→ BPL_TEST2_Batch script with FMPy ver 0.3.15

The key library FMPy ver 0.3.15 is installed.

After the installation a small application BPL_YEAST_COB_Batch 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 07:38:12-- https://repo.anaconda.com/miniconda/Miniconda3-py310 23.1
    Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.131.3, 104.16.130.3, 260
    Connecting to repo.anaconda.com (repo.anaconda.com) | 104.16.131.3 | :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'
    in 0.3s
    2023-09-13 07:38:12 (217 MB/s) - 'Miniconda3-py310 23.1.0-1-Linux-x86 64.sh' saved
    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

 $\verb|!conda| install -c conda-forge fmpy -- yes \# Install the key package$

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

```
!conda install matplotlib --yes
```

```
brotli-1.0.9
                    | 375 KB
                               : 4% 0.042610296794865124/1 [00:00<00:08,
                                                                             8.
                                | : 100% 1.0/1 [00:00<00:00, 2.76it/s]
matplotlib-3.7.1
                    | 8 KB
munkres-1.1.4
                    | 13 KB
                                : 100% 1.0/1 [00:00<00:00, 2.69it/s]
                                : 8% 0.0782994341642453/1 [00:00<00:04, 4.79</pre>
contourpy-1.0.5
                    204 KB
                    | 8 KB
                                : 100% 1.0/1 [00:00<00:00, 2.76it/s]
matplotlib-3.7.1
                    | 375 KB
                               : 100% 1.0/1 [00:00<00:00,
brotli-1.0.9
                                                            2.68it/s]
                               : 100% 1.0/1 [00:00<00:00, 2.69it/s]
munkres-1.1.4
                    | 13 KB
matplotlib-base-3.7. | 6.7 MB
                               : 69% 0.6942129235320452/1 [00:00<00:00, 1.75
contourpy-1.0.5
                    204 KB
                               | : 100% 1.0/1 [00:00<00:00, 2.27it/s]
                    204 KB
                                | : 100% 1.0/1 [00:00<00:00, 2.27it/s]
contourpy-1.0.5
                                 : 100% 1.0/1 [00:00<00:00, 1.40it/s]
fonttools-4.25.0
                      632 KB
fonttools-4.25.0
                    632 KB
                                : 100% 1.0/1 [00:00<00:00, 1.40it/s]
```

: 100% 1.0/1 [00:01<00:00, 1.59s/it]

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

matplotlib-base-3.7. | 6.7 MB

```
#!conda install xlrd --yes
#!conda install openpyxl --yes
# For some reason conda installation does not work for optlang
!pip install optlang
    Collecting optlang
      Downloading optlang-1.7.0-py2.py3-none-any.whl (138 kB)
                                              --- 138.3/138.3 kB 2.9 MB/s eta 0:00:00
    Requirement already satisfied: six>=1.9 in /usr/local/lib/python3.10/site-packages
    Collecting swiglpk>=5.0.8
      Downloading swiglpk-5.0.8-cp310-cp310-manylinux_2_17_x86_64.manylinux2014_x86_64
                                                 - 2.3/2.3 MB 51.8 MB/s eta 0:00:00
    Collecting sympy>=1.12.0
      Downloading sympy-1.12-py3-none-any.whl (5.7 MB)
                                               --- 5.7/5.7 MB 57.7 MB/s eta 0:00:00
    Collecting mpmath>=0.19
      Downloading mpmath-1.3.0-py3-none-any.whl (536 kB)
                                               - 536.2/536.2 kB 39.1 MB/s eta 0:00:00
    Installing collected packages: swiglpk, mpmath, sympy, optlang
    Successfully installed mpmath-1.3.0 optlang-1.7.0 swiglpk-5.0.8 sympy-1.12
    WARNING: Running pip as the 'root' user can result in broken permissions and confl
```

BPL_YEAST_COB_Batch setup

Now specific installation and the run simulations. Start with connecting to Github. Then upload the two files:

- FMU BPL_YEAST_COB_Batch_linux_om_me.fmu
- Setup-file BPL_YEAST_COB_Batch_fmpy_explore.py

```
%%bash
git clone https://github.com/janpeter19/BPL YEAST COB Batch
    Cloning into 'BPL_YEAST_COB_Batch'...
%cd BPL YEAST COB Batch
     /content/BPL_YEAST_COB_Batch
run -i BPL_YEAST_COB_Batch_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

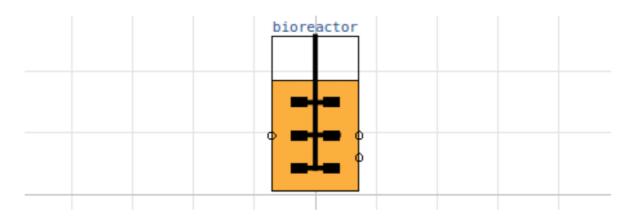
Brief information about a command by help(), eg help(simu) Key system information is listed with the command system info()

```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
import warnings
warnings.filterwarnings("ignore")
```

▼ BPL_YEAST_COB_Batch - demo

from optlang import Model, Variable, Constraint, Objective

process_diagram()



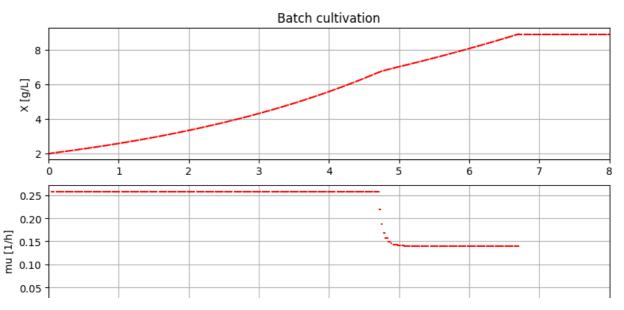
```
describe('culture'); print(); #describe('liquidphase')
```

Saccharomyces cerevisae - default parameters for strain H1022

```
# Define culture constraint-based model
def culture(G, E):
   # LP calculation of the optimal qGr, qEr based on G and E values
   # - parameters
    q02max = 6.9e-3; kog = 2.3; koe = 1.6; YGr = 3.5; YEr = 1.32;
    alpha = 0.01; beta = 1.0
    # - transfer data from dynamic reactor model to static LP model
```

qGr opt = Variable('qGr opt', lb=0)

```
qEr_opt = Variable('qEr_opt', lb=0)
    # - LP model constraint and objective
   mu max = Objective(YGr*qGr opt + YEr*qEr opt, direction='max')
    q02lim = Constraint(kog*qGr opt + koe*qEr opt, ub=q02max)
    qGlim = Constraint(qGr_opt, ub=alpha*max(0,G))
    qElim = Constraint(qEr_opt, ub=beta*max(0,E))
   # - put together the LP model
   yeast model = Model(name='Yeast bottleneck model')
   yeast model.objective = mu max
   yeast model.add(qO2lim)
   yeast model.add(qGlim)
   yeast_model.add(qElim)
   # - do LP optimization
   yeast model.optimize()
   return (yeast model.objective.value, yeast model.variables.qGr opt.primal, yeast mo
# Initialization
V 0=1.0
init(V_0=V_0, VX_0=V_0*2.0, VG_0=V_0*10, VE_0=3.0)
# Loop of simulations
t final = 8.0
t samp = 0.0333
n samp = t final/t samp + 1
# Simulate n sample steps
newplot(title='Batch cultivation', plotType='TimeSeries2')
ax1.set_xlim([0, t_final]); ax2.set_xlim([0, t_final]); ax3.set_xlim([0, t_final])
simu(t samp, options=opts fast)
for i in range(int(n samp)):
    (mum_opt, qGr_opt, qEr_opt, qO2_opt) = culture(sim_res['bioreactor.c[2]'][-1], sim_
    par(mum=mum_opt, qGr=qGr_opt, qEr=qEr_opt, qO2=qO2_opt)
    simu(t_samp, 'cont', options=opts_fast)
```



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_YEAST_COB.Batch

-Generated: 2023-05-31T09:43:28Z

-MSL: 3.2.3

-Description: Bioprocess Library version 2.1.1 -Interaction: FMU-explore for FMPy version 0.9.8

1.7.0

!conda list optlang

optlang

packages in environment at /usr/local: # Name Version

Build Channel pypi_0 pypi

✓ 2s completed at 09:45

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