

✓ 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-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/')
```

```
--2024-03-05 20:42:52-- https://repo.anaconda.com/miniconda/Miniconda3-py310\_23.1.0-1-Linux-x86\_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.131.3, 104.16.130.3, 260
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.131.3|: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 131MB/s in 0.5s
```

```
2024-03-05 20:42:53 (131 MB/s) - 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh' saved
```

```
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 24.1.2  
Python 3.10.13
```

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

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

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

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

Package Plan

```
environment location: /usr/local

added / updated specs:
- matplotlib
```

The following packages will be downloaded:

package	build	
matplotlib-3.8.0	py310h06a4308_0	8 KB
matplotlib-base-3.8.0	py310h1128e8f_0	6.8 MB
pyparsing-3.0.9	py310h06a4308_0	153 KB
Total:		7.0 MB

The following NEW packages will be INSTALLED:

```
matplotlib      pkgs/main/linux-64::matplotlib-3.8.0-py310h06a4308_0
```

The following packages will be UPDATED:

```
matplotlib-base  conda-forge::matplotlib-base-3.5.2-py~ --> pkgs/main::matplot
```

The following packages will be SUPERSEDED by a higher-priority channel:

```
certifi          conda-forge/noarch::certifi-2024.2.2~ --> pkgs/main/linux-64
conda             conda-forge::conda-24.1.2-py310hff520~ --> pkgs/main::conda-2
pyparsing         conda-forge/noarch::pyparsing-3.1.1-p~ --> pkgs/main/linux-64
```

```
Downloading and Extracting Packages:
matplotlib-base-3.8. | 6.8 MB | : 0% 0/1 [00:00<?, ?it/s]
pyparsing-3.0.9      | 153 KB | : 0% 0/1 [00:00<?, ?it/s]

matplotlib-3.8.0     | 8 KB | : 0% 0/1 [00:00<?, ?it/s]

matplotlib-3.8.0     | 8 KB | : 100% 1.0/1 [00:00<00:00, 8.76it/s]
matplotlib-base-3.8. | 6.8 MB | : 0% 0.0022928172852449986/1 [00:00<00:55, 56

matplotlib-3.8.0     | 8 KB | : 100% 1.0/1 [00:00<00:00, 8.76it/s]
```

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

```
#!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-compiled 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")
```

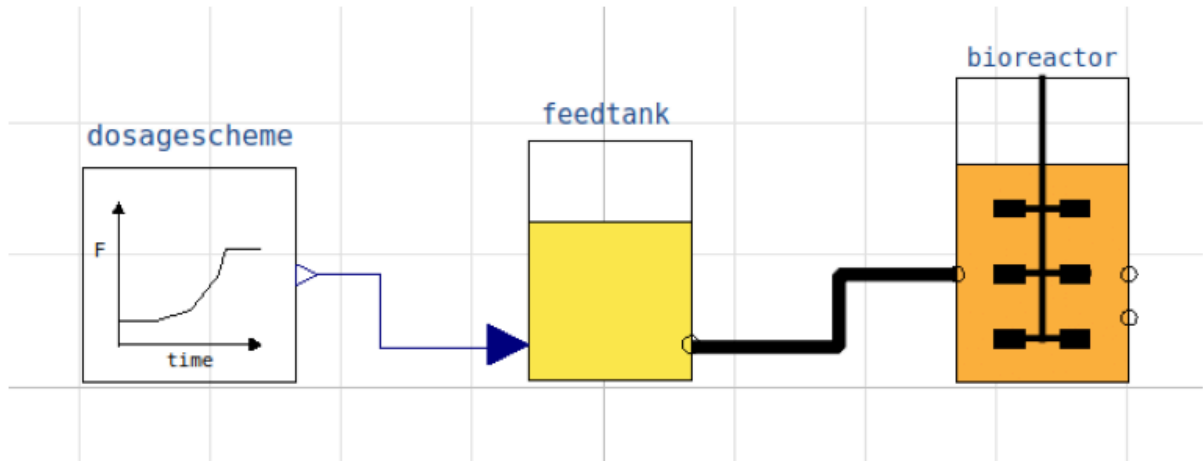
✓ BPL_TEST2_Fedbatch - demo

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

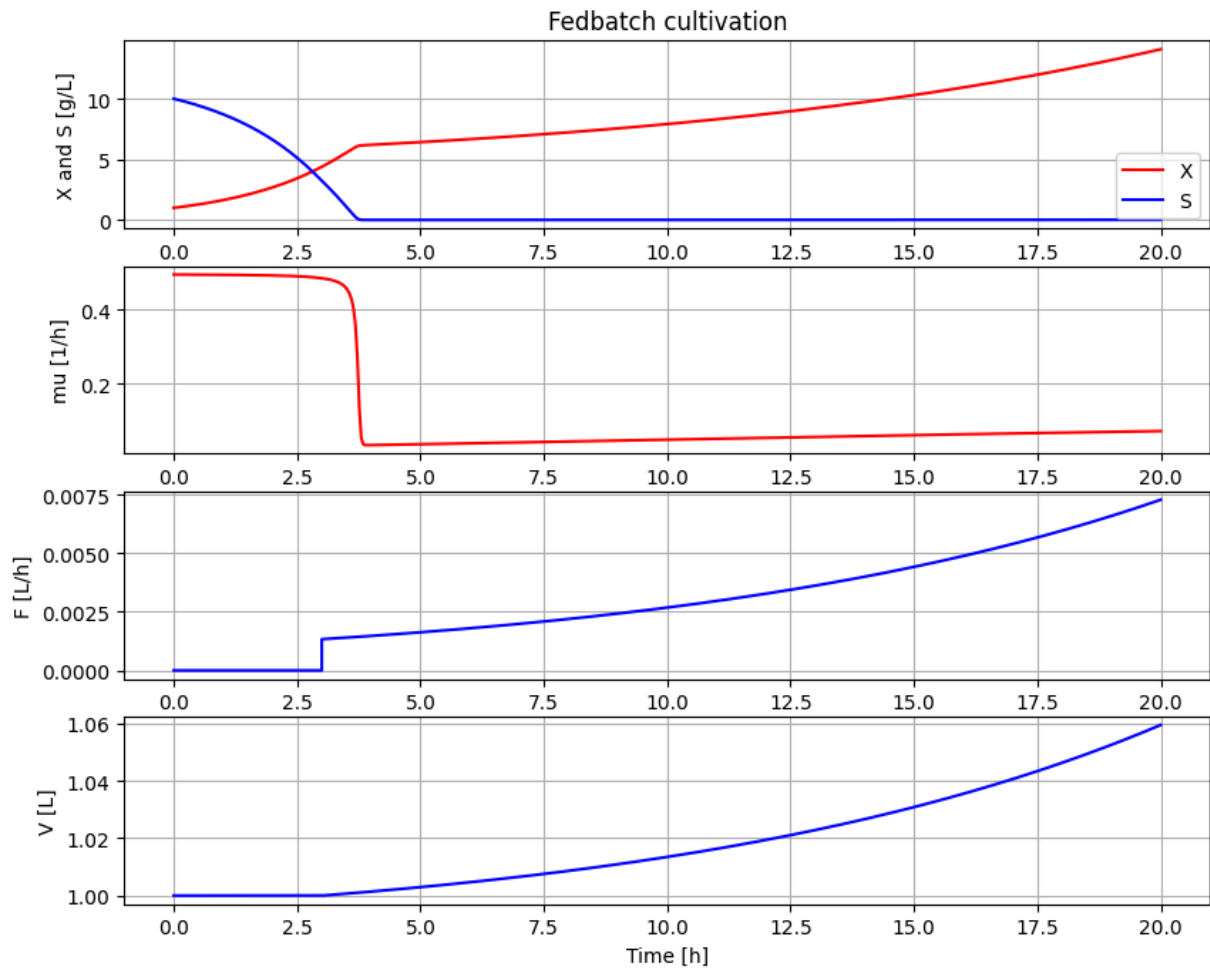
Simplified text book model – only substrate S and cell concentration X

```
process_diagram()
```

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



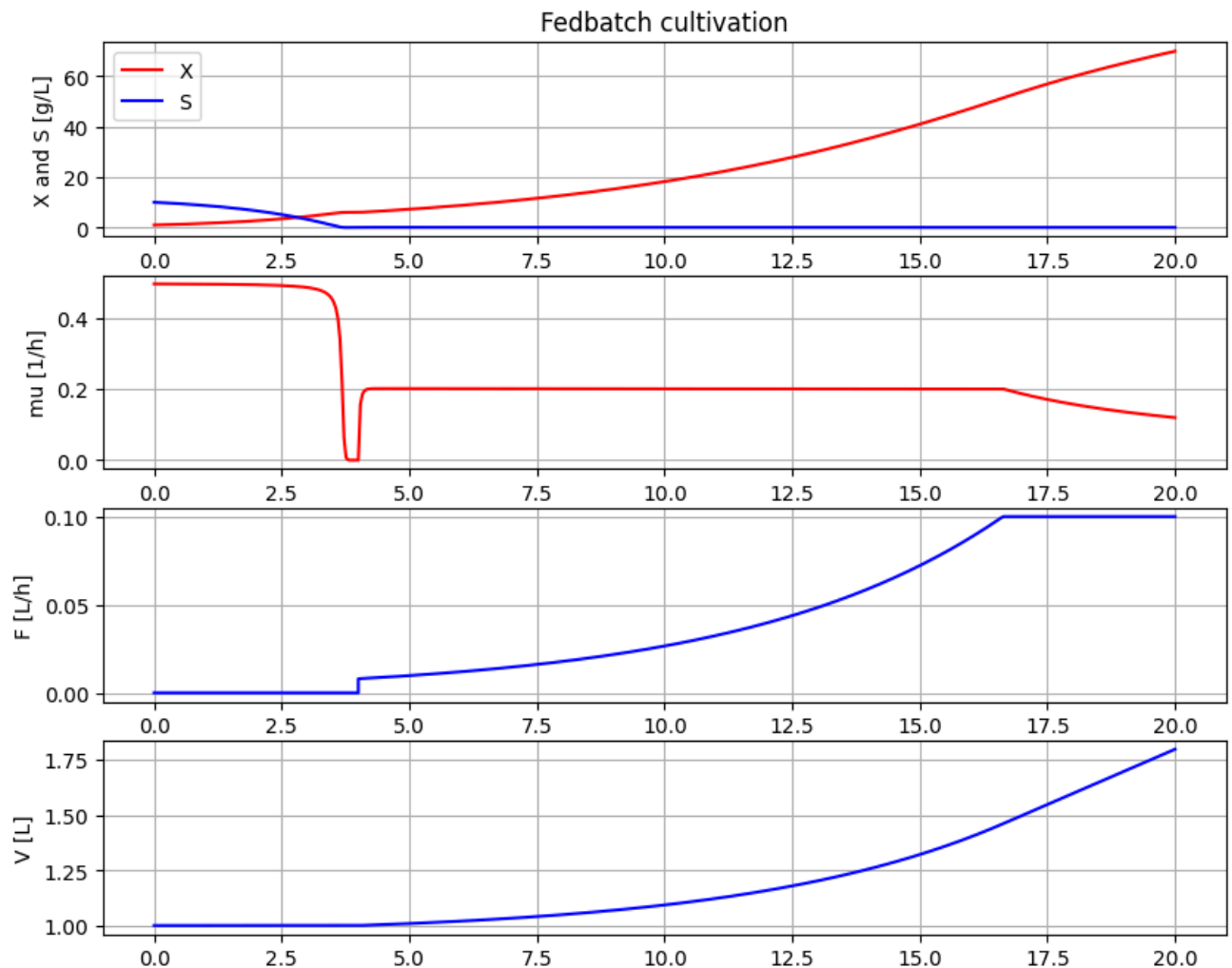
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)
```



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

```
bioreactor.V_start : V_start : 1.0
bioreactor.m_start[1] : VX_start : 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.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)
```



```
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: 0.3.19
-FMU by: OpenModelica Compiler OpenModelica 1.21.0
-FMT: 2.0
```