

## ▼ BPL\_TEST2\_Fedbatch script with PyFMI

The key library PyFMI 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/')

--2023-08-19 11:26:59-- 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.2'

Miniconda3-py310_23 100%[=====] 70.96M 248MB/s in 0.3s

2023-08-19 11:27:00 (248 MB/s) - 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh.2' 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
```

```
assimulo -> scipy
pyfmi -> scipy
```

Package mpfr conflicts for:

```
sundials -> suitesparse[version='>=5.10.1,<6.0a0'] -> mpfr[version='>=4.0.2,<5.0a0']
suitesparse -> mpfr[version='>=4.0.2,<5.0a0']
```

Package setuptools conflicts for:

```
python=3.10 -> pip -> setuptools
conda[version='>=23.1.0'] -> ruamel.yaml[version='>=0.11.14,<0.18'] -> setuptools
wheel -> setuptools
conda[version='>=23.1.0'] -> setuptools[version='>=31.0.1|>=60.0.0']
pip -> setuptoolsThe following specifications were found to be incompatible with your system:
```

```
- feature:/linux-64::__glibc==2.35=0
- feature:|@/linux-64::__glibc==2.35=0
- assimulo -> libgfortran-ng -> __glibc[version='>=2.17']
- libopenblas -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
- libxslt -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
- lxml -> libgcc-ng[version='>=11.2.0'] -> __glibc[version='>=2.17']
- metis -> libgcc-ng[version='>=7.2.0'] -> __glibc[version='>=2.17']
- mpfr -> libgcc-ng[version='>=7.3.0'] -> __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=3.10 -> 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']
```

Your installed version is: 2.35

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

```
conda 23.1.0
Python 3.10.9
```

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

```
- conda-forge/linux-64::suitesparse==5.10.1=hd8046ac_0
- conda-forge/linux-64::libxslt==1.1.37=h873f0b0_0
- conda-forge/linux-64::mpfr==4.2.0=hb012696_0
- conda-forge/linux-64::fmilib==2.4.1=h59595ed_0
- conda-forge/linux-64::liblapack==3.9.0=17_linux64_openblas
- conda-forge/linux-64::assimulo==3.4.1=py310h48d6207_4
- conda-forge/linux-64::libcblas==3.9.0=17_linux64_openblas
- defaults/linux-64::lxml==4.9.2=py310h5eee18b_0
- conda-forge/linux-64::sundials==6.6.0=h777d08e_done
```

```
==> WARNING: A newer version of conda exists. <==
current version: 23.1.0
latest version: 23.7.2
```

Please update conda by running

```
$ conda update -n base -c defaults conda
```

Or to minimize the number of packages updated during conda update use

```
conda install conda=23.7.2
```

```
## Package Plan ##
```

```
environment location: /usr/local
```

```
added / updated specs:
- pyfmi
```

The following packages will be REMOVED:

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
```

Downloading and Extracting Packages

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

## ▼ BPL\_TEST2\_Fedbatch setup

This notebook just produce the Figure 2 in the paper "Design ideas behind Bioprocess Library for Modelica", by J P Axelsson, to be presented at the 15th International Modelica Conference in Aachen, Germany, October 9-11, 2023.

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/CONF_2023_10_MODELICA15

Cloning into 'CONF_2023_10_MODELICA15'...

%cd CONF_2023_10_MODELICA15

/content/CONF_2023_10_MODELICA15

run -i BPL_TEST2_Fedbatch_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

Brief information about a command by help(), eg help(simu)
Key system information is listed with the command system_info()

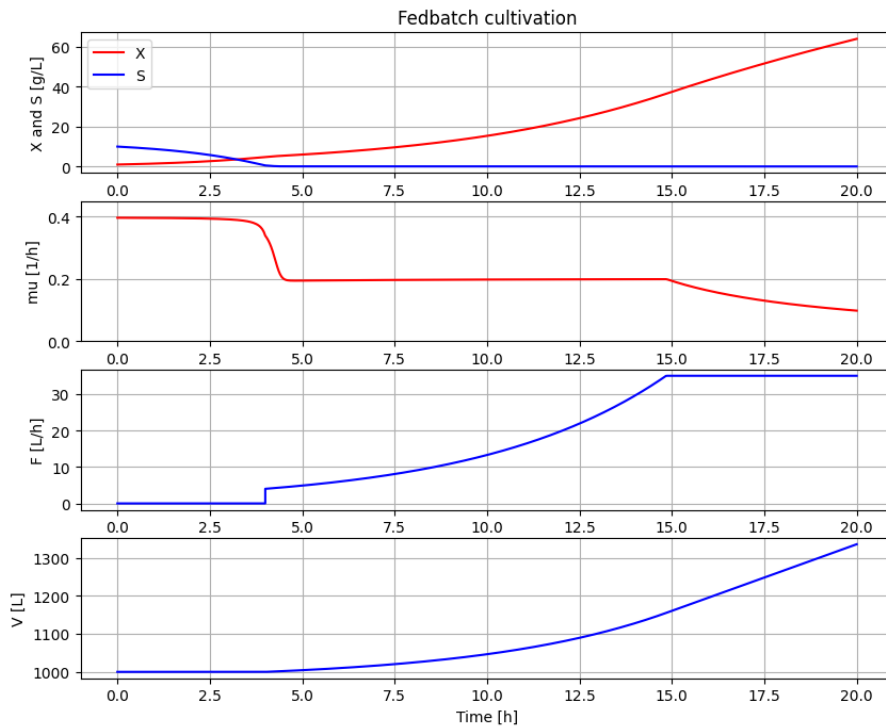
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]

import warnings
warnings.filterwarnings("ignore")

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

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

# Simulation 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('culture')
```

```
Y : 0.4
qSmax : 1.0
Ks : 0.1
```

```
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
-PyFMI: 2.11.0
-FMU by: OpenModelica Compiler OpenModelica 1.21.0
-FMI: 2.0
-Type: FMUModelME2
-Name: BPL_TEST2.Fedbatch
-Generated: 2023-04-20T12:24:29Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.1.1
-Interaction: FMU-explore version 0.9.7
```

---

✓ 0s    completed at 13:37

● ×