# 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.

```
!lsb_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/')
```

```
--2023-01-21 09:18:29--  https://repo.anaconda.com/miniconda/Miniconda3-py38_22.11.1-1-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.131.3, 104.16.130.3, 2606:4700::6810:8203, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.131.3|: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   167MB/s    in 0.4s

2023-01-21 09:18:29 (167 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
```

```
sundials -> suitesparse[version='>=5.10.1,<6.0a0']

Package sundials conflicts for:
assimulo -> sundials[version='>=6.4.0,<6.5.0a0']
pyfmi -> assimulo[version='>=3.0'] -> sundials[version='>=6.4.0,<6.5.0a0']

Package scipy conflicts for:
assimulo -> scipy
pyfmi -> scipy

Package enum34 conflicts for:
conda -> enum34
conda-content-trust -> cryptography -> enum34The following specifications were found to be incompatible with your system:

  - feature:/linux-64::__glibc==2.31=0
  - feature:|@/linux-64::__glibc==2.31=0
  - assimulo -> libgfortran-ng -> __glibc[version='>=2.17']
  - libopenblas -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
  - numpy -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
  - openssl -> libgcc-ng[version='>=7.5.0'] -> __glibc[version='>=2.17']
  - python=3.8 -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
  - scipy -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
  - suitesparse -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
  - tbb -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']

Your installed version is: 2.31
```

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

```
conda 22.11.1
Python 3.8.15
```

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

```
Collecting package metadata (current_repodata.json): done
Solving environment: |
The environment is inconsistent, please check the package plan carefully
The following packages are causing the inconsistency:

  - conda-forge/linux-64::tbb==2021.7.0=h924138e_1
  - conda-forge/linux-64::numpy==1.24.1=py38hab0fcb9_0
  - conda-forge/linux-64::suitesparse==5.10.1=h9e50725_1
  - conda-forge/linux-64::scipy==1.10.0=py38h10c12cc_0
  - conda-forge/linux-64::libcblas==3.9.0=16_linux64_openblas
  - conda-forge/linux-64::libopenblas==0.3.21=pthreads_h78a6416_3
  - conda-forge/linux-64::pyfmi==2.9.8=py38h26c90d9_1
  - conda-forge/linux-64::assimulo==3.3=py38h71f17ff_1
  - conda-forge/linux-64::libblas==3.9.0=16_linux64_openblas
  - conda-forge/linux-64::liblapack==3.9.0=16_linux64_openblas
  - conda-forge/linux-64::libhwloc==2.8.0=h32351e8_1
  - conda-forge/linux-64::fmilib==2.4.1=h27087fc_0
  - conda-forge/linux-64::sundials==6.4.1=h89a52a3_done

## Package Plan ##

  environment location: /usr/local

  added / updated specs:
    - pyfmi


The following packages will be REMOVED:

  libgomp-11.2.0-h1234567_1

The following packages will be UPDATED:

  ca-certificates    pkgs/main::ca-certificates-2022.10.11~ --> conda-forge::ca-certificates-2022.12.7-ha878542_0
  libgcc-ng          pkgs/main::libgcc-ng-11.2.0-h1234567_1 --> conda-forge::libgcc-ng-12.2.0-h65d4601_19
  libstdcxx-ng       pkgs/main::libstdcxx-ng-11.2.0-h12345~ --> conda-forge::libstdcxx-ng-12.2.0-h46fd767_19
  openssl              pkgs/main::openssl-1.1.1s-h7f8727e_0 --> conda-forge::openssl-1.1.1s-h0b41bf4_1

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

  _libgcc_mutex           pkgs/main::_libgcc_mutex-0.1-main --> conda-forge::_libgcc_mutex-0.1-conda_forge
  _openmp_mutex          pkgs/main::_openmp_mutex-5.1-1_gnu --> conda-forge::_openmp_mutex-4.5-2_kmp_llvm
  certifi            pkgs/main/linux-64::certifi-2022.12.7~ --> conda-forge/noarch::certifi-2022.12.7-pyhd8ed1ab_0
  conda              pkgs/main::conda-22.11.1-py38h06a4308~ --> conda-forge::conda-22.11.1-py38h578d9bd_1



Downloading and Extracting Packages

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

```
%%bash
git clone https://github.com/janpeter19/BPL_TEST2_Fedbatch
```

```
Cloning into 'BPL_TEST2_Fedbatch'...
```

```
%cd BPL_TEST2_Fedbatch
```

```
/content/BPL_TEST2_Fedbatch/BPL_TEST2_Fedbatch/BPL_TEST2_Fedbatch/BPL_TEST2_Fedbatch
```

```
run -i BPL_TEST2_Fedbatch_explore_me.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 simula
 - describe()  - describe culture, broth, parameters, variables with values

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()
<Figure size 708.661x566.929 with 0 Axes>
```

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

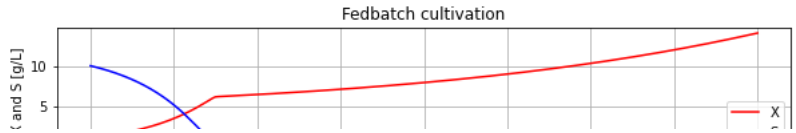
```
import warnings
warnings.filterwarnings("ignore")
```

# BPL_TEST2_Fedbatch - demo

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

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

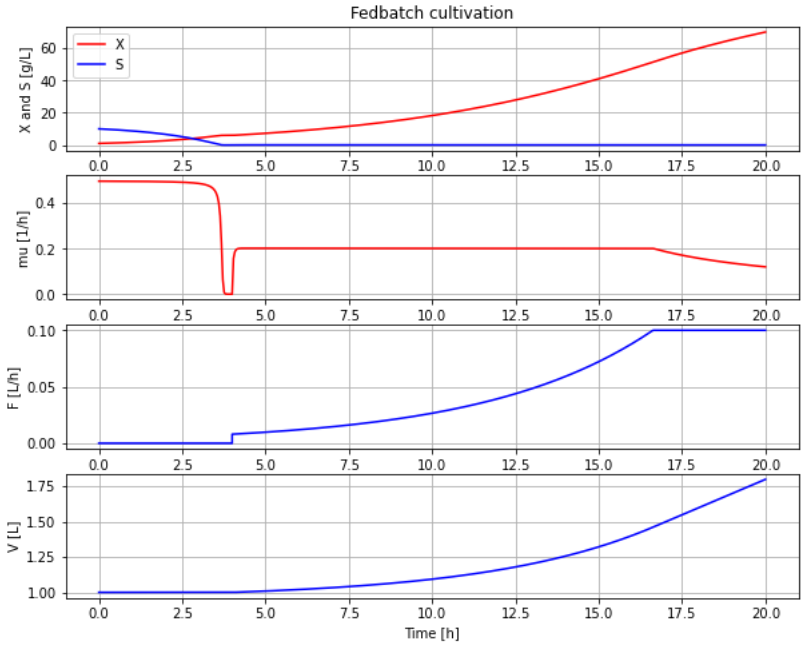
```
# Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)
```




```
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: 3.2.3 - used components: RealInput, RealOutput, CombiTimeTable, Types
```

```
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.Fedbatch
-Generated: 2023-01-19T09:29:14Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.1.1-beta
-Interaction: FMU-explore version 0.9.6e
```



✓ 0s completed at 10:22