

▼ BPL_TEST2_Fedbatch script with FMPy 0.3.15

The key library FMPy ver 0.3.15 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 22.04.2 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/')

--2023-09-13 06:21:11-- https://repo.anaconda.com/miniconda/Miniconda3-py310\_23.1.0-1-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: 74403966 (71M) [application/x-sh]
Saving to: 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh'

Miniconda3-py310_23 100%[=====>] 70.96M 145MB/s in 0.5s

2023-09-13 06:21:11 (145 MB/s) - 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh' saved [74403966/74403966]

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 23.7.4  
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

brotdli-1.0.9	375 KB	:	4% 0.042610296794865124/1	[00:00<00:06, 6.79s/it]
matplotlib-base-3.7.	6.7 MB	:	0% 0.002337417250949647/1	[00:00<02:06, 126.77s/it]
munkres-1.1.4	13 KB	:	100% 1.0/1	[00:00<00:00, 3.78it/s]
fonttools-4.25.0	632 KB	:	3% 0.02530132575611338/1	[00:00<00:13, 14.04s/it]
matplotlib-3.7.1	8 KB	:	100% 1.0/1	[00:00<00:00, 2.68it/s]
contourpy-1.0.5	204 KB	:	100% 1.0/1	[00:00<00:00, 2.93it/s]
contourpy-1.0.5	204 KB	:	100% 1.0/1	[00:00<00:00, 2.93it/s]
brotdli-1.0.9	375 KB	:	100% 1.0/1	[00:00<00:00, 2.83it/s]
matplotlib-3.7.1	8 KB	:	100% 1.0/1	[00:00<00:00, 2.68it/s]
matplotlib-base-3.7.	6.7 MB	:	81% 0.8134212033304772/1	[00:00<00:00, 2.29it/s]
fonttools-4.25.0	632 KB	:	100% 1.0/1	[00:00<00:00, 1.55it/s]
fonttools-4.25.0	632 KB	:	100% 1.0/1	[00:00<00:00, 1.55it/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/CONF_2023_10_MODELICA15

Cloning into 'CONF_2023_10_MODELICA15'...

%cd CONF_2023_10_MODELICA15

/content/CONF_2023_10_MODELICA15/CONF_2023_10_MODELICA15

run -i BPL_TEST2_Fedbatch_fmpy_explore.py

Linux - run FMU pre-comiled 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

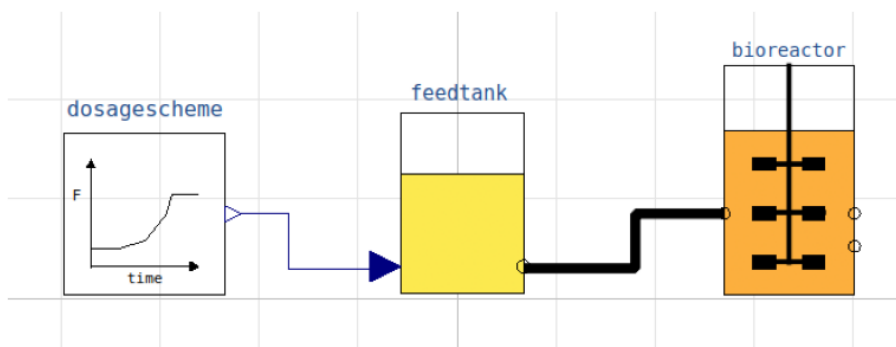
Brief information about a command by help(), eg help(simu)
Key system information is listed with the command system_info()
<Figure size 984.252x787.402 with 0 Axes>

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

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

▼ BPL_TEST2_Fedbatch - demo

```
process_diagram()
```

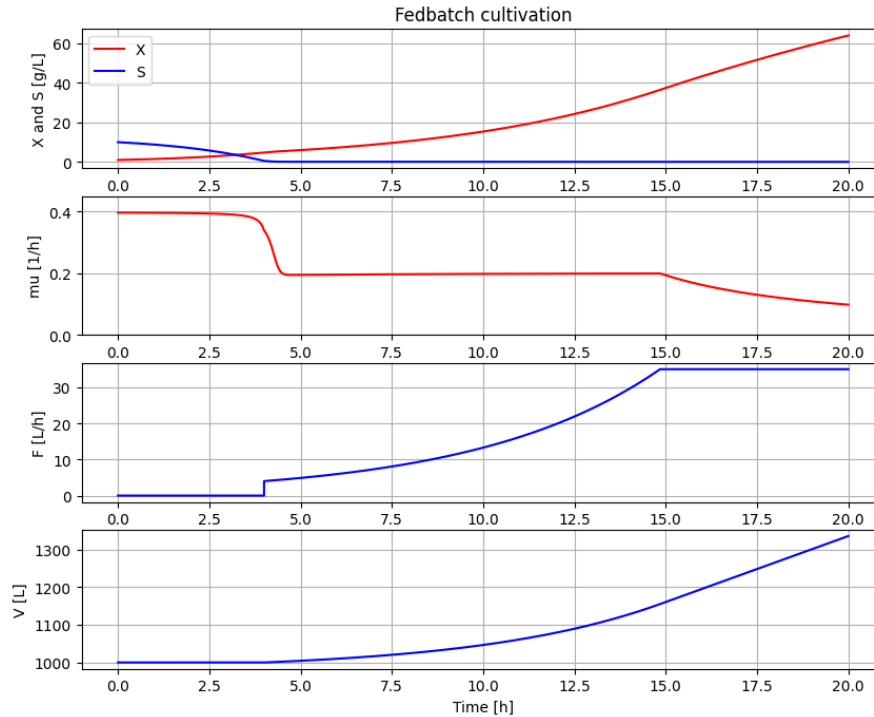


```
describe('culture'); print(); #describe('liquidphase')
```

```
# Pump schedule parameter
```

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

```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
ax2.set_ylim([0, 0.45])
init(V_0=1000, VX_0=1*1e3, VS_0=10*1e3)
par(feedtank_S_in=600, Ks=0.1, Y=0.40)
par(t_start=4, F_start=4.0, mu_feed=0.2, F_max=35)
simu(20)
```



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

```
bioreactor.V_0 : V_0 : 1000
bioreactor.m_0[1] : VX_0 : 1000.0
bioreactor.m_0[2] : VS_0 : 10000.0
bioreactor.culture.Y : Y : 0.4
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1
feedtank.c_in[2] : feedtank_S_in : 600
feedtank.V_0 : feedtank_V_0 : 10.0
dosagescheme.mu_feed : mu_feed : 0.2
dosagescheme.t_start : t_start : 4
dosagescheme.F_start : F_start : 4.0
dosagescheme.F_max : F_max : 35
```

```
describe('mu')
```

```
Cell specific growth rate variable : 0.098 [ 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: 0.3.15  
-FMU by: OpenModelica Compiler OpenModelica 1.21.0  
-FMI: 2.0  
-Type: ME  
-Name: BPL_TEST2.Fedbatch  
-Generated: 2023-04-20T12:24:29Z  
-MSL: 3.2.3  
-Description: Bioprocess Library version 2.1.1  
-Interaction: FMU-explore for FMPy version 0.9.8
```

✓ 0s completed at 08:31

