

✓ 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 22.04.3 LTS
  Release:       22.04
  Codename:      jammy
```

```
%env PYTHONPATH=
```

```
➦ env: PYTHONPATH=
```

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
```

```
!chmod +x Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
```

```
!bash ./Miniconda3-py312_24.3.0-0-Linux-x86_64.sh -b -f -p /usr/local
```

```
import sys
```

```
sys.path.append('/usr/local/lib/python3.12/site-packages/')
```

```
➦ --2024-10-24 08:38:11-- https://repo.anaconda.com/miniconda/Miniconda3-py312_24.3.0-0-Linux-x86_64.sh
  Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.158, 2606:4700::6810:20f1, ...
  Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... connected.
  HTTP request sent, awaiting response... 200 OK
  Length: 143351488 (137M) [application/octet-stream]
  Saving to: 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh'
```

```
Miniconda3-py312_24 100%[=====>] 136.71M 97.1MB/s in 1.4s
```

```
2024-10-24 08:38:13 (97.1 MB/s) - 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh' saved [143351488/143351488]
```

```
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
```

```
➦ frozendict          pkgs/main/linux-64::frozendict-2.4.2-py312h06a4308_0
```

The following packages will be UPDATED:

```
openssl-3.0.15      | 5.2 MB      | :    0% 0.003007460830410892/1 [00:00<01:35, 96.20s/it]
```

```
frozendict-2.4.2    | 36 KB       | :   44% 0.43853215920344746/1 [00:00<00:00, 1.52it/s]
```

```
frozendict-2.4.2    | 36 KB       | : 100% 1.0/1 [00:00<00:00, 1.52it/s]  
conda-24.9.2        | 1.1 MB      | : 100% 1.0/1 [00:00<00:00, 1.37it/s]
```

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

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

```
🔄 conda 24.9.2  
   Python 3.12.2
```

```
!conda install -c conda-forge fmpy --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")

```

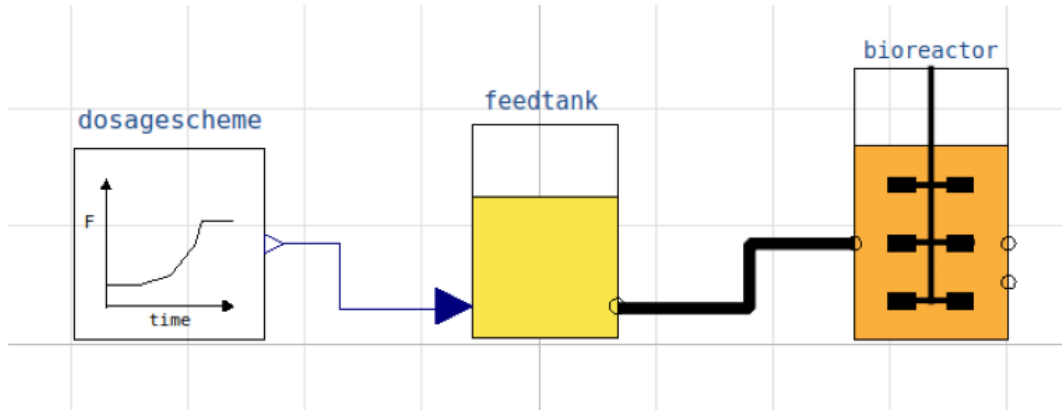
✓ BPL_TEST2_Fedbatch - demo

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

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

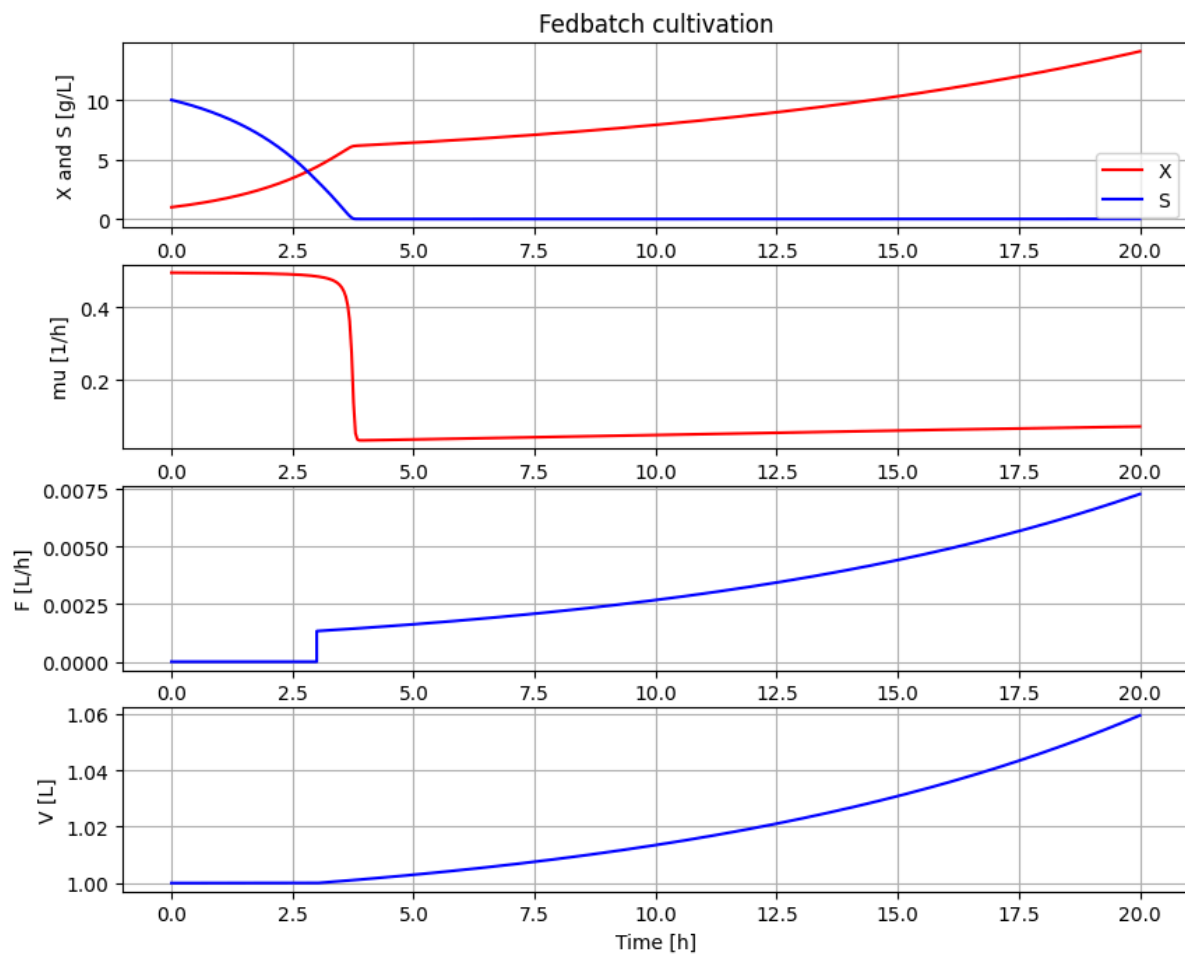
```
process_diagram()
```

🔄 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)
```

🔄



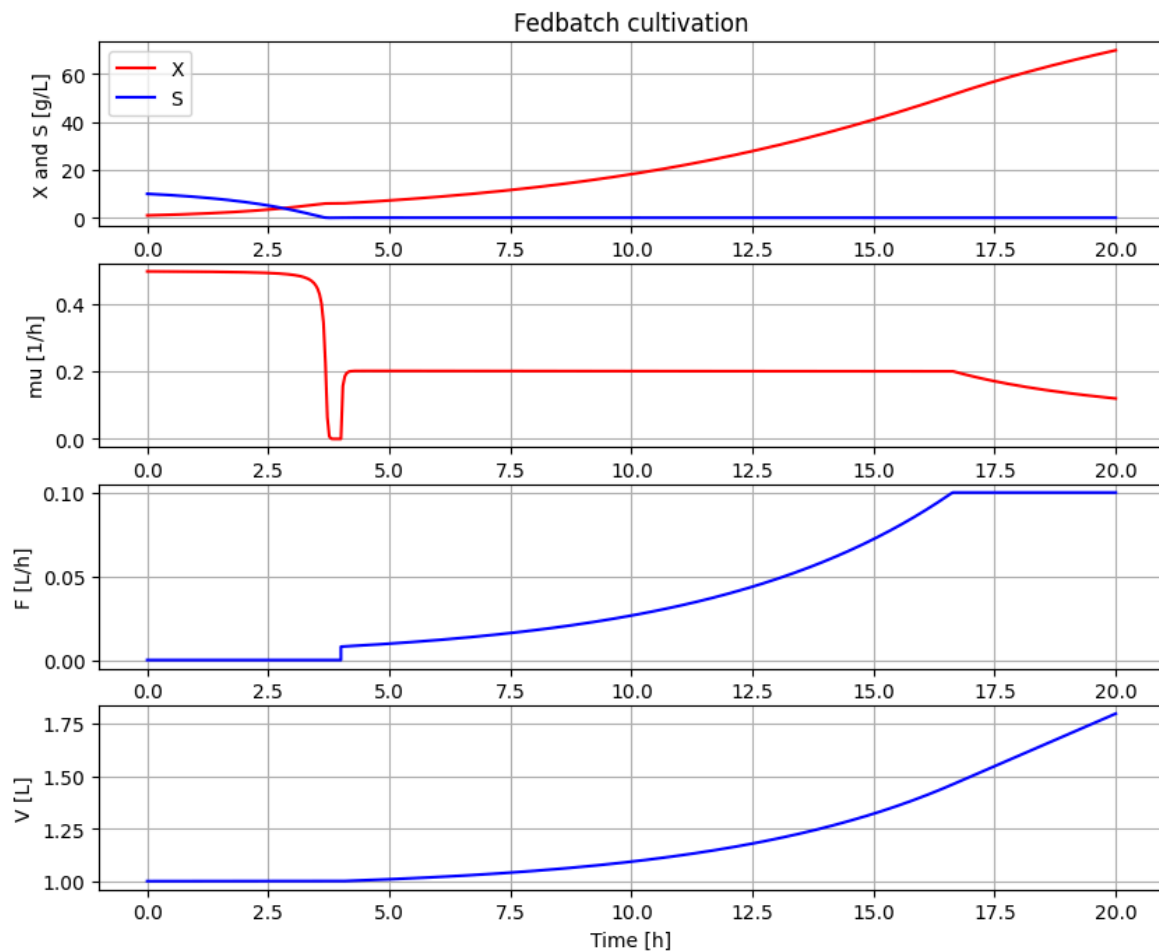
```
disp(mode='long')
```

🔄

```
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: 3.10.12
-Scipy: not installed in the notebook
-FMPy: 0.3.20
-FMU by: OpenModelica Compiler OpenModelica 1.25.0~dev-51-ge672d09
-FMI: 2.0
-Type: ME
-Name: BPL.Examples_TEST2.Fedbatch
-Generated: 2024-10-12T15:10:24Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.2.2 - GUI
-Interaction: FMU-explore for FMPy version 1.0.1
```

Start coding or [generate](#) with AI.

