BPL_TEST2_Fedbatch script with FMPy

The key library FMPy 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 Ubuntu 22.04.3 LTS Description: Release: 22.04 Codename: jammy %env PYTH0NPATH= → env: PYTHONPATH= !wget https://repo.anaconda.com/miniconda/Miniconda3-py312 24.3.0-0-Linux-x86 64.5 !chmod +x Miniconda3-py312 24.3.0-0-Linux-x86 64.sh !bash ./Miniconda3-py312_24.3.0-0-Linux-x86_64.sh -b -f -p /usr/local import sys sys.path.append('/usr/local/lib/python3.12/site-packages/') → --2024-05-21 06:24:39-- https://repo.anaconda.com/miniconda/Miniconda3-py312 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... con HTTP request sent, awaiting response... 200 OK Length: 143351488 (137M) [application/octet-stream] Saving to: 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh' Miniconda3-py312_24 100%[==========] 136.71M 193MB/s in 0.7s 2024-05-21 06:24:40 (193 MB/s) - 'Miniconda3-py312_24.3.0-0-Linux-x86_64.sh' s 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 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		
conda-24.5.0 frozendict-2.4.2 openssl-3.0.13	py312h06a4308_0 py312h06a4308_0 h7f8727e_1	1.2 36 5.2	KB
	Total:	6.5	MB

The following NEW packages will be INSTALLED:

frozendict pkgs/main/linux-64::frozendict-2.4.2-py312h06a4308_0

The following packages will be UPDATED:

conda 24.3.0-py312h06a4308_0 --> 24.5.0-py312h0 openssl 3.0.13-h7f8727e_0 --> 3.0.13-h7f8727

Downloading and Extracting Packages:

openssl-3.0.13 | 5.2 MB | : 0% 0/1 [00:00<?, ?it/s] conda-24.5.0 | 1.2 MB | : 0% 0/1 [00:00<?, ?it/s]

frozendict-2.4.2 | 36 KB | : 0% 0/1 [00:00<?, ?it/s]

openssl-3.0.13 | 5.2 MB | : 0% 0.002997347135570501/1 [00:00<00:48, conda-24.5.0 | 1.2 MB | : 1% 0.01293349794914382/1 [00:00<00:12,

frozendict-2.4.2 | 36 KB | : 100% 1.0/1 [00:00<00:00, 3.14it/s] conda-24.5.0 | 1.2 MB | : 100% 1.0/1 [00:00<00:00, 1.96it/s]

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

!conda --version
!python --version

→ conda 24.5.0
Python 3.12.2

!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/BPL_TEST2_Fedbatch
→ Cloning into 'BPL_TEST2_Fedbatch'...
%cd BPL_TEST2_Fedbatch
/content/BPL_TEST2_Fedbatch
run -i BPL TEST2 Fedbatch fmpy explore.py

→ Linux – run FMU pre-comiled OpenModelica 1.23.0-dev

    Model for bioreactor has been setup. Key commands:
     - par()

    change of parameters and initial values

     - init()
- simu()

    change initial values only

    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/un

    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")
```

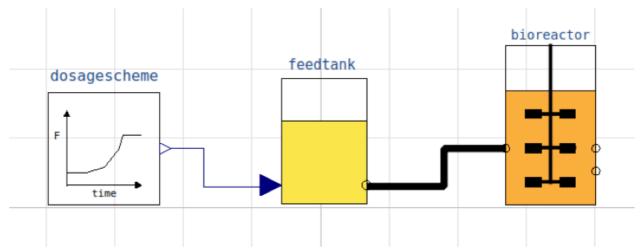
BPL_TEST2_Fedbatch - demo

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

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

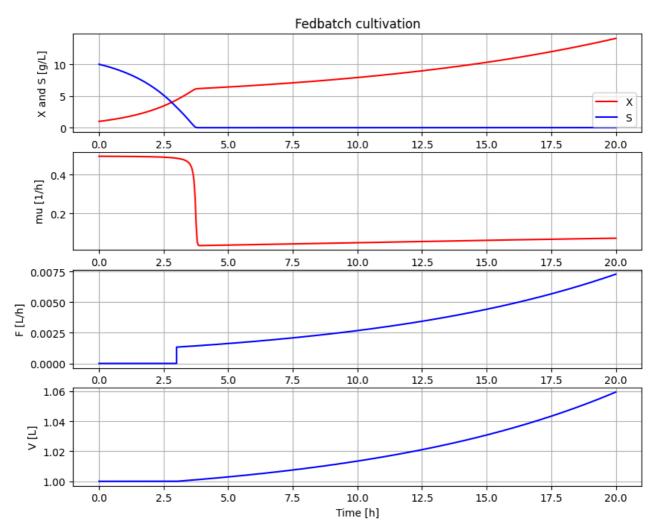
process_diagram()

No processDiagram.png file in the FMU, but try the file on disk.



Simulation with default values of the process
newplot(plotType='TimeSeries')
simu(20)

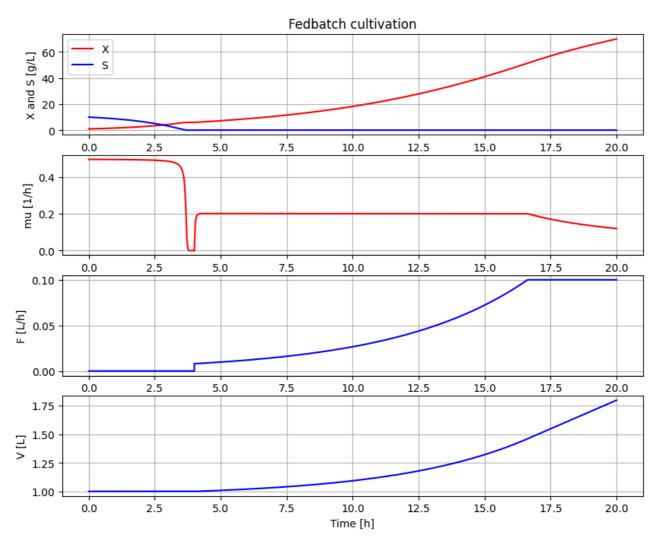




disp(mode='long')

```
\rightarrow
    bioreactor.V_start : V_start : 1.0
    bioreactor.m_start[1] : VX_start : 1.0
    bioreactor.m_start[2] : VS_start : 10.0
    bioreactor.culture.Y: Y: 0.5
    bioreactor.culture.qSmax : qSmax : 1.0
    bioreactor.culture.Ks: Ks: 0.1
    feedtank.c in[2] : feedtank.S in : 300.0
    feedtank.V_start : feedtank.V_start : 10.0
    dosagescheme.mu_feed : mu_feed : 0.1
    dosagescheme.t_startExp : t_startExp : 3.0
    dosagescheme.F_startExp : F_startExp : 0.001
    dosagescheme.F_max : F_max : 0.3
# A more typical feed scheme for the culture at hand
newplot(plotType='TimeSeries')
par(t_startExp=4, F_startExp=0.008, mu_feed=0.2, F_max=0.1)
simu(20)
```





```
disp('culture')

Y: 0.5
qSmax: 1.0
Ks: 0.1

describe('mu')

Cell specific growth rate variable: 0.12 [ 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

-FMPy: 0.3.20

-FMU by: OpenModelica Compiler OpenModelica 1.23.0~dev.beta.1-1-g379f714

-FMI: 2.0 -Type: ME

-Name: BPL_TEST2.Fedbatch

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