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 22.04.4 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/')
```

```
--2025-02-10 09:48:45--  https://repo.anaconda.com/miniconda/Miniconda3-py311_24.11.1-0-Linux-x86_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.191.158, 104.16.32.241, 2606:4700::6810:20f1, ..
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.191.158|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 145900576 (139M) [application/octet-stream]
Saving to: ‘Miniconda3-py311_24.11.1-0-Linux-x86_64.sh’

Miniconda3-py311_24 100%[===================>] 139.14M   253MB/s    in 0.5s

2025-02-10 09:48:46 (253 MB/s) - ‘Miniconda3-py311_24.11.1-0-Linux-x86_64.sh’ saved [145900576/145900576]

PREFIX=/usr/local
Unpacking payload ...

Installing base environment...

Preparing transaction: ...working... done
Executing transaction: ...working... done
installation finished.
```

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

```
Channels:
 - defaults
Platform: linux-64
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 |       h06a4308_0         128 KB
```

```
    certifi-2025.1.31          |  py311h06a4308_0         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:
certifi-2025.1.31    | 163 KB    | :   0% 0/1 [00:00<?, ?it/s]
certifi-2025.1.31    | 163 KB    | : 100% 1.0/1 [00:00<00:00, 16.02it/s]
ca-certificates-2024 | 128 KB    | : 100% 1.0/1 [00:00<00:00, 14.41it/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 fmpy --yes # Install the key package
```

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

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

```
#!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
```

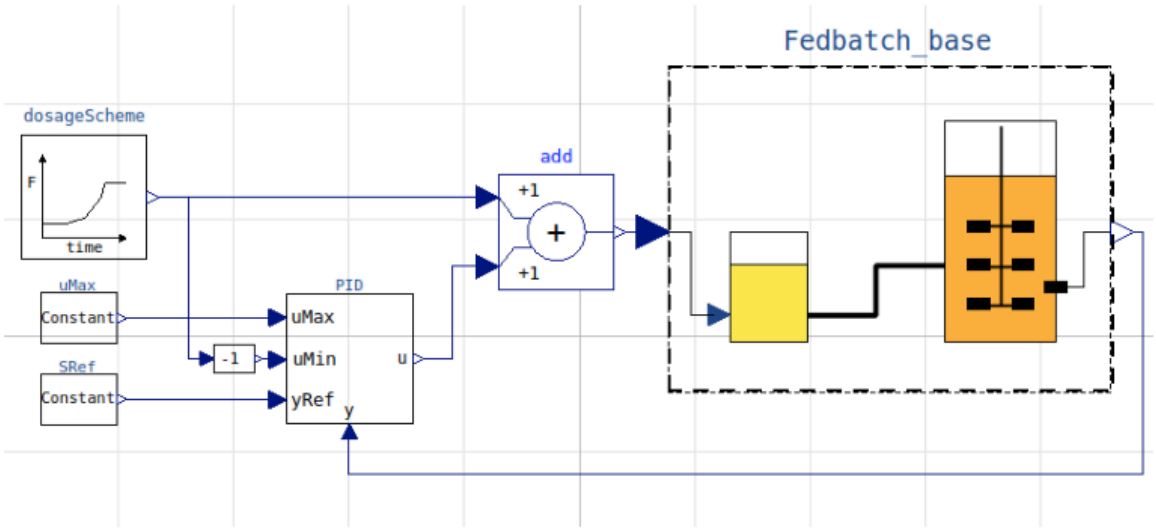
```
Linux - run FMU pre-comiled OpenModelica 1.21.0

    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_TEST2_Fedbatch - demo

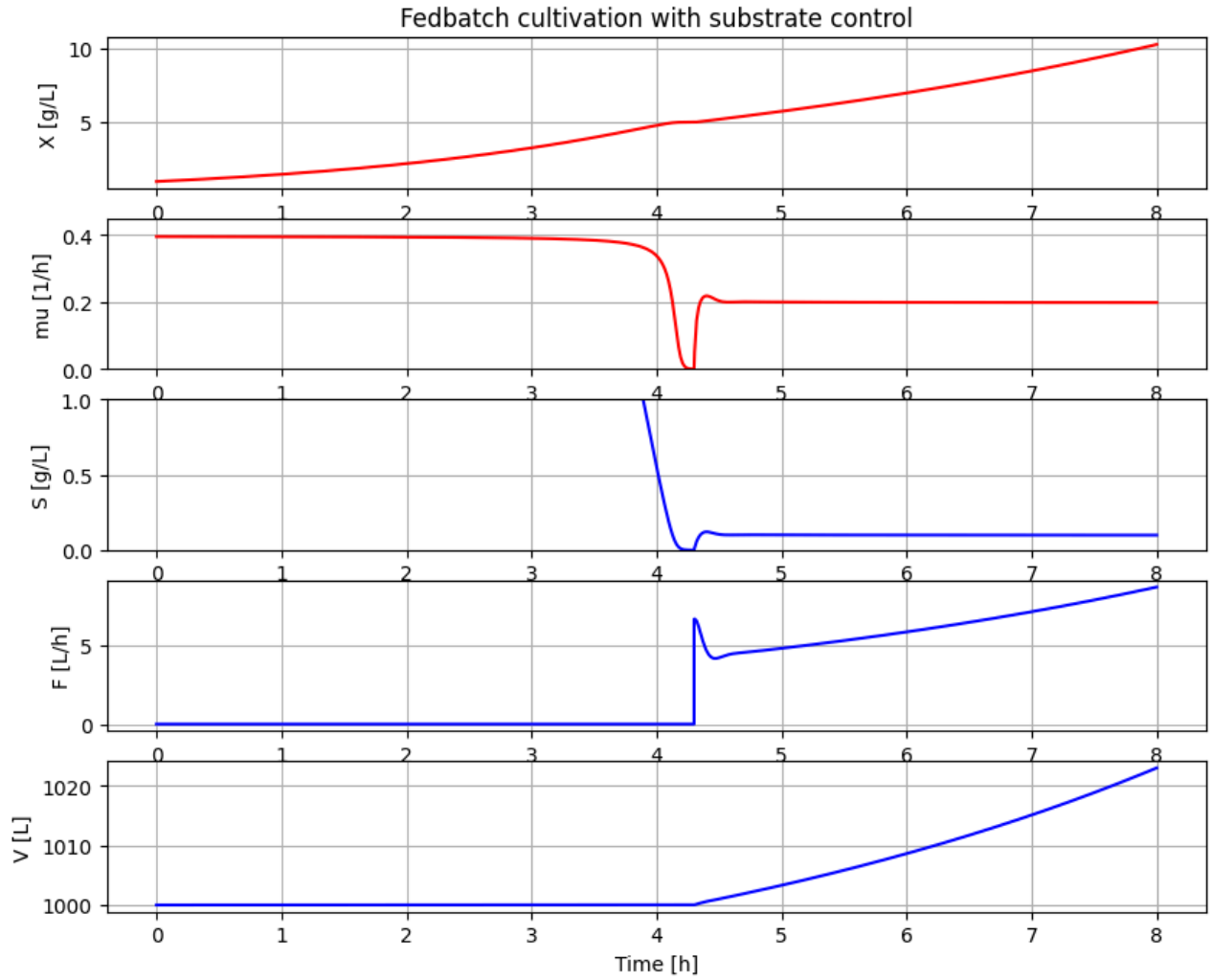
```
process_diagram()
```




```
describe('culture'); print(); #describe('liquidphase')                                    # Pump schedule param
```

```
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', 'substrateSens
```

```
describe('MSL')
```

```
MSL: 3.2.3 - used components: RealInput, RealOutput
```

```
system_info()
```

```
System information
 -OS: Linux
 -Python: 3.11.11
 -Scipy: not installed in the notebook
 -FMPy: 0.3.19
 -FMU by: OpenModelica Compiler OpenModelica 1.21.0
 -FMI: 2.0
 -Type: ME
```