→ BPL_TEST2_Chemostat script with PyFMI ver 2.7.4

The key library PyFMI v2.7.4 is installed and downgrading is done Numpy v1.19.1. To simplify this we first install conda.

After the installation a small application BPL_TEST2_Chemostat 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 18.04.6 LTS

18.04 Release: Codename: bionic

%env PYTHONPATH=



env: PYTHONPATH=

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py37 4.12.0-Linux-x86 64.sh
!chmod +x Miniconda3-py37_4.12.0-Linux-x86_64.sh
!bash ./Miniconda3-py37 4.12.0-Linux-x86 64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.7/site-packages/')
    --2022-10-18 06:12:30-- https://repo.anaconda.com/miniconda/Miniconda3-py37 4
    Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.130.3, 104.16.131.3,
    Connecting to repo.anaconda.com (repo.anaconda.com) | 104.16.130.3 | :443... conne
    HTTP request sent, awaiting response... 200 OK
    Length: 104996770 (100M) [application/x-sh]
    Saving to: 'Miniconda3-py37 4.12.0-Linux-x86 64.sh'
    2022-10-18 06:12:31 (131 MB/s) - 'Miniconda3-py37 4.12.0-Linux-x86 64.sh' save
    PREFIX=/usr/local
    Unpacking payload ...
    Collecting package metadata (current_repodata.json): done
    Solving environment: failed with initial frozen solve. Retrying with flexible
    Solving environment: failed with repodata from current repodata.json, will ret
    Collecting package metadata (repodata.json): done
    Solving environment: failed with initial frozen solve. Retrying with flexible
    Solving environment: /
    Found conflicts! Looking for incompatible packages.
    This can take several minutes. Press CTRL-C to abortfailed
    UnsatisfiableError: The following specifications were found to be incompatible
    Output in format: Requested package -> Available versions
```

```
Package libgcc-ng conflicts for:
    setuptools==61.2.0=py37h06a4308 0 -> python[version='>=3.7,<3.8.0a0'] -> libgc
    conda-package-handling==1.8.1=py37h7f8727e 0 -> libgcc-ng[version='>=7.5.0']
    numpy -> libgcc-ng[version='>=10.3.0|>=7.3.0']
    python==3.7.13=h12debd9 0 -> libgcc-ng[version='>=7.5.0']
    cffi==1.15.0=py37hd667e15 1 -> libffi[version='>=3.3'] -> libgcc-ng[version='>
    assimulo -> libgcc-ng[version='>=9.4.0']
    scipy -> numpy[version='>=1.18.5,<2.0a0'] -> libgcc-ng[version='>=10.3.0|>=7.3
    tbb -> libgcc-ng[version='>=10.3.0']
    readline==8.1.2=h7f8727e 1 -> ncurses[version='>=6.3,<7.0a0'] -> libgcc-ng[ver
    libiconv -> libgcc-ng[version='>=10.3.0']
    pyfmi -> assimulo[version='>=3.0'] -> libgcc-ng[version='>=10.3.0|>=9.4.0|>=7.
    ruamel_yaml==0.15.100=py37h27cfd23_0 -> python[version='>=3.7,<3.8.0a0'] -> li
    lxml -> libxml2[version='>=2.9.10,<2.11.0a0'] -> libqcc-ng[version='>=7.5.0|>=
    yaml==0.2.5=h7b6447c 0 -> libgcc-ng[version='>=7.3.0']
    pycosat==0.6.3=py37h27cfd23_0 -> python[version='>=3.7,<3.8.0a0'] -> libgcc-nc
    ncurses==6.3=h7f8727e 2 -> libgcc-ng[version='>=7.5.0']
    openssl==1.1.1n=h7f8727e 0 -> libgcc-ng[version='>=7.5.0']
    icu -> libgcc-ng[version='>=9.4.0']
    cryptography==36.0.0=py37h9cele76 0 -> cffi[version='>=1.12'] -> libgcc-ng[ver
    libopenblas -> libgcc-ng[version='>=10.3.0']
    pyfmi -> libgcc-ng[version='>=7.5.0']
    pip==21.2.2=py37h06a4308 0 -> python[version='>=3.7,<3.8.0a0'] -> libgcc-ng[ve
    pycparser==2.21=pyhd3eb1b0_0 -> python[version='>=3.6'] -> libgcc-ng[version='
    suitesparse -> metis[version='>=5.1.0,<5.2.0a0'] -> libgcc-ng[version='>=10.3.
    toolz -> python[version='>=3.5'] -> libgcc-ng[version='>=7.5.0']
    sqlite=3.38.2=hc218d9a 0 -> zlib[version='>=1.2.11,<1.3.0a0'] -> libgcc-ng[ve
    sqlite==3.38.2=hc218d9a 0 -> libqcc-ng[version='>=7.5.0']
    libblas -> libopenblas[version='>=0.3.20,<0.3.21.0a0'] -> libgcc-ng[version='>
    libgcc-ng==9.3.0=h5101ec6 17
    conda-content-trust==0.1.1=pyhd3eb1b0_0 -> cryptography -> libgcc-ng[version='
          !conda update -n base -c defaults conda --yes
    Collecting package metadata (current repodata.json): done
    Solving environment: done
    ## Package Plan ##
      environment location: /usr/local
      added / updated specs:
        - conda
    The following packages will be SUPERSEDED by a higher-priority channel:
      ca-certificates
                         conda-forge::ca-certificates-2022.9.2~ --> pkgs/main::ca-
      certifi
                         conda-forge/noarch::certifi-2022.9.24~ --> pkgs/main/linu
                         conda-forge::conda-22.9.0-py37h89c186~ --> pkgs/main::cor
      conda
    Preparing transaction: done
    Verifying transaction: done
    Executing transaction: done
    Retrieving notices: ...working... done
```

```
!python --version
    conda 22.9.0
    Python 3.7.13
!conda install -c conda-forge pyfmi==2.7.4 --yes # Install the key package
    Collecting package metadata (current repodata.json): done
    Solving environment: done
    ## Package Plan ##
      environment location: /usr/local
      added / updated specs:
        - pyfmi==2.7.4
    The following packages will be UPDATED:
                         pkgs/main::ca-certificates-2022.07.19~ --> conda-forge::c
      ca-certificates
      conda
                         pkgs/main::conda-22.9.0-py37h06a4308 0 --> conda-forge::c
    The following packages will be SUPERSEDED by a higher-priority channel:
      certifi
                         pkgs/main/linux-64::certifi-2022.9.24~ --> conda-forge/nc
    Preparing transaction: done
    Verifying transaction: done
    Executing transaction: done
    Retrieving notices: ...working... done
!conda install numpy=1.19.1 --yes # Need to downgrade numpy
    Collecting package metadata (current_repodata.json): done
    Solving environment: failed with initial frozen solve. Retrying with flexible
    Collecting package metadata (repodata.json): done
    Solving environment: done
    ## Package Plan ##
      environment location: /usr/local
      added / updated specs:
        - numpy=1.19.1
    The following packages will be downloaded:
        package
                                                               46 KB
        blas-1.0
                                            openblas
```

The following NEW packages will be INSTALLED:

Total:

46 KB

conda-forge/noarch::certifi-2022.9.24~ --> pkgs/main/linu

conda-forge::conda-22.9.0-py37h89c186~ --> pkgs/main::cor conda-forge::numpy-1.21.6-py37h976b52~ --> pkgs/main::num

certifi

conda

numpy

```
blas
                     pkgs/main/linux-64::blas-1.0-openblas None
                     pkgs/main/linux-64::numpy-base-1.19.1-py37h75fe3a5 0 None
 numpy-base
The following packages will be SUPERSEDED by a higher-priority channel:
 ca-certificates
                     conda-forge::ca-certificates-2022.9.2~ --> pkgs/main::ca-
```

```
Downloading and Extracting Packages
blas-1.0
                                : 100% 1.0/1 [00:00<00:00, 18.26it/s]
                     | 46 KB
```

ChecksumMismatchError: Conda detected a mismatch between the expected content for url 'https://repo.anaconda.com/pkgs/main/linux-64/blas-1.0-openblas.conda' download saved to: /usr/local/pkgs/blas-1.0-openblas.conda expected sha256: c85b5d0a336b5be0f415c71fd7fe2eca59e09f42221bfa684aafef5510k actual sha256: 5dc5483db0d9785b19e021cee418a8ee03e0ff0e5ebd0b75af4927746604e

Now specific installation run a simulation and notebook for that

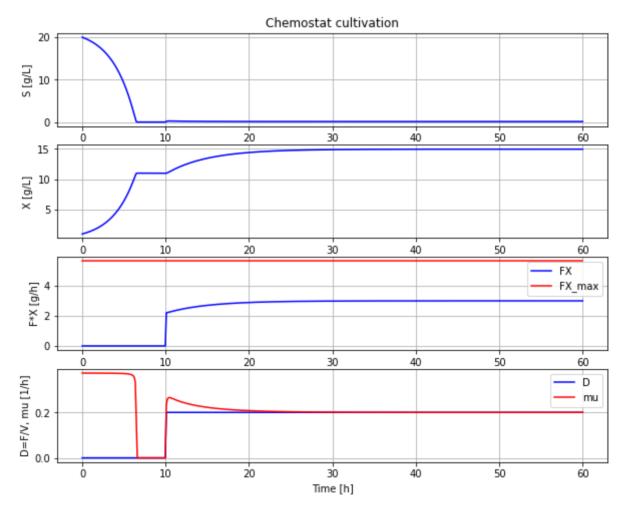
Start with connecting to Github. Then upload the two files:

- FMU BPL_TEST2_Chemostat_linux_im_cs.fmu
- Setup-file BPL_TEST2_Chemostat_explore.py

```
# Filter out DepracationWarnings for 'np.float as alias' is needed - wish I could m
import warnings
warnings.filterwarnings("ignore")
%%bash
git clone https://github.com/janpeter19/BPL TEST2 Chemostat
    Cloning into 'BPL TEST2 Chemostat'...
%cd BPL TEST2 Chemostat
    /content/BPL TEST2 Chemostat/BPL TEST2 Chemostat/BPL TEST2 Chemostat/BPL TEST2
run -i BPL TEST2 Chemostat explore.py
```

Linux - run FMU pre-compiled JModelica 2.4

```
Model for bioreactor has been setup. Key commands:
                   - change of parameters and initial values
     - par()
     - init()
                   - change initial values only
     - simu()
                   - simulate and plot
                   - make a new plot
     - newplot()
     - show()
                   - show plot from previous simulation
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
    MOLE CHAL DOCH ALBY() AND DESCRIPC() CARES VALUES ITOM CHE TASC SIMULACION
newplot()
par(Y=0.50, qSmax=0.75, Ks=0.1)
                                         # Culture parameters
init(V 0=1.0, VX 0=1.0, VS 0=20)
                                        # Bioreactor startup
par(S in=30, t0=0, F0=0, t1=10, F1=0.2) # Substrate feeding
simu(60)
```



The maximal biomass productivity $FX_max[g/h]$ marked red in the diagram above # can be calculated for CSTR from the FMU and is cstrProdMax(model)

5.625

describe('cstrProdMax')

```
describe('parts')
    ['bioreactor', 'bioreactor.culture', 'D', 'dosagescheme', 'feedtank', 'harvest
system info()
    System information
     -OS: Linux
     -Python: 3.7.15
     -Scipy: not installed in the notebook
     -PyFMI: 2.7.4
     -FMU by: JModelica.org
     -FMI: 2.0
     -Type: FMUModelCS2
     -Name: BPL TEST2.Chemostat
     -Generated: 2022-10-17T11:45:49
     -MSL: 3.2.2 build 3
     -Description: Bioprocess Library version 2.1.0
     -Interaction: FMU-explore version 0.9.5
```

Colab paid products - Cancel contracts here

Os completed at 08:19

X