

✓ BPL_TEST2_PID_Fedbatch_reg6 script with FMPy

The key library FMPy is installed.

After the installation a small application BPL_TEST2_PID_Fedbatch_reg6 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 22.04.3 LTS
Release:        22.04
Codename:       jammy

%env PYTHONPATH=

env: PYTHONPATH=

# @title
!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/')

Show hidden output

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

Show hidden output

!conda --version
!python --version

conda 23.11.0
Python 3.10.13

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

Show hidden output

!conda install matplotlib --yes

Show hidden output

#!conda install scipy --yes

#!conda install xlrd --yes

#!conda install openpyxl --yes
```

✓ 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_fmpy_explore.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_PID_Fedbatch_reg6_fmpy_explore.py
```

Linux – run FMU pre-compiled 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)

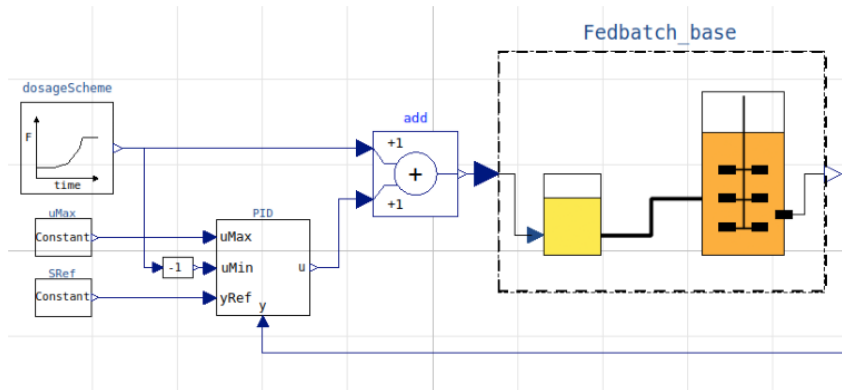
Key system information is listed with the command system_info()

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

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

✓ BPL_TEST2_Fedbatch - demo

```
process_diagram()
```



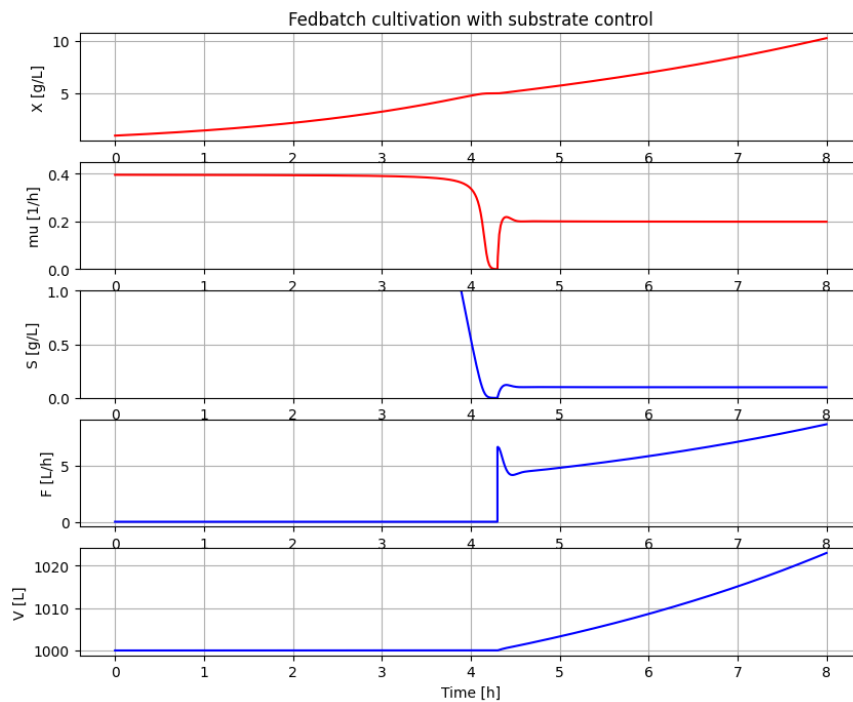
```
describe('culture'); print(); #describe('liquidphase')
```

```
# Pump schedule parameter
```

Simplified text book mode – only substrate S and cell concentration X

```
par(Y=0.40, qSmax=1.0, Ks=0.1)
init(V_0=1e3, VX_0=1e3, VS_0=10*1e3)
# Culture parameters
# Process initialization
par(S_in=600)
par(t_start=4.3, F_start=4, mu_feed=0.2, F_max=35)
par(S_ref=0.1) # Substrate controller
par(t_regStart=4.3)
par(uMax=50)

newplot()
ax2.set_ylim([0, 0.45]); ax3.set_ylim([0, 1])
setLines(['-']);
par(K=30, Ti=0.5)
simu(8)
```



```
disp(mode='long')
```

```
bioreactor.V_0 : V_0 : 1000.0
bioreactor.m_0[1] : VX_0 : 1000.0
bioreactor.m_0[2] : VS_0 : 10000.0
bioreactor.culture.Y : Y : 0.4
bioreactor.culture.qSmax : qSmax : 1.0
bioreactor.culture.Ks : Ks : 0.1
feedtank.V_0 : feedtank_V_0 : 10.0
feedtank.c_in[2] : S_in : 600
dosagescheme.mu_feed : mu_feed : 0.2
dosagescheme.F_0 : F_0 : 0.0
dosagescheme.t_start : t_start : 4.3
dosagescheme.F_start : F_start : 4
dosagescheme.F_max : F_max : 35
substrateSensor.x_0 : Sensor_x_0 : 0
substrateRef.k : S_ref : 0.1
t_regStart : t_regStart : 4.3
PIDreg.K : K : 30
PIDreg.Ti : Ti : 0.5
PIDreg.I_0 : I_0 : 0
uMax : uMax : 50
```

```
describe('mu')
```

```
Cell specific growth rate variable : 0.199 [ 1/h ]
```

```
describe('parts')
```

```
👤 ['bioreactor', 'bioreactor.culture', 'dosagescheme', 'feedtank', 'PIDreg', 'substrateRef', 'substrateSensor', 't_regStar
```

```
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
-FMPy: 0.3.19
-FMU by: OpenModelica Compiler OpenModelica 1.21.0
```

-FMI: 2.0
-Type: ME
-Name: BPL_TEST2_PID.Fedbatch_reg6
-Generated: 2023-08-22T10:54:51Z
-MSL: 3.2.3
-Description: Bioprocess Library version 2.1.1
-Interaction: FMU-explore for FMPy version 0.9.8