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

Ubuntu 22.04.4 LTS Description:

Release: 22.04 Codename: iammv

!python --version

→ Python 3.11.11

!pip install fmpy

→ Collecting fmpy

Downloading FMPy-0.3.22-py3-none-any.whl.metadata (1.9 kB)

Requirement already satisfied: attrs in /usr/local/lib/python3.11/dist-package Requirement already satisfied: Jinja2 in /usr/local/lib/python3.11/dist-package Collecting lark (from fmpy)

Downloading lark-1.2.2-py3-none-any.whl.metadata (1.8 kB)

Requirement already satisfied: lxml in /usr/local/lib/python3.11/dist-package: Requirement already satisfied: msgpack in /usr/local/lib/python3.11/dist-packa Requirement already satisfied: numpy in /usr/local/lib/python3.11/dist-package Requirement already satisfied: MarkupSafe>=2.0 in /usr/local/lib/python3.11/d: Downloading FMPy-0.3.22-py3-none-any.whl (4.9 MB)

- 4.9/4.9 MB 33.4 MB/s eta 0:00:00 Downloading lark-1.2.2-py3-none-any.whl (111 kB)

- 111.0/111.0 kB 3.2 MB/s eta 0:00:0

Installing collected packages: lark, fmpy Successfully installed fmpy-0.3.22 lark-1.2.2

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

```
BPL_TEST2_PID_Fedbatch_reg6_fmpy_colab.ipynb - Colab
%%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-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

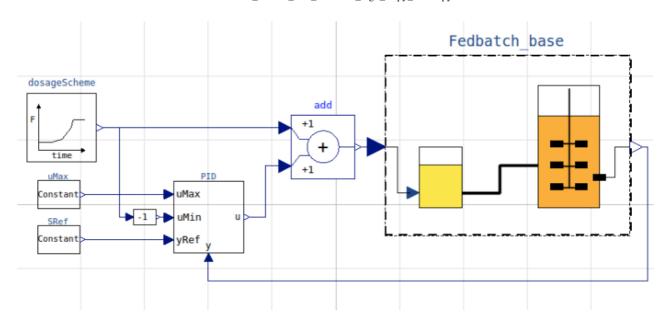
     - newplot() - make a new plot
     - show()
                   - show plot from previous simulation
                   - display parameters and initial values from the last simulation
     - disp()
     - describe() - describe culture, broth, parameters, variables with values/ur
    Note that both disp() 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()
```





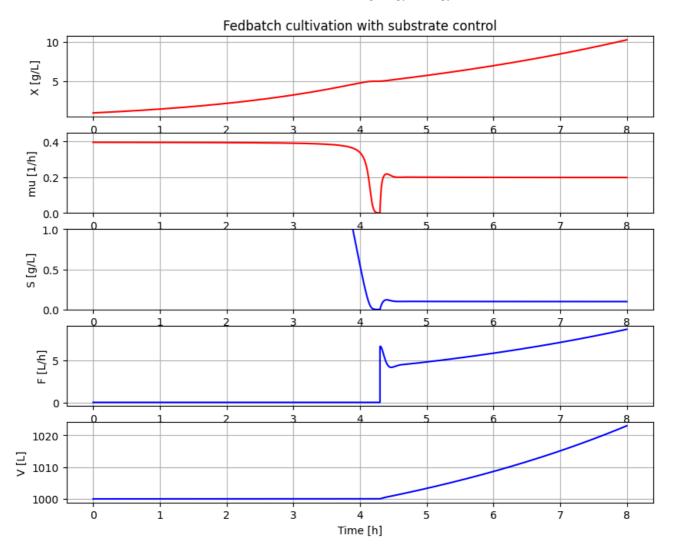
describe('culture'); print(); #describe('liquidphase')

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
```

```
BPL_TEST2_PID_Fedbatch_reg6_fmpy_colab.ipynb - Colab
    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', 'su
describe('MSL')
→ MSL: 3.2.3 – used components: RealInput, RealOutput
system_info()
\rightarrow
    System information
     -OS: Linux
     -Python: 3.11.11
     -Scipy: not installed in the notebook
     -FMPy: 0.3.22
     -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
```