## 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 22.04.3 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/')
    --2024-01-18 09:52:29-- 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::6810:8303, ...
    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'
    2024-01-18 09:52:29 (122 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 23.11.0 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
                                        py310h1128e8f_0
                                                                 6.8 MB
        matplotlib-base-3.8.0
        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::matplotlib-base-3.8.0-py310h1128e8f_0
    The following packages will be SUPERSEDED by a higher-priority channel:
                          \label{local-conda-forge/noarch::certifi-2023.11.17-py310h06a4308_0 conda-forge::conda-23.11.0-py310hff52^- --> pkgs/main::conda-23.11.0-py310h06a4308_0 \\
       certifi
      conda
                          conda-forge/noarch::pyparsing-3.1.1-p~ --> pkgs/main/linux-64::pyparsing-3.0.9-py310h06a4308_0
      pyparsing
    Downloading and Extracting Packages:
                                             0% 0/1 [00:00<?, ?it/s]
    matplotlib-base-3.8. | 6.8 MB
                                      | :
     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]
    pyparsing-3.0.9
                          | 153 KB
                                       | : 10% 0.10471552197977783/1 [00:00<00:01, 1.26s/it]
    matplotlib-base-3.8. | 6.8 MB
                                            0% 0.0022928172852449986/1 [00:00<01:08, 68.60s/it]
                                       1:
                          | 8 KB
    matplotlib-3.8.0
                                       | : 100% 1.0/1 [00:00<00:00, 7.35it/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-comiled OpenModelica 1.21.0
    Model for bioreactor has been setup. Key commands:
                   - change of parameters and initial values
     - par()
                   - change initial values only
     - init()
                   - simulate and plot
     - simu()
     - newplot()

    make a new plot

                   - show plot from previous simulation
     - show()
                    - 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]
```

## BPL\_TEST2\_Fedbatch - demo

warnings.filterwarnings("ignore")

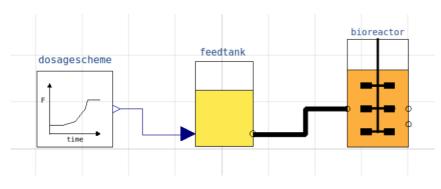
```
describe('culture'); print(); #describe('liquidphase')
```

# Pump schedule parameter

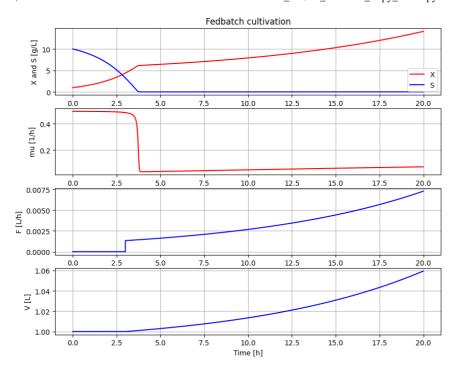
Simplified text book model – only substrate S and cell concentration  $\boldsymbol{X}$ 

process\_diagram()

import warnings



# 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.Ysmax: 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)

```
Fedbatch cultivation
      60 40 20
40 20
        0.4
      mu [1/h]
        0.2
disp('culture')
    Y: 0.5
    qSmax : 1.0
    Ks : 0.1
          1 1
describe('mu')
    Cell specific growth rate variable : 0.12 [ 1/h ]
     ⊒ 1.50
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
-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
```