

BPL_TEST2_Perfusion - demo

This notebook explore perfusion cultivation in comparison with ordinary continuous cultivation (chemostat) and use comparable settings to earlier notebook. Further you see here examples of interaction with the simplified commands `par()`, `init()`, `simu()` etc as well as direct interaction with the FMU which is called "model" here. The last simulation is always available in the workspace and called "sim_res". Note that `describe()` brings mainly up from descriptive information from the Modelica code from the FMU but is complemented by some information given in the Python setup file.

```
In [1]: run -i BPL_TEST2_Perfusion_fmpy_explore.py
```

Windows - run FMU pre-compiled JModelica 2.14

Model for the process 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

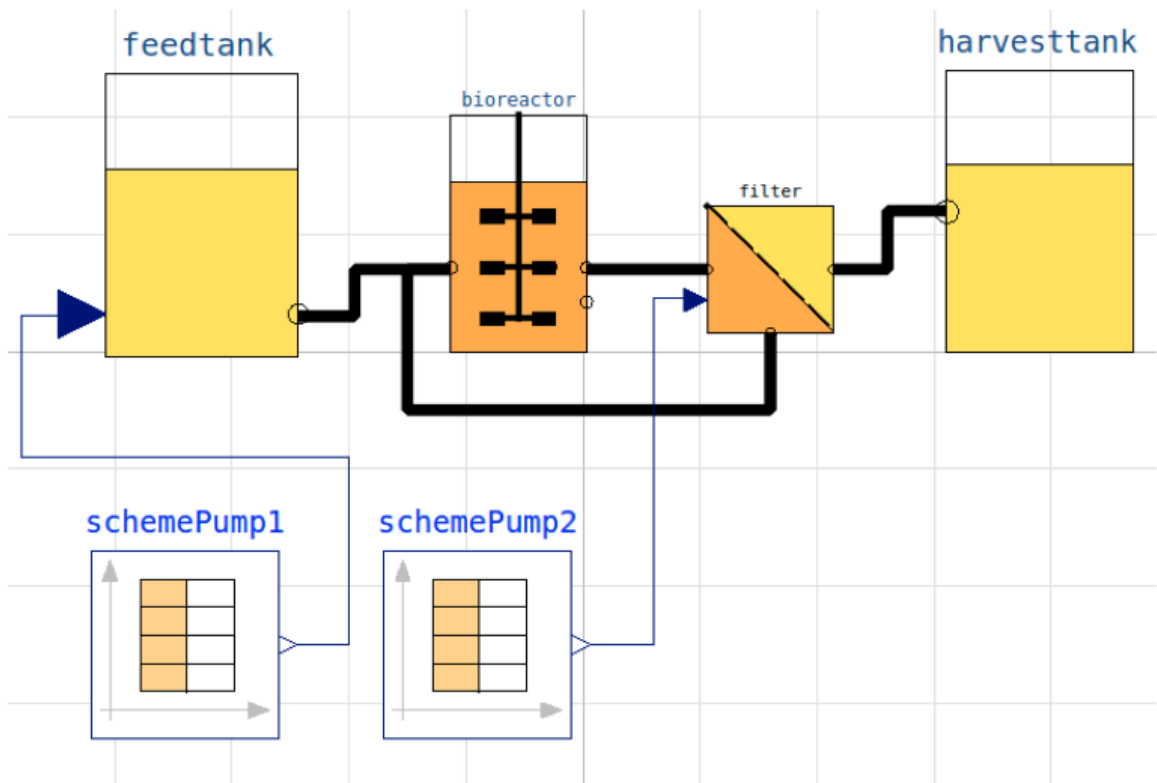
Brief information about a command by `help()`, eg `help(simu)`

Key system information is listed with the command `system_info()`

```
In [2]: %matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

```
In [3]: process_diagram()
```

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

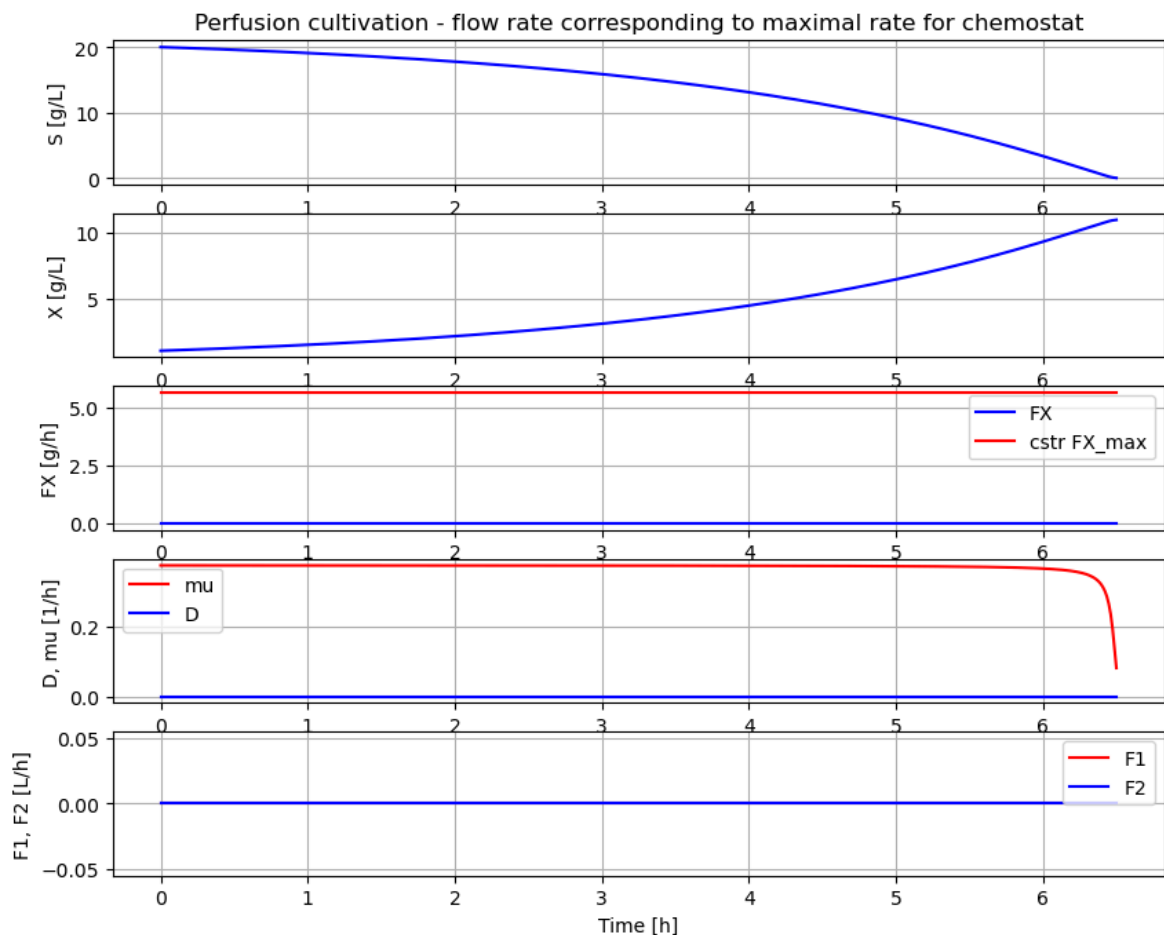


```
In [5]: # Process parameters used throughout
par(Y=0.5, qSmax=0.75, Ks=0.1) # Culture
par(filter_eps=0.10, filter_alpha_X=0.02, filter_alpha_S=0.10) # Filter
par(S_in=30.0) # Inlet subs
init(V_start=1.0, VX_start=1.0) # Process in
eps = parValue['filter_eps'] # Pump sche
```

```
In [6]: # Simulation of process with flow rate clot to wash-out for chemostat

init(VS_start=20) # Process initial
par(pump1_t1=10, pump2_t1=10) # Pump schedule - recyc
par(pump1_F1=2.5*0.155, pump2_F1=2.5*0.155/eps)
par(pump1_t2=940, pump2_t2=940, pump1_t3=950, pump2_t3=950, pump1_t4=960, pump2_

newplot(title='Perfusion cultivation - flow rate corresponding to maximal rate f
simu(6.5)
```



```
In [7]: # Concentration factor of the filter
c=model_get('filter.retentate.c[1]')/model_get('filter.inlet.c[1]')
print('Conc factor of perfusion filter =', np.round(c,3))
```

Conc factor of perfusion filter = 1.186

```
In [8]: c_data=sim_res['filter.retentate.c[1]']/sim_res['filter.inlet.c[1]']
print('Conc factor variation', np.round(min(c_data[151:]), 3),'to', np.round(max
```

Conc factor variation 1.186 to 1.186

```
In [9]: # Simulation of process with step-wise increase of perfusion rate until wash-out.
# This means that re-circulation rate change at the same time as the perfusion rate

init(VS_start=150) # Process initial variables

par(pump1_t1=12, pump2_t1=12) # Pump schedule - recirculation
par(pump1_F1=2.5*0.155, pump2_F1=2.5*0.155/eps)
par(pump1_t2=22, pump2_t2=22)
par(pump1_F2=2.5*0.35, pump2_F2=2.5*0.35/eps)
par(pump1_t3=32, pump2_t3=32)
par(pump1_F3=2.5*0.63, pump2_F3=2.5*0.63/eps)
par(pump1_t4=42, pump2_t4=42)
par(pump1_F4=2.5*0.83, pump2_F4=2.5*0.83/eps)

newplot(title='Perfusion cultivation - step wise increase of perfusion rate and
simu(60)
```

```

-----
FMIException                                         Traceback (most recent call last)
Cell In[9], line 16
    13 par(pump1_F4=2.5*0.83, pump2_F4=2.5*0.83/eps)
    15 newplot(title='Perfusion cultivation - step wise increase of perfusion ra
te and max productivity 4x chemostat')
--> 16 simu(60)

File \\VBoxSvr\Modelica\GitHub\Colab\BPL_TEST2_Perfusion\BPL_TEST2_Perfusion_fmpy
_explore.py:579, in simu(simulationTime, mode, options, diagrams, timeDiscreteSta
tes, stateValue, stateValueInitial, stateValueInitialLoc, parValue, parLocation,
fmu_model)
    576 start_values = {parLocation[k]:parValue[k] for k in parValue.keys()}
    577 # Simulate
--> 579 sim_res = simulate_fmu(
    580     filename = fmu_model,
    581     validate = False,
    582     start_time = 0,
    583     stop_time = simulationTime,
    584     output_interval = simulationTime/options[ ],
    585     record_events = True,
    586     start_values = start_values,
    587     fmi_call_logger = None,
    588     output = list(set(extract_variables(diagrams) + list(stateValue.key
s()) + key_variables))
    589 )
    591 simulationDone = True
    593 elif mode in ['Continued', 'continued', 'cont']:

File ~\miniconda3\envs\fmpy0325\Lib\site-packages\fmpy\simulation.py:789, in simu
late_fmu(filename, validate, start_time, stop_time, solver, step_size, relative_t
olerance, output_interval, record_events, fmi_type, start_values, apply_default_s
tart_values, input, output, timeout, debug_logging, visible, logger, fmi_call_log
ger, step_finished, model_description, fmu_instance, set_input_derivatives, remot
e_platform, early_return_allowed, use_event_mode, initialize, terminate, fmu_stat
e, set_stop_time)
    787 result = simulateME(model_description, fmu, start_time, stop_time, so
lver, step_size, relative_tolerance, start_values, apply_default_start_values, in
put, output, output_interval, record_events, timeout, step_finished, validate, se
t_stop_time)
    788 elif fmi_type == 'CoSimulation':
--> 789 result = simulateCS(model_description, fmu, start_time, stop_time, re
lative_tolerance, start_values, apply_default_start_values, input, output, output
_interval, timeout, step_finished, set_input_derivatives, use_event_mode, early_r
eturn_allowed, validate, initialize, terminate, set_stop_time)
    791 if fmu_instance is None:
    792     fmu.freeInstance()

File ~\miniconda3\envs\fmpy0325\Lib\site-packages\fmpy\simulation.py:1322, in sim
ulateCS(model_description, fmu, start_time, stop_time, relative_tolerance, start
_values, apply_default_start_values, input_signals, output, output_interval, timeo
ut, step_finished, set_input_derivatives, use_event_mode, early_return_allowed, v
alidate, initialize, terminate, set_stop_time)
    1320         break
    1321     else:
-> 1322         raise exception
    1324 recorder.sample(time)
    1326 else:

File ~\miniconda3\envs\fmpy0325\Lib\site-packages\fmpy\simulation.py:1307, in sim

```

```

ulateCS(model_description, fmu, start_time, stop_time, relative_tolerance, start_
values, apply_default_start_values, input_signals, output, output_interval, timeo
ut, step_finished, set_input_derivatives, use_event_mode, early_return_allowed, v
alidate, initialize, terminate, set_stop_time)
    1304 input.apply(time, continuous=True, discrete=True, after_event=True)
    1306 try:
-> 1307     fmu.doStep(currentCommunicationPoint=time, communicationStepSize=step
_size)
    1309     time = next_communication_point
    1311 except FMICallException as exception:

```

File ~\miniconda3\envs\fmipy0325\Lib\site-packages\fmipy\fmipy2.py:580, in FMU2Slave.doStep(self, currentCommunicationPoint, communicationStepSize, noSetFMUStatePriorToCurrentPoint)

```

    579 def doStep(self, currentCommunicationPoint, communicationStepSize, noSetF
MUStatePriorToCurrentPoint=fmipy2True):
--> 580     self.fmipy2DoStep(self.component, currentCommunicationPoint, communicat
ionStepSize, noSetFMUStatePriorToCurrentPoint)

```

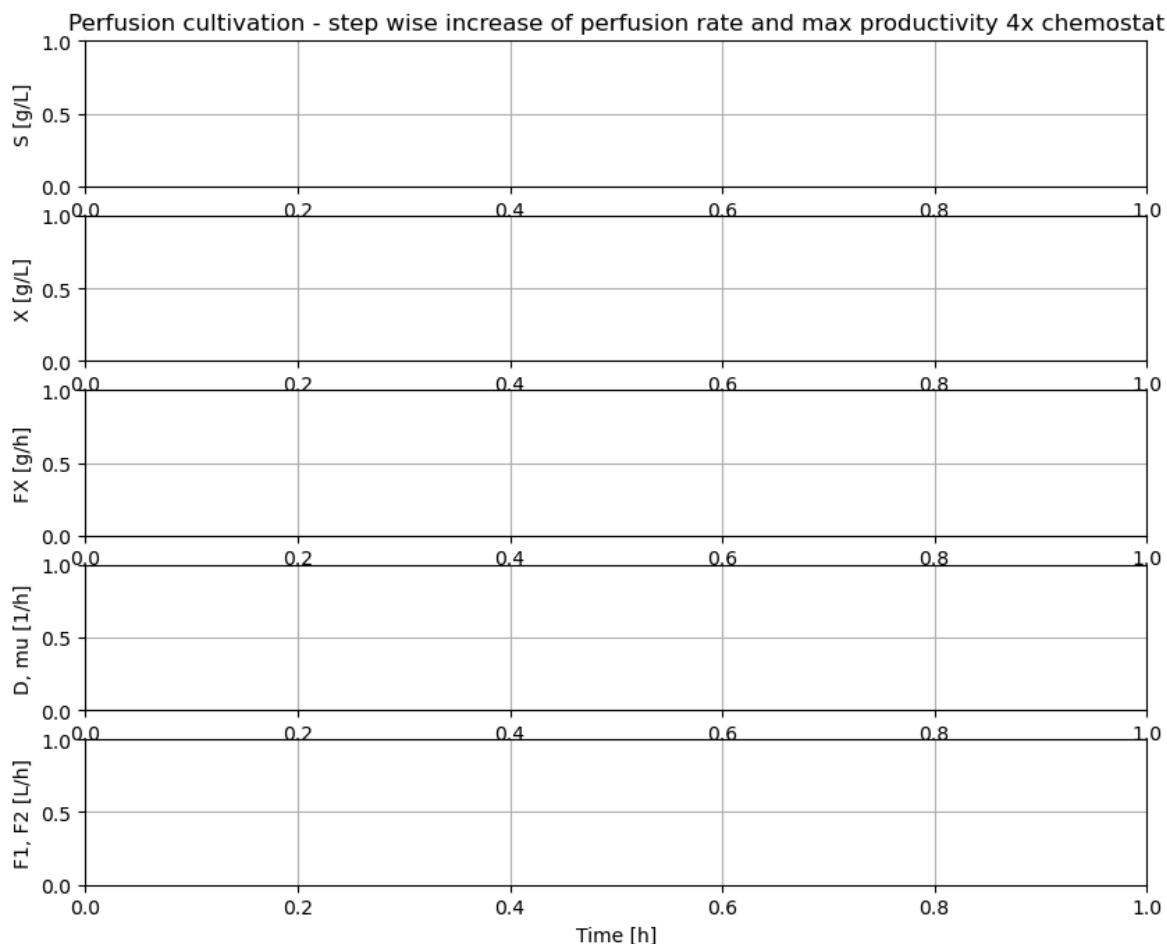
File ~\miniconda3\envs\fmipy0325\Lib\site-packages\fmipy\fmipy2.py:215, in _FMU2._fmipy2Function.<locals>.w(*args)

```

    212 if restype == fmipy2Status: # status code
    213     # check the status code
    214     if res > fmipy2Warning:
--> 215         raise FMICallException(function=fname, status=res)
    217 return res

```

FMICallException: fmipy2DoStep failed with status 3 (error).



```

In [ ]: # Simulation without a plot and just to check typical values at high production
        simu(40)

```

```
c_data=sim_res['filter.retentate.c[1]'][304:]/sim_res['filter.inlet.c[1]'][304:]
print('Conc factor variation', np.round(min(c_data[304:]), 3), 'to', np.round(max(c_data[304:]), 3))
```

```
In [ ]: #describe('cstrProdMax')
```

```
In [ ]: # The maximal biomass productivity before washout is obtained around 40 hours
np.round(model_get('harvesttank.inlet.F')*model_get('harvesttank.inlet.c[1]'),1)
```

```
In [10]: # Thus perfusion (with this filter) brings a productivity improvement of about
np.round(23.5/5.6,1)
```

```
Out[10]: np.float64(4.2)
```

```
In [11]: # Finally we check the filter flow rates at time 40 hour - note the negative sign
model_get('filter.inlet.F')
```

```
Out[11]: np.float64(0.0)
```

```
In [12]: model_get('filter.filtrate.F')
```

```
Out[12]: np.float64(-0.0)
```

```
In [13]: model_get('filter.retentate.F')
```

```
Out[13]: np.float64(-0.0)
```

Summary

- The perfusion filter had a concentration factor of cells around 1.08 and re-cycling flow was set to a factor 10 higher than the perfusion rate and changed when perfusion rate was change to keep the ratio factor 10.
- The first simulation showed that by cell retention using perfusion filter the process could be run at a perfusion flow rate at the maximal flow rate possible for corresponding chemostat culture and cell concentration increased steadily.
- The second simulation showed that with a proper startup cell concentration, the cell concentration remained constant when perfusion rate increased in a similar way as what we see in a chemostat.
- The second simulation also showed that biomass productivity in this case was increased by a factor 4.2 compared to chemostat.
- If the perfusion rate increased to higher levels washout started but the decrease of cell concentration was slow.

Some of you who read this may have your perfusion experience with CHO-cultures. For such cultures the cell concentration do increase with increase of perfusion rate and there are understood reasons for that. But for this simplified process as well as microbial processes they typically keep cell concentration constant when flow rate is chaged, and that under quite wide conditions. I will try come back to this phenomena in a later notebook.

Appendix

```
In [14]: disp('culture')
```

```
Y : 0.5  
qSmax : 0.75  
Ks : 0.1
```

```
In [15]: describe('mu')
```

```
Cell specific growth rate variable : 0.081 [ 1/h ]
```

```
In [16]: # List of components in the process setup and also a couple of other things like  
describe('parts')
```

```
['bioreactor', 'bioreactor.culture', 'D', 'feedtank', 'filter', 'harvesttank', 'MSL', 'schemePump1', 'schemePump2']
```

```
In [17]: describe('MSL')
```

```
MSL: RealInput, RealOutput, CombiTimeTable, Types
```

```
In [18]: system_info()
```

```
System information  
-OS: Windows  
-Python: 3.12.11  
-Scipy: not installed in the notebook  
-FMPy: 0.3.25  
-FMU by: JModelica.org  
-FMI: 2.0  
-Type: CS  
-Name: BPL.Examples_TEST2.Perfusion  
-Generated: 2025-07-26T09:41:00  
-MSL: 3.2.2 build 3  
-Description: Bioprocess Library version 2.3.1  
-Interaction: FMU-explore for FMPy version 1.0.2
```

```
In [ ]:
```

```
In [ ]:
```