⌄ BPL_TEST2_Fedbatch script with PyFMI

The key library PyFMI is installed.

After the installation a small application BPL_TEST2_Fedbatch 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=
```

```
!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/')

    ––2024–01–22 10:42:26––  https://repo.anaconda.com/miniconda/Miniconda3–py310_23.1.0–1–Linux–x86_64.sh
    Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.130.3, 104.16.131.3, 2606:4700::6810:8303, ...
    Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.130.3|: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'

    Miniconda3–py310_23 100%[===================>]  70.96M  131MB/s    in 0.5s

    2024–01–22 10:42:27 (131 MB/s) – 'Miniconda3–py310_23.1.0–1–Linux–x86_64.sh' saved [74403966/74403966]

    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 23.11.0
      Python 3.10.13
```

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

⌄ Notes: BPL_TEST2_PID_Fedbatch_reg

This notebook just produce the Figure 6 in the paper "Design ideas behind Bioprocess Library for Modelica", by J P Axelsson, to be presented in the 15th International Modelica Conference in Aachen, Germany, October 9-11, 2023.

Test run for in BPL_TEST2_PID test-case fedbatch_reg that demonstarate substrate control of the feed flow around fixed exponential dosage scheme. Note, that here is a small drift from mu_ref at the end.

Note For the JModelica compilation the derivative part and thus Td, and N cannot be used. Likely due to usage of MSL 3.2.2

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

- FMU - BPL_TEST2_PID_Fedbatch_reg6_linux_om_me.fmu
- Setup-file - BPL_TEST2_PID_Fedbatch_reg6_explore.me.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_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()
```
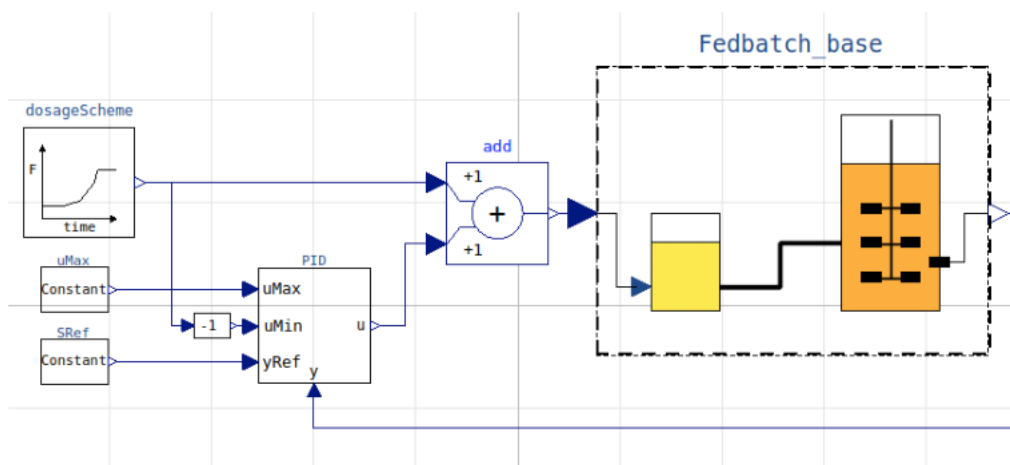
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

```
process_diagram()
```

```
# Simulation of the process with controller
par(Y=0.40, qSmax=1.0, Ks=0.1)              # Culture parameters
init(V_0=1e3, VX_0=1e3, VS_0=10*1e3)        # Process initialization

par(S_in=600)                               # Feed profile
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)
```


Fedbatch cultivation with substrate control
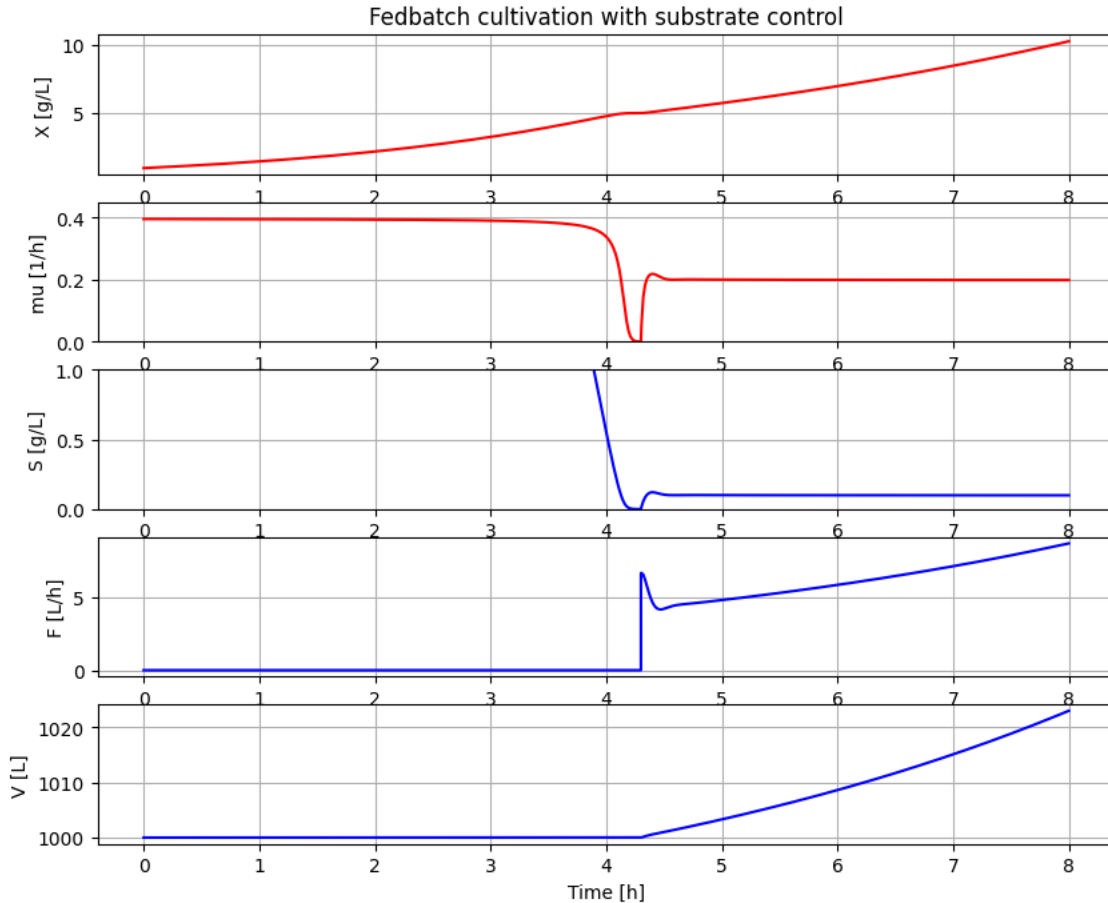
```
describe('MSL')
```

> MSL: 3.2.3 – used components: RealInput, RealOutput, LimPID-components

```
system_info()
```

> System information
> –OS: Linux
> –Python: 3.10.12
> –Scipy: not installed in the notebook
> –PyFMI: 2.11.0
> –FMU by: OpenModelica Compiler OpenModelica 1.21.0
> –FMI: 2.0
> –Type: FMUModelME2
> –Name: BPL_TEST2_PID.Fedbatch_reg6
> –Generated: 2023-08-22T10:54:51Z
> –MSL: 3.2.3
> –Description: Bioprocess Library version 2.1.1-beta
> –Interaction: FMU-explore version 0.9.8