▾ 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 22.04.2 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/')
```

```
    --2023-09-26 05:59:41--  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::6810:8203, ...
    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  29.3MB/s    in 2.4s

    2023-09-26 05:59:45 (29.3 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 23.7.4
     Python 3.10.13
```

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

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

▾ BPL_TEST2_Fedbatch setup

This notebook just produce the Figure 2 in the paper "Design ideas behind Bioprocess Library for Modelica", by J P Axelsson, to be presented at the 15th International Modelica Conference in Aachen, Germany, October 9-11, 2023.

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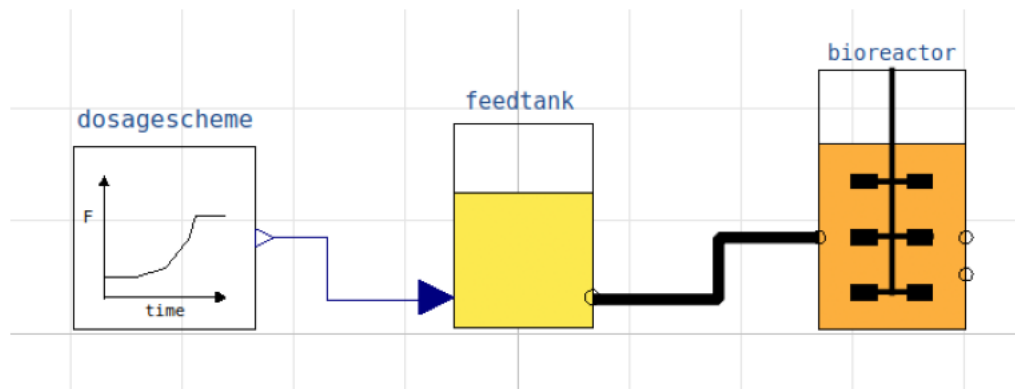
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

```
process_diagram()
```
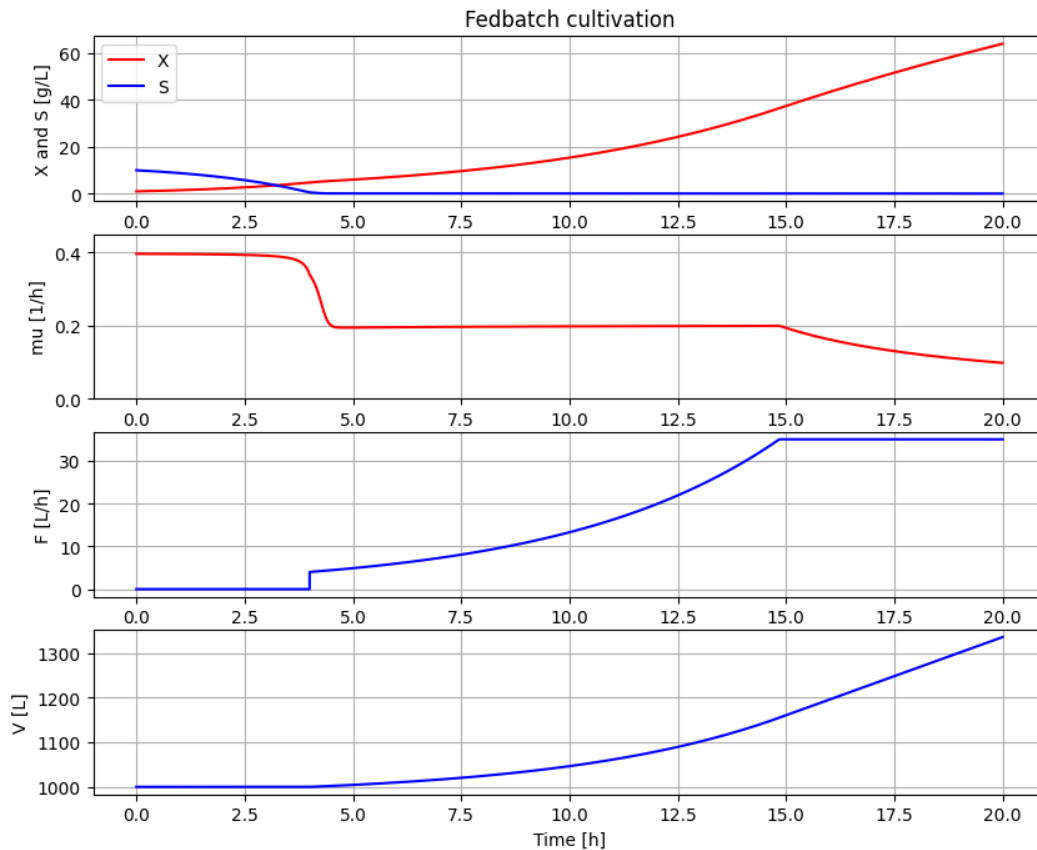


```
describe('culture'); print(); #describe('liquidphase')                                          # Pump schedule parameter
```

```
    Simplified text book model - only substrate S and cell concentration X
```

```
# Simulation of the process
newplot(plotType='TimeSeries')
ax2.set_ylim([0, 0.45])
init(V_0=1000, VX_0=1*1e3, VS_0=10*1e3)
par(feedtank_S_in=600, Ks=0.1, Y=0.40)
par(t_start=4, F_start=4.0, mu_feed=0.2, F_max=35)
simu(20)
```

Fedbatch cultivation


```
disp('culture')

    Y : 0.4
    qSmax : 1.0
    Ks : 0.1
```

```
describe('mu')

    Cell specific growth rate variable : 0.098 [ 1/h ]
```

```
describe('parts')

    ['bioreactor', 'bioreactor.culture', 'dosagescheme', 'feedtank']
```

```
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
     -PyFMI: 2.11.0
     -FMU by: OpenModelica Compiler OpenModelica 1.21.0
     -FMI: 2.0
     -Type: FMUModelME2
     -Name: BPL_TEST2.Fedbatch
     -Generated: 2023-04-20T12:24:29Z
     -MSL: 3.2.3
     -Description: Bioprocess Library version 2.1.1
     -Interaction: FMU-explore version 0.9.8
```