

## ✓ 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 22.04.4 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.sh
```

```
!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/')
```

```
➦ --2025-02-06 09:17:53-- 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, 104.16.191.158, 2606:4700::6810:bf9e, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... connected.
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 224MB/s in 0.6s
```

```
2025-02-06 09:17:54 (224 MB/s) - 'Miniconda3-py311_24.11.1-0-Linux-x86_64.sh' saved [145900576/145900576]
```

```
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]
ca-certificates-2024 | 128 KB | : 0% 0/1 [00:00<?, ?it/s]
certifi-2025.1.31 | 163 KB | : 100% 1.0/1 [00:00<00:00, 17.35it/s]
```

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

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

```
🔄 conda 24.11.1
    Python 3.11.11
```

```
!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-compiled 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()
```

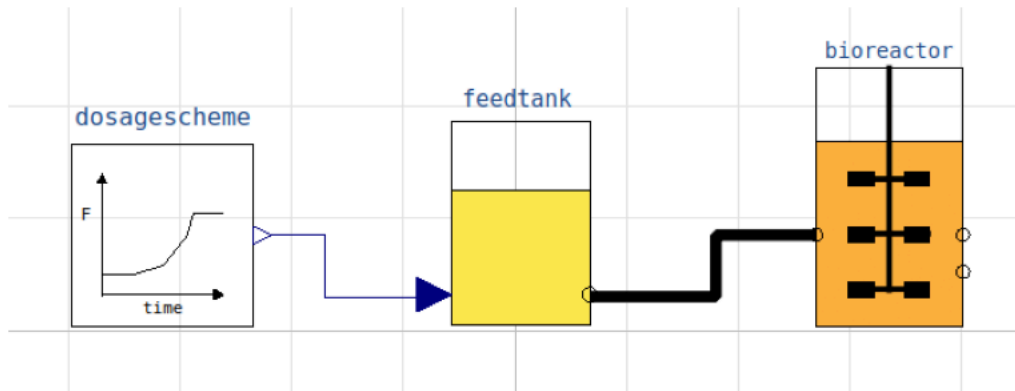
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

## ✓ BPL\_TEST2\_Fedbatch - demo

```
process_diagram()
```

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

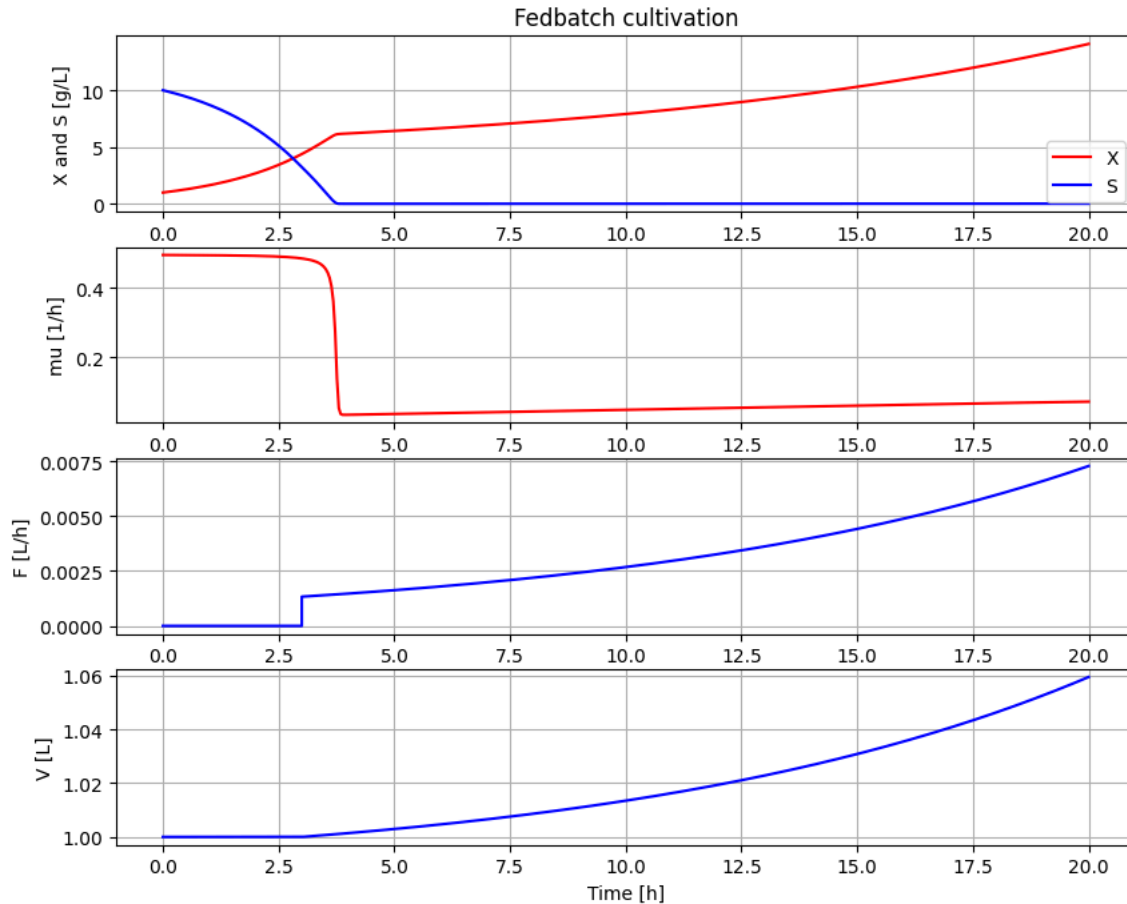


```
describe('culture'); print(); #describe('liquidphase') # Pump schedule parameter
```

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

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

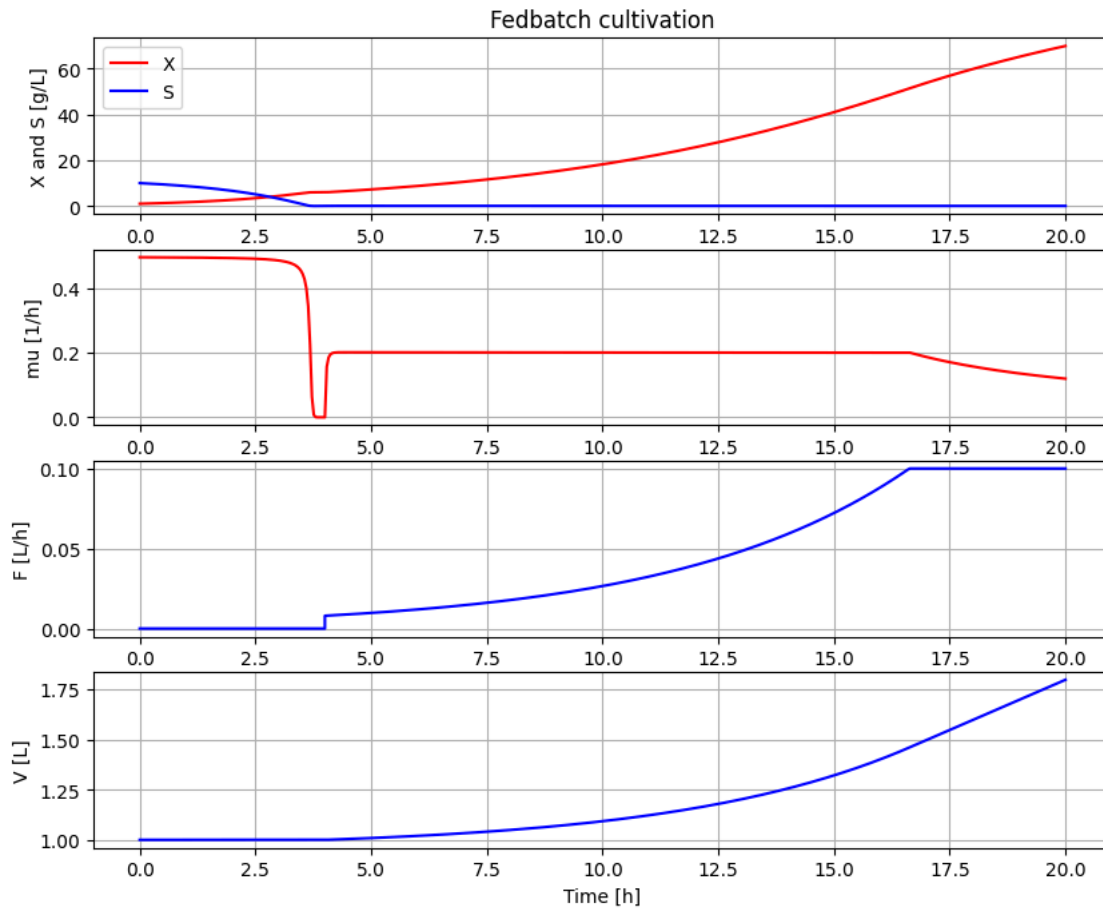
Could not find cannot import name 'dopri5' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/\_\_\_i  
 Could not find cannot import name 'rodas' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/\_\_\_in  
 Could not find cannot import name 'odassl' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/\_\_\_i  
 Could not find ODEPACK functions.  
 Could not find RADAR5  
 Could not find GLIMDA.



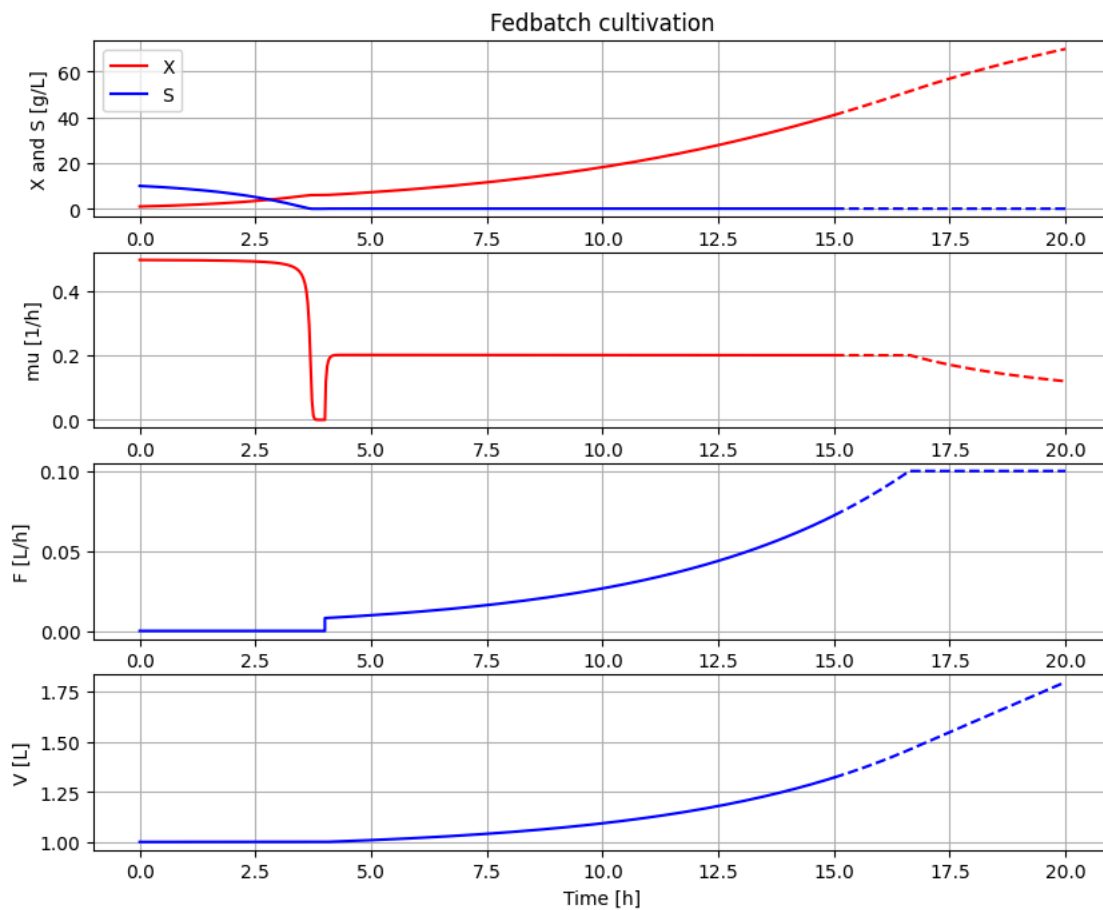
```
disp(mode='long')
```

```
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')
```



```
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
```