

▼ BPL_TEST2_Fedbatch script with PyFMI ver 2.9.8

The key library PyFMI ver 2.9.8 is installed.

After the installation a small application BPL_CHO_Fedbatch is loaded and run. You can continue with this example if you like.

```
lslsb_release -a # Actual VM Ubuntu version used by Google

No LSB modules are available.
Distributor ID: Ubuntu
Description:   Ubuntu 20.04.5 LTS
Release:      20.04
Codename:     focal

%env PYTHONPATH=

env: PYTHONPATH=

!wget https://repo.anaconda.com/miniconda/Miniconda3-py38_22.11.1-1-Linux-x86_64.sh
!chmod +x Miniconda3-py38_22.11.1-1-Linux-x86_64.sh
!bash ./Miniconda3-py38_22.11.1-1-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.8/site-packages/')

--2023-01-18 14:09:40--  https://repo.anaconda.com/miniconda/Miniconda3-py38_22.11.1-1-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.130.3, 104.16.131.3, 2606:4700::6810:8203, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.130.3|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 64630241 (62M) [application/x-sh]
Saving to: 'Miniconda3-py38_22.11.1-1-Linux-x86_64.sh'

Miniconda3-py38_22. 100%[=====] 61.64M  146MB/s   in 0.4s

2023-01-18 14:09:41 (146 MB/s) - 'Miniconda3-py38_22.11.1-1-Linux-x86_64.sh' saved [64630241/64630241]

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
```

xz-5.2.10	431 KB	: 100% 1.0/1 [00:00<00:00, 3.82it/s]
xz-5.2.10	431 KB	: 100% 1.0/1 [00:00<00:00, 3.82it/s]
sqlite-3.40.1	1.2 MB	: 100% 1.0/1 [00:00<00:00, 2.95it/s]

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

!conda --version
!python --version

conda 22.11.1
Python 3.8.15

!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

```
# Filter out DeprecationWarnings for 'np.float as alias' is needed - wish I could make filter more narrow
#import warnings
#warnings.filterwarnings("ignore")
```

```
%%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_me.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
```

```
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")
```

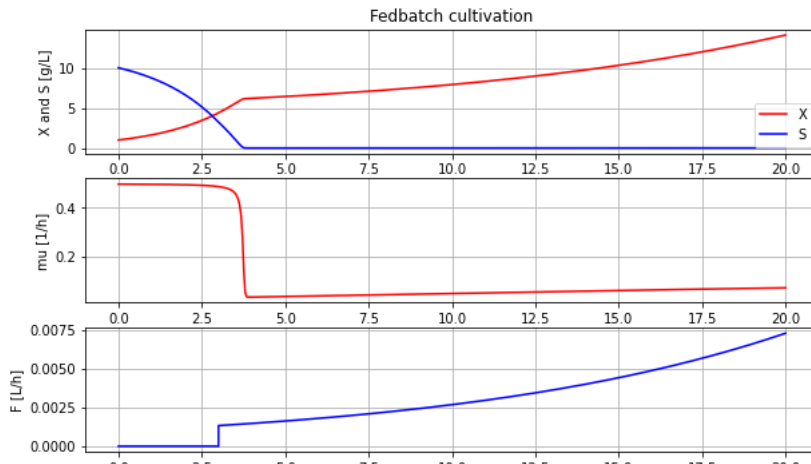
▼ 1 About the process model

We can get information about the process and liquid phase by the command describe(). Here is no gas-phase included. This command can also be used to bring up information about a specific variable or parameter. However, you should use describe() after a simulation to get the values used during the simulation.

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

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

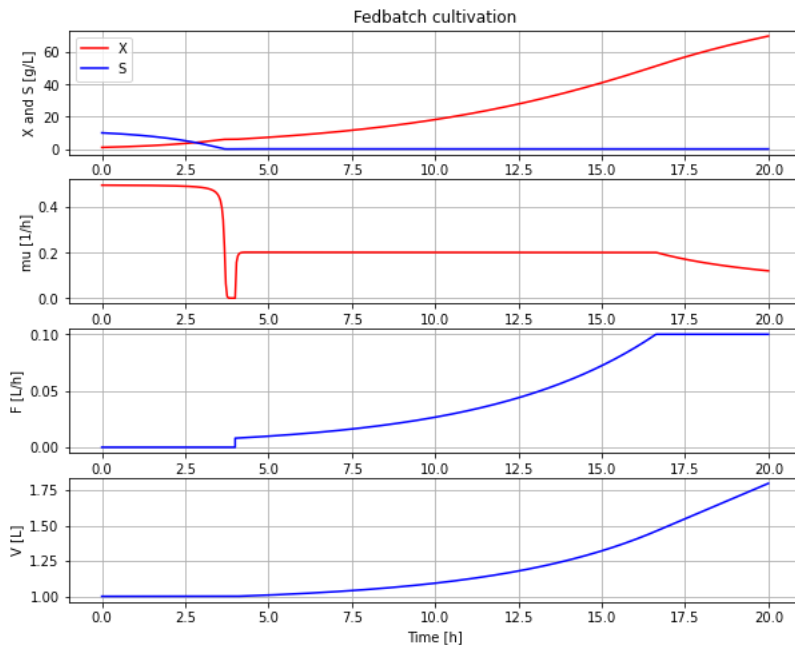
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)
```



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

```
bioreactor.V_0 : V_0 : 1.0
bioreactor.m_0[1] : VX_0 : 1.0
bioreactor.m_0[2] : VS_0 : 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_0 : feedtank.V_0 : 10.0
dosagescheme.mu_feed : mu_feed : 0.1
dosagescheme.t_start : t_start : 3.0
dosagescheme.F_start : F_start : 0.001
dosagescheme.F_max : F_max : 0.3
```

```
# A more typical feed scheme for the culture at hand
newplot(plotType='TimeSeries')
par(t_start=4, F_start=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: information not accessible from this FMU
```

```
system_info()
```



System information

```
-OS: Linux  
-Python: 3.8.10  
-Scipy: not installed in the notebook  
-PyFMI: 2.9.8  
-FMU by: OpenModelica Compiler OpenModelica 1.21.0~dev-185-g9d983b8  
-FMI: 2.0  
-Type: FMUModelME2  
-Name: BPL.TEST2_INTERNAL.Fedbatch  
-Generated: 2023-01-17T13:48:34Z  
-MSL: MSL.version information not accessible  
-Description: BPL.version information not accessible  
-Interaction: FMU-explore version 0.9.6d
```

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✓ 0s completed at 15:11

