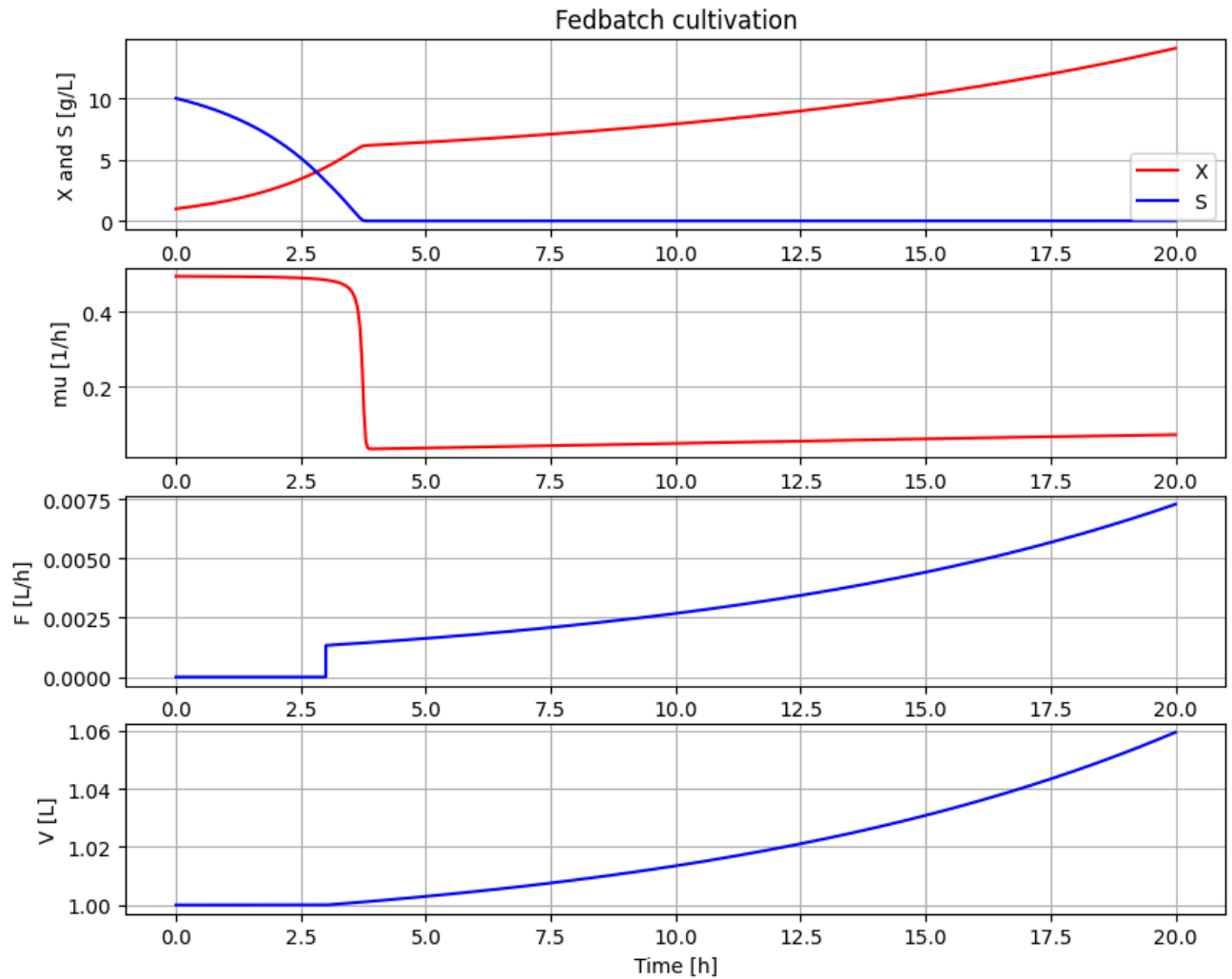
⇒ Simplified text book model – only substrate S and cell concentration X

```
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)
```

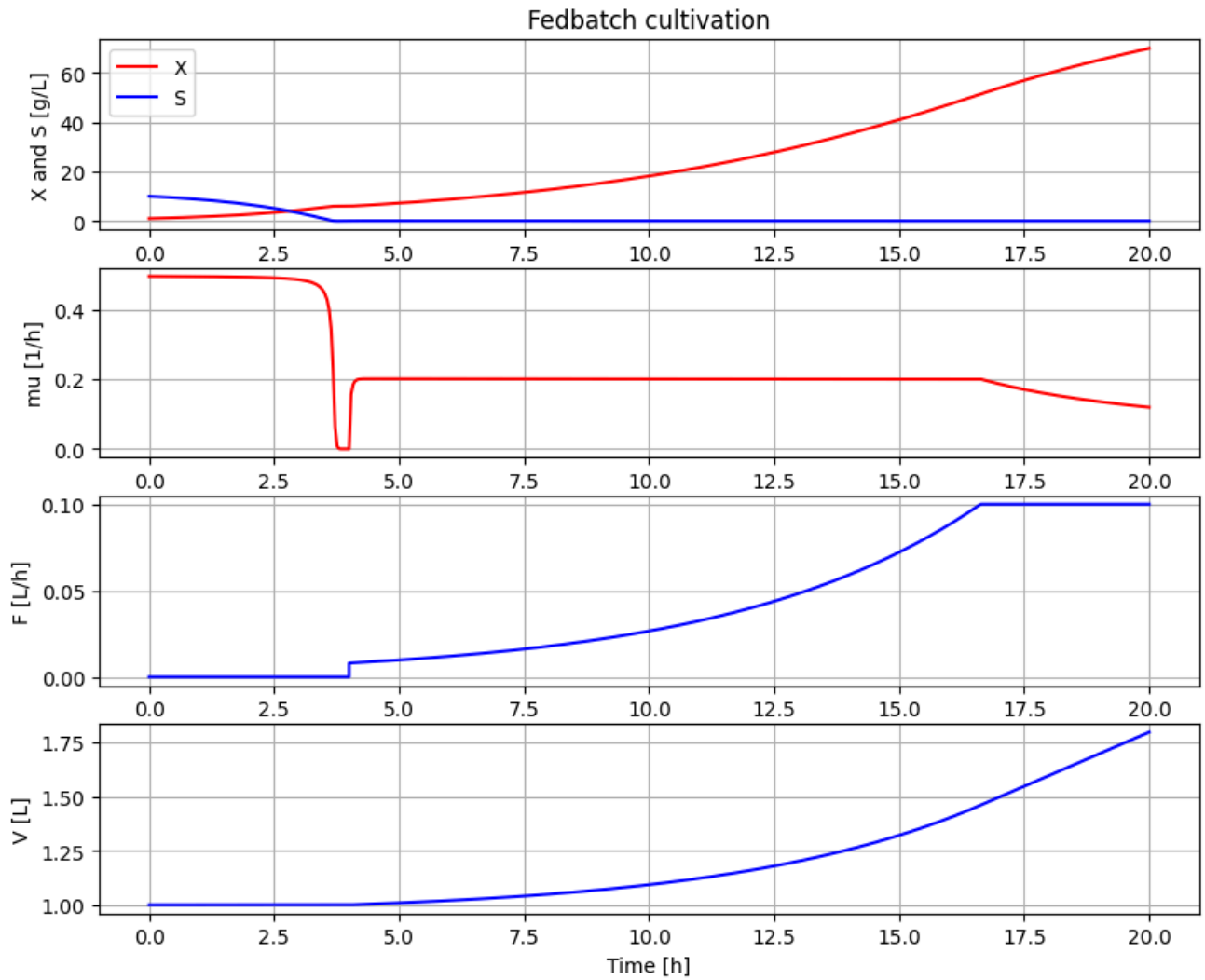


```
disp(mode='long')
```



```
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