BPL_TEST2_Batch_calibration - demo

This notebook shows the possibilities for calibration of the model BPL_TEST2_Batch using scipy.optimize.minimize() routine.

The text-book model of batch cultivation we simulate is the following where S is substrate, X is cell concentration, and V is volume of the broth

$$\frac{d(VS)}{dt} = -q_S(S) \cdot VX$$
$$\frac{d(VX)}{dt} = \mu(S) \cdot VX$$

and where specific cell growth rate μ and substrate uptake rate q_S are

$$\mu(S) = Y \cdot q_S(S)$$

$$q_S(S) = q_S^{max} rac{S}{K_s + S}$$

where Y is yield, q_S^{max} is maximal specific substrate uptake rate and K_s is the saturation constant for the substrate uptake.

```
In [1]:    run -i BPL_TEST2_Batch_explore.py
```

Windows - run FMU pre-compiled JModelica 2.14

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 plot from previous simulation - show()
- display parameters and initial values from the last simulation - disp()
- describe() describe culture, broth, parameters, variables with values / units

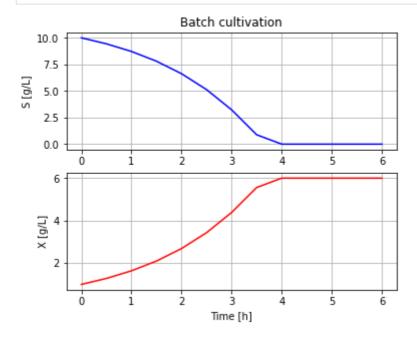
Note that both disp() and describe() takes values from the last simulation

Brief information about a command by help(), eg help(simu) Key system information is listed with the command system info()

```
In [2]:
         # Adjust the size of diagrams
         plt.rcParams['figure.figsize'] = [15/2.54, 12/2.54]
```

A first simulation and store data in a dataframe

```
In [3]:
         import pandas as pd
In [4]:
         par(Y=0.5, qSmax=1.0, Ks=0.1)
         init(V_0=1.0, VS_0=10, VX_0=1.0)
         newplot(plotType='Demo_1')
         opts['ncp'] = 12
         simu(6)
```



```
In [5]: # Store data in a DataFrame for Later use
    data = pd.DataFrame(data={'time':sim_res['time'], 'X':sim_res['bioreactor.c[1]'], 'S
    data
```

Out[5]:		time	х	S
-	0	0.0	1.000000	1.000000e+01
	U	0.0	1.000000	1.0000000e+01
	1	0.5	1.280773	9.438453e+00
	2	1.0	1.640079	8.719842e+00
	3	1.5	2.099615	7.800770e+00
	4	2.0	2.686770	6.626459e+00
	5	2.5	3.435479	5.129043e+00
	6	3.0	4.385325	3.229350e+00
	7	3.5	5.559252	8.814967e-01
	8	4.0	6.000000	1.048375e-08
	9	4.5	6.000000	-1.936268e-10
	10	5.0	6.000000	2.156125e-12
	11	5.5	6.000000	9.975889e-14
	12	6.0	6.000000	4.189854e-15

Try minimize() for parameter estimation

Here we try the same scipy-algorithm family that is actually used in pyfmi model.estimate()

```
In [6]: # For clarity of code here we import again
import scipy.optimize

In [7]: # Parameters to be estimated using parDict names and their bounds
```

localhost:8889/nbconvert/html/BPL_TEST2_Batch_calibration.ipynb?download=false

parEstim = ['Y', 'qSmax', 'Ks']

```
parEstim_0 = np.array([0.4, 1.2, 0.15])
          extra_args = (parEstim, data, 'BPL_TEST2_Batch_windows_jm_cs.fmu', parDict, parLocat
 In [8]:
          # Modified evaluation function tailored for Python optimization algorithms
          def evaluation(x, parEstim, data=data, fmu_model=fmu_model,
                          parDict=parDict, parLocation=parLocation):
              """The parameter list is tailored for scipy optimization algorithms interface,
                 where the first parameter x is an array with parameters that are tuned
                 and evalauted."""
              # Load model
              global model
              if model is None:
                  model = load_fmu(fmu_model)
              model.reset()
              # Change parameters and initial values from default
              for i, p in enumerate(parEstim): model.set(parLocation[p], x[i])
              for p in set(parDict)-set(parEstim): model.set(parLocation[p], parDict[p])
              # Simulation options
              opts = model.simulate_options()
              opts['ncp'] = 12
              opts['result_handling'] = 'memory'
              opts['silent mode'] = True
              # Simulate
              sim_res = model.simulate(start_time=0.0, final_time=6.0, options=opts)
              # Calculate loss
              V={}
              V['X'] = np.linalg.norm(data['X'] - np.interp(data['time'], sim_res['time'], sim_
              V['S'] = np.linalg.norm(data['S'] - np.interp(data['time'], sim_res['time'], sim
              return V['X'] + V['S']
In [9]:
          # Run minimize()
          result = scipy.optimize.minimize(evaluation, x0=parEstim 0, args=extra args,
                                            method='Nelder-Mead', options={"disp":True})
                                             method='BFGS', options={"disp":True})
          #
         Optimization terminated successfully.
                  Current function value: 0.069422
                  Iterations: 42
                  Function evaluations: 83
In [10]:
          result
          final simplex: (array([[0.50010848, 1.01030323, 0.16246785],
Out[10]:
                [0.50010547, 1.01023377, 0.16248744],
                [0.50007476, 1.01031636, 0.16249674],
                [0.50015623, 1.01021132, 0.16250092]]), array([0.06942214, 0.06944698, 0.0694
         6086, 0.06947121]))
                    fun: 0.06942213758121146
                message: 'Optimization terminated successfully.'
                   nfev: 83
                    nit: 42
                 status: 0
```

```
success: True
    x: array([0.50010848, 1.01030323, 0.16246785])
```

The estimated parameters x are very close to the original, but why not a success?

But if a use method 'Nelder-Mead' instead of the default 'BFGS' then I get success but needs double amount of function evaluations.

Concluding remarks

- It is rather easy to make scipy function evaluations with flexibility to use compiled FMUs and provide parameters different fram default and that should not be tuned.
- FMU-explore with workspace dictionaries parDict[] and parLocation[] etc are useful also in this scipy-optimization context. We see also that the broad optimization family scipy.minimization() used in pyfmi for model.estimate() does work.

Appendix

```
In [11]:
          describe('parts')
         ['bioreactor', 'bioreactor.culture', 'liquidphase', 'MSL']
In [12]:
          describe('MSL')
         MSL: 3.2.2 build 3 - used components:
In [13]:
          system_info()
         System information
          -OS: Windows
           -Python: 3.9.5
           -PyFMI: 2.9.5
           -FMU by: JModelica.org
           -FMI: 2.0
           -Type: FMUModelCS2
           -Name: BPL TEST2.Batch
           -Generated: 2022-09-13T11:19:04
           -MSL: 3.2.2 build 3
           -Description: Bioprocess Library version 2.1.0 beta
           -Interaction: FMU-explore ver 0.9.3
In [14]:
          optse = model.estimate options()
In [15]:
          optse
         {'tolerance': 1e-06,
Out[15]:
           'result_file_name': '',
           'filter': None,
           'method': 'Nelder-Mead',
           'scaling': 'Default',
           'simulate options': 'Default'}
 In [ ]:
```