∨ 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.
!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/')
```

⇥ --2025-01-15 07:30:40-- https://repo.anaconda.com/miniconda/Miniconda3-py310
    Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.191.158, 104.16.32.2
    Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.191.158|:443... co
    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 49.3MB/s   in 1.4s

    2025-01-15 07:30:42 (49.3 MB/s) - 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh'

    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 23.1.0
Python 3.10.16
```

```
!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
%%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 simulatic
    - describe()  - describe culture, broth, parameters, variables with values/ui

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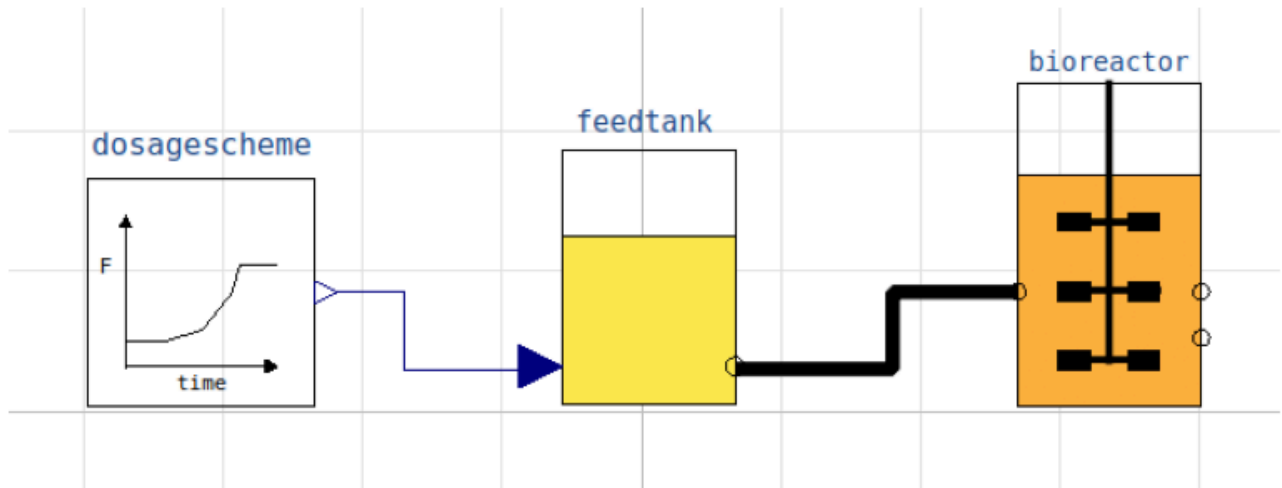
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

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

```
process_diagram()
```



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

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)
```

Could not find cannot import name 'dopri5' from 'assimulo.lib' (/usr/local/lil
Could not find cannot import name 'rodas' from 'assimulo.lib' (/usr/local/lib,
Could not find cannot import name 'odassl' from 'assimulo.lib' (/usr/local/lil
Could not find ODEPACK functions.
Could not find RADAR5
Could not find GLIMDA.

Fedbatch cultivation
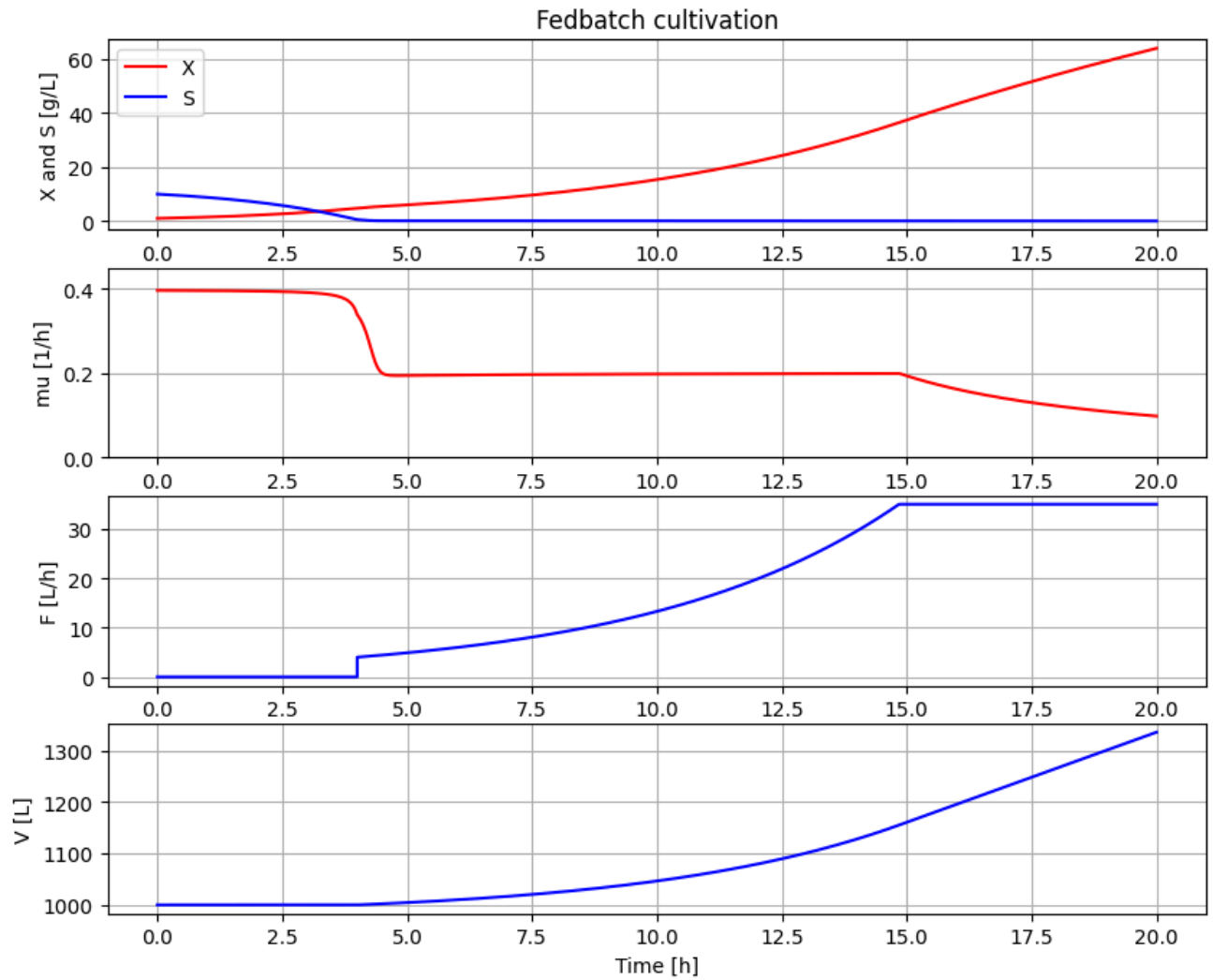
```
disp('culture')
```

Y : 0.4
qSmax : 1.0
Ks : 0.1

Start coding or generate with AI.

```
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: 2.16.1
 -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
```

Start coding or generate with AI.