## BPL\_YEAST\_COB\_Batch script with PyFMI

The key library PyFMI 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 22.04.4 LTS
Release: 22.04
Codename: jammy
```

%env PYTHONPATH=

```
env: PYTHONPATH=
```

!python --version

→ Python 3.11.11

```
!wget https://repo.anaconda.com/miniconda/Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
!chmod +x Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
!bash ./Miniconda3-py311_24.11.1-0-Linux-x86_64.sh -b -f -p /usr/local
import sys
sys.path.append('/usr/local/lib/python3.11/site-packages/')
```

!conda update -n base -c defaults conda --yes

Preparing transaction: ...working... done Executing transaction: ...working... done

→ Channels:
- defaults

Platform: linux-64

installation finished.

Collecting package metadata (repodata.json): done

Solving environment: done

## Package Plan ##

environment location: /usr/local

added / updated specs:

- conda

The following packages will be downloaded:

package	build	
ca-certificates-2024.12.31 certifi-2025.1.31	   h06a4308_0   py311h06a4308_0	128 KB 163 KB
	 Total:	291 KB

The following packages will be UPDATED:

```
ca-certificates 2024.11.26-h06a4308_0 --> 2024.12.31-h06a4308_0
certifi 2024.8.30-py311h06a4308_0 --> 2025.1.31-py311h06a4308_0
```

Downloading and Extracting Packages:

```
0% 0/1 [00:00<?, ?it/s]
0% 0/1 [00:00<?, ?it/s]
    certifi-2025.1.31
                       | 163 KB
                                      |:
    ca-certificates-2024 | 128 KB
                                      |:
                                      | : 100% 1.0/1 [00:00<00:00, 9.54it/s]
    certifi-2025.1.31 | 163 KB
    ca-certificates-2024 | 128 KB
                                      | : 100% 1.0/1 [00:00<00:00, 8.22it/s]
    Preparing transaction: done
    Verifying transaction: done
    Executing transaction: done
!conda --version
!python --version
→ conda 24.11.1
    Python 3.11.11
!conda config --set channel_priority strict
!conda install -c conda-forge pyfmi --yes # Install the key package
₹
```

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

!pip install optlang

```
Collecting optlang
Downloading optlang-1.8.3-py2.py3-none-any.whl.metadata (8.2 kB)
Collecting swiglpk>=5.0.12 (from optlang)
Downloading swiglpk-5.0.12-cp311-cp311-manylinux_2_17_x86_64.manylinux2014_x86_64.whl.metadata (5.5 kB)
Collecting sympy>=1.12.0 (from optlang)
```

## Notes YEAST\_COB\_Batch constraint-based approach

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

- FMU BPL\_YEAST\_AIR\_Fedbatch\_linux\_jm\_cs.fmu
- Setup-file BPL\_YEAST\_AIR\_Fedbatch\_explore

```
%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_explore.py
Fr Linux - run FMU pre-comiled OpenModelica
    Model for bioreactor has been setup. Key commands:
                   - change of parameters and initial values
     - par()
     - init()
                   - change initial values only
     - simu()
                   simulate and plot
     - newplot()
                   - make a new plot
                   - 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()
plt.rcParams['figure.figsize'] = [20/2.54, 16/2.54]
process_diagram()
No processDiagram.png file in the FMU, but try the file on disk.
                                    bioreactor
```

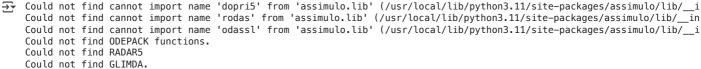
## Try using LP in each step

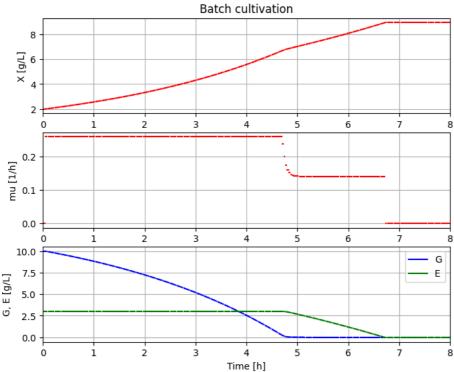
```
from optlang import Model, Variable, Constraint, Objective

# 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(q02lim)
    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_model.variables.qEr_opt.primal, qO2lim.
# Initialization
V_start=1.0
init(V_start=V_start, VX_start=V_start*2.0, VG_start=V_start*10, VE_start=V_start*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)):
    (\texttt{mum\_opt, qGr\_opt, qEr\_opt, q02\_opt}) = \texttt{culture}(\texttt{sim\_res['bioreactor.c[2]'][-1]}, \texttt{sim\_res['bioreactor.c[3]'][-1]})
    par(mum=mum_opt, qGr=qGr_opt, qEr=qEr_opt, q02=q02_opt)
    simu(t_samp, 'cont', options=opts_fast)
    Could not find cannot import name 'dopri5' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/__i
     Could not find cannot import name 'rodas' from 'assimulo.lib' (/usr/local/lib/python3.11/site-packages/assimulo/lib/_
     Could not find ODEPACK functions.
     Could not find RADAR5
     Could not find GLIMDA.
```





```
describe('MSL')
→ MSL: 3.2.3 – used components: none
system_info()
₹
    System information -OS: Linux
      -Python: 3.11.11
      -Scipy: not installed in the notebook
      -PyFMI: 2.16.3
      -FMU by: OpenModelica Compiler OpenModelica 1.25.0~dev-133-ga5470be
      -FMI: 2.0
      -Type: FMUModelME2
      -Name: BPL_YEAST_COB.Batch
      -Generated: 2024-11-08T08:21:20Z
      -MSL: 3.2.3
      -Description: Bioprocess Library version 2.3.0 -Interaction: FMU-explore version 1.0.0 \,
!conda list optlang
# packages in environment at /usr/local:
     # Name
                                 Version
                                                            Build Channel
    optlang
                                                            pypi_0
                                                                       pypi
```