

✓ BPL_CHO_Fedbatch script with FMPy

The key library FMPy is installed.

After the installation a small application BPL_CHO_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/')
```

```
--2024-03-07 09:27:00-- https://repo.anaconda.com/miniconda/Miniconda3-py310\_23.1.0-1-Linux-x86\_64.sh
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.131.3, 104.16.130.3
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.131.3|:443... conn
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 92.0MB/s in 0.8s
```

```
2024-03-07 09:27:01 (92.0 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 24.1.2  
Python 3.10.13
```

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

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

```
!conda install matplotlib --yes
```

```
Channels:
- defaults
- conda-forge
Platform: linux-64
Collecting package metadata (repodata.json): done
Solving environment: done
```

Package Plan

```
environment location: /usr/local

added / updated specs:
- matplotlib
```

The following packages will be downloaded:

package	build	
matplotlib-3.8.0	py310h06a4308_0	8 KB
matplotlib-base-3.8.0	py310h1128e8f_0	6.8 MB
pyparsing-3.0.9	py310h06a4308_0	153 KB
Total:		7.0 MB

The following NEW packages will be INSTALLED:

```
matplotlib      pkgs/main/linux-64::matplotlib-3.8.0-py310h06a4308_0
```

The following packages will be UPDATED:

```
matplotlib-base  conda-forge::matplotlib-base-3.5.2-py~ --> pkgs/main::ma
```

The following packages will be SUPERSEDED by a higher-priority channel:

```
certifi          conda-forge/noarch::certifi-2024.2.2~ --> pkgs/main/lini
conda            conda-forge::conda-24.1.2-py310hff520~ --> pkgs/main::co
pyparsing        conda-forge/noarch::pyparsing-3.1.2-p~ --> pkgs/main/lini
```

Downloading and Extracting Packages:

```
matplotlib-base-3.8.0 | 6.8 MB | : 0% 0/1 [00:00<?, ?it/s]
pyparsing-3.0.9       | 153 KB | : 0% 0/1 [00:00<?, ?it/s]
```

```

matplotlib-3.8.0      | 8 KB      | : 0% 0/1 [00:00<?, ?it/s]
matplotlib-base-3.8. | 6.8 MB    | : 0% 0.0022928172852449986/1 [00:00<00:40, 7.77it/s]

matplotlib-3.8.0      | 8 KB      | : 100% 1.0/1 [00:00<00:00, 7.77it/s]
matplotlib-3.8.0      | 8 KB      | : 100% 1.0/1 [00:00<00:00, 7.77it/s]

```

```

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

```

```
#!/conda install scipy --yes
```

```
#!/conda install openpyxl --yes
```

```
#!/conda install xlrd --yes
```

✓ BPL_CHO_Fedbatch setup

Now specific installation and the run simulations. Start with connecting to Github. Then upload the two files:

- FMU - BPL_CHO_Fedbatch_linux_om_me.fmu
- Setup-file - BPL_CHO_Fedbatch_fmpy_explore

```

# Filter out DeprecationWarnings for 'np.float as alias' is needed - wish I could
import warnings
warnings.filterwarnings("ignore")

```

```

%%bash
git clone https://github.com/janpeter19/BPL_CHO_Fedbatch

```

```
Cloning into 'BPL_CHO_Fedbatch'...
```

```

%cd BPL_CHO_Fedbatch

/content/BPL_CHO_Fedbatch

```

✓ BPL_CHO_Fedbatch - demo

Author: Jan Peter Axelson

This notebook deals with CHO fedbatch cultivation and recombinant protein production is included. First we make a check of the model by comparing a simulation result with corresponding published diagram. Then we take a closer look at the start-up strategy to keep the by-product formation low. After that we investigate at a whole cultivation and see the impact of feeding strategy on both cell growth and protein production where a trade-off is needed in this case.

The model used takes its inspiration from the microbial bottleneck models as described in the original papers [1] and [2] and reformulated and studied in [3]. The laboratory cultures used for model validation in [1] did produce MAb (against part of IgG) but no MAb-data was presented. The paper focus on viable and non-viable cell concentrations only. The original model is in section 5 expanded with the classical empirical Luedeking-Piret model recombinant protein production, see chapter 5 in [4]. In this way can get more insight into choice of feeding profile.

Interaction with the compiled model as FMU is mainly through the simplified commands: `par()`, `init()`, `newplot()`, `simu()` etc. The last simulation is always available in the workspace and called 'sim_res'. The command `describe()` brings mainly up description information from the actual Modelica code from the FMU but is complemented with information given in the dedicated Python setup-file.

The idea here is to demonstrate how simulations and varying conditions can provide some process insight that can support the experimental work. I hope that at the end of this session you are ready to formulate your own questions you want to address with simulations - and you can just go on in this notebook! Just press the field "+Code" in the upper left part of notebook interface and you get a new "cell" where you write your own code. You can copy and paste from cells above using `ctrl-c` and `ctrl-v` as usual and edit the cell. When you are ready to execute the cell just press the "play button" to the left in the cell or press `shift-enter` as in "ordinary" Jupyter notebooks.

After a session you may want to save your own notebook. That you can do on your Google Drive account and I refer to Colab instructions for how to do this. It is easy.

Good luck!

```
run -i BPL_CHO_Fedbatch_fmpy_explore.py
```

```
Linux - run FMU pre-compiled 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/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()`

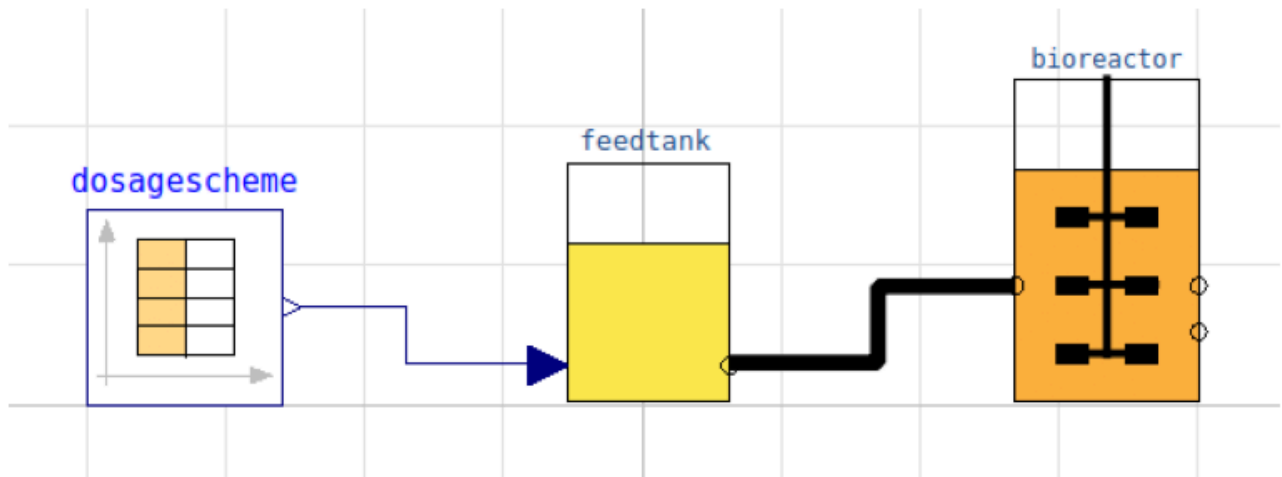
```
%matplotlib inline
plt.rcParams['figure.figsize'] = [25/2.54, 20/2.54]
```

✓ 1 About the process model

We can get information about the process and liquid phase by the command `describe()`. Here is no gas-phase included. This command can also be used to bring up information about a specific variable or parameter. However, you should use `describe()` after a simulation to get the values used during the simulation.

```
process_diagram()
```

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



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

Reactor culture CHO-MAb – cell line HB-58 American Culture Collection ATCC

The molecular weight of the recombinant protein (MAb) is somewhat arbitrarily chosen and the value not used in the simulations.

✓ 2 Simulation reproducing the original paper

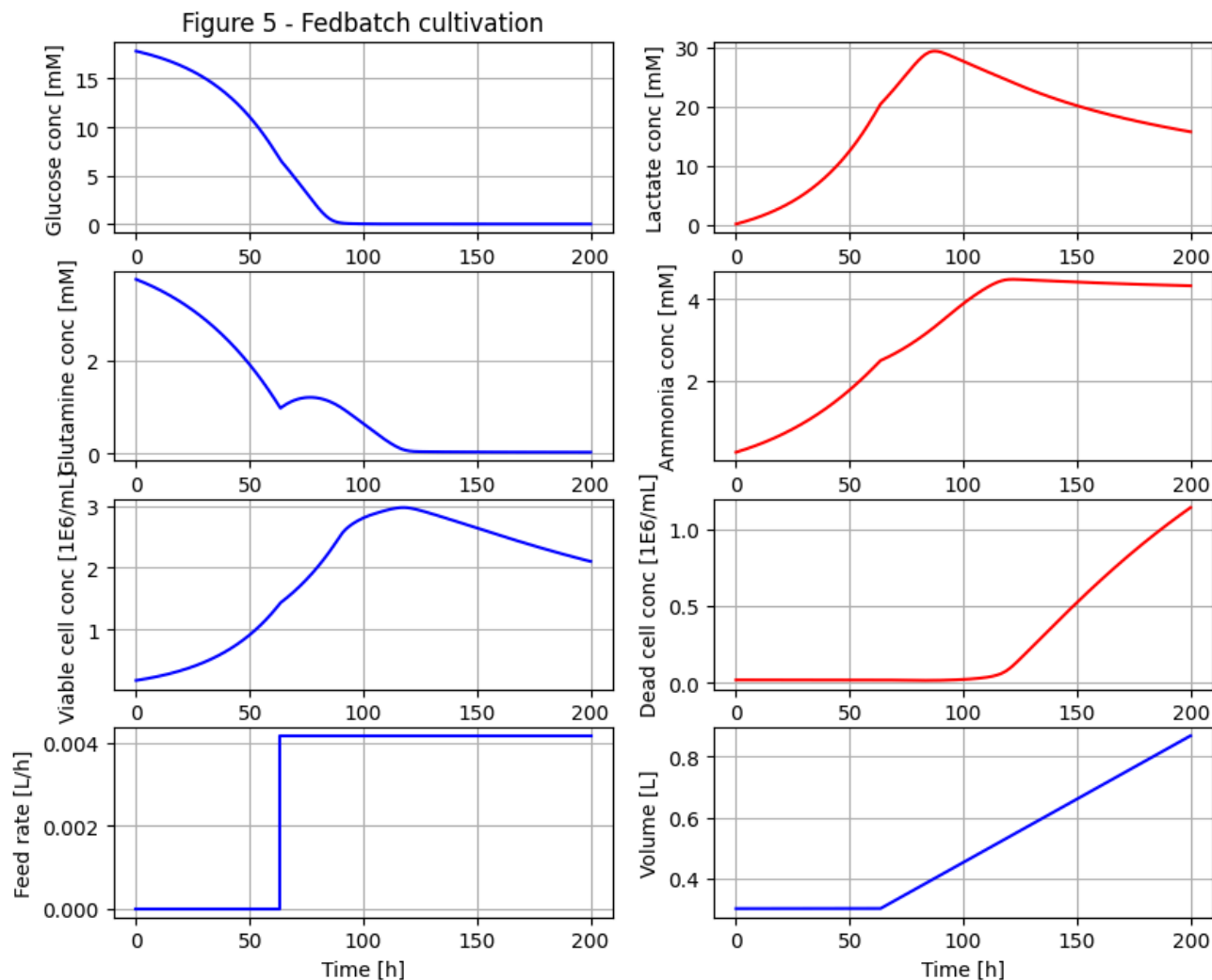
The simulation below reproduce diagrams in Figure 5 in the original paper. There are several simulation in the paper showing how well the model describe different experiments and here I just choose one of them.

```
# Data from Table 1 and 2 for experiment 4 shown in Figure 5 in paper [1]
# -culture parameters taken from Table 5 identified parameters for cultures 1,2,a

# Initial process conditions
V_start=0.30
init(V_start=V_start, VXv_start=V_start*0.172, VXd_start=V_start*0.020)
init(VG_start=V_start*17.83, VGn_start=V_start*3.74, VL_start=V_start*0.12, VN_st

# Feeding
Feed=0.1/24
par(G_in=15, Gn_in=9.3)
par(t0=0, F0=0, t1=63.5, F1=Feed, t2=300, F2=Feed)

# Simulation
newplot(title='Figure 5 - Fedbatch cultivation')
simu(200)
```

Comment: The simulation results look very similar to the published diagram Figure 5 in [1]. The model passes this quality check.

✓ 3 Simulation of different start-up feeding strategies

```
# Figur 5
V_0=0.30
init(V_start=V_start, VXv_start=V_start*0.172, VXd_start=V_start*0.020)
init(VG_start=V_start*17.83, VGn_start=V_start*3.74, VL_start=V_start*0.12, VN_st

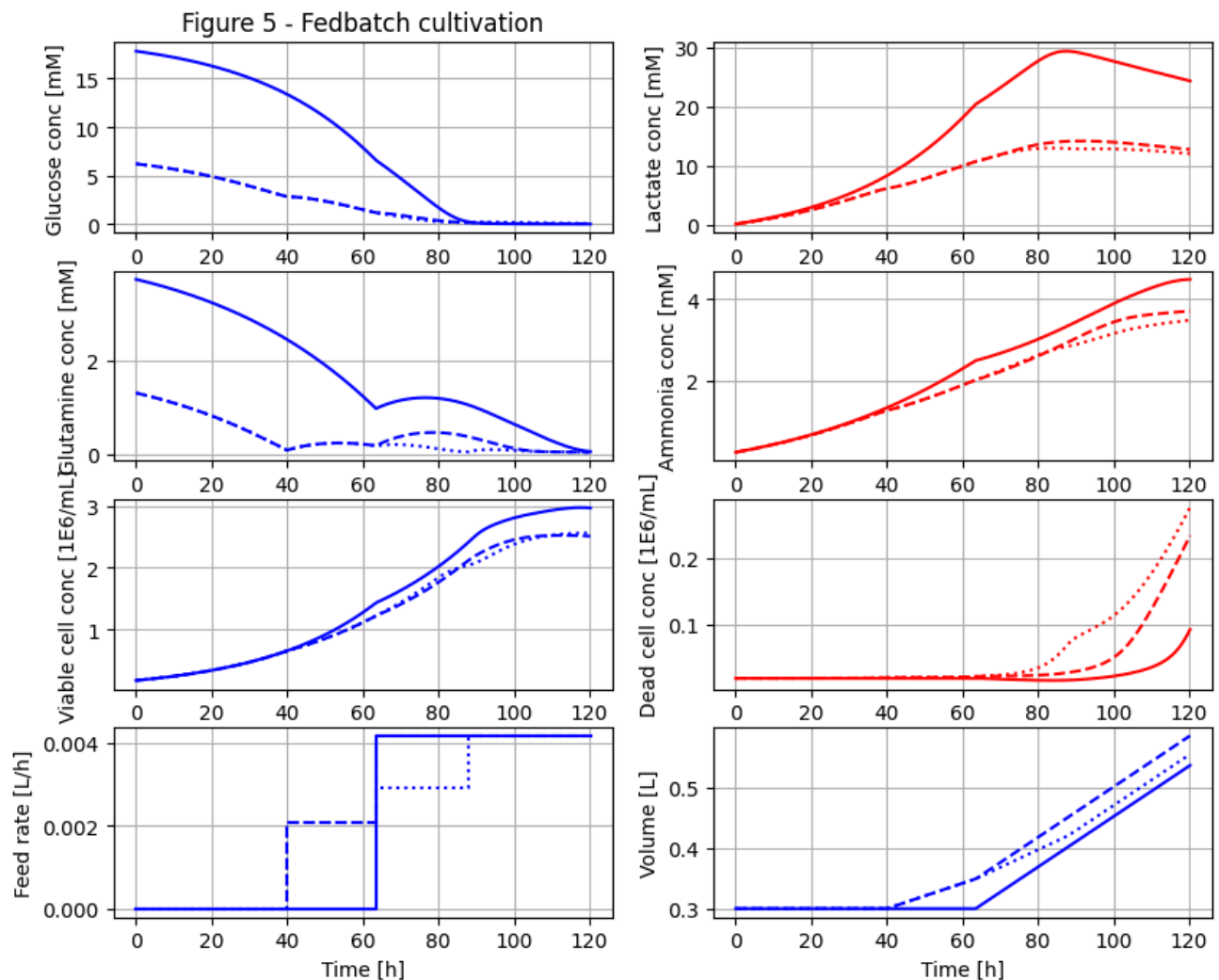
# Feeding
Feed=0.1/24
par(G_in=15, Gn_in=9.3)
par(t0=0, F0=0, t1=63.5, F1=Feed, t2=300, F2=Feed)

newplot(title='Figure 5 - Fedbatch cultivation')
simu(120)

init(VG_start=0.35*V_start*17.83, VGn_start=0.35*V_start*3.74)
par(t0=0, F0=0, t1=40.0, F1=0.5*Feed, t2=63.5, F2=Feed, t3=300, F3=Feed)
simu(120)

init(VG_start=0.35*V_start*17.83, VGn_start=0.35*V_start*3.74)
par(t0=0, F0=0, t1=40.0, F1=0.5*Feed, t2=63.5, F2=0.7*Feed, t3=88.0, F3=Feed, t4=
simu(120)

# Reset time table to avoid problems below
par(t1=1001, t2=1002, t3=1003, t4=1004, t5=1005, t6=1006)
```



Comment: We see that starting the feed a day earlier at lower rate and then increase decreases lactate formation to half, while the cell concentration is just slightly lower. With a more careful design of the feedprofile the ammonia formation can be decreased more than shown here.

✓ 4 Simulation of optimal feed profile for cell growth

At the end of the original paper section 5 in [1], the derived model is used to find an optimal feeding profile for high final cell concentration. It is stated that protein productivity is assumed to be mainly positively growth associated and therefore optimization of cell concentration is very similar to optimization of protein product. The optimization of feed profile is done with different

structures of the feed profile. All of them have a start-time and all of them has a fixed amount of substrate and concentrations in the media are also the same.

- The first optimization is for a feed profile similar to the experimental, i.e. after start the feed rate remains constant throughout the cultivation. Thus the start time and the actual feed rate are optimized. The result was that the start time was about the same as experimentally but the feed rate was 50% higher, see Figure 7 and Figure 10 in [1].
- The second optimization is for a feed profile with not just one increase but three steps of increase of feed rate. The results is a somewhat higher final cell concentration, see Figure 11.
- The third optimization is for a feed profile with five steps of increase of feed rate. The results is a slightly higher final cell concentration than for three steps, see Figure 12.
- The fourth optimization is for a feed profile with continuous exponential increase of the feed rate. The result is a bit higher final concentration than the previous with five steps, see Figure 13 but not shown in the figure below.

Below we just show the results of the original experimental cultivation, compared with results from three and five steps. It is possible to do the optimization in Python with the FMU, but we save that for a future notebook.

```
# Culture parameters taken from Table 5 identified parameters for cultures 1,2,an

# Data chosen
V_start=0.35
init(V_start=V_start, VXv_start=V_start*0.20, VXd_start=V_start*0.0)
init(VG_start=V_start*18.0, VGn_start=V_start*2.4, VL_start=V_start*0, VN_start=V

# Feeding n=1 – experimental and lower feed rate
par(G_in=15, Gn_in=4.0)
par(t0=0, F0=0, t1=49, F1=0.00417)
par(t2=1002, t3=1003, t4=1004, t5=1005)

# Simulation
newplot(title='Figure 12 – Fedbatch with optimal step-wise feed')
simu(125)

# Feeding n=1
par(G_in=15, Gn_in=4.0)
par(t0=0, F0=0, t1=52, F1=0.00625)
par(t2=1002, t3=1003, t4=1004, t5=1005, t6=1006)

# Simulation
simu(125)

# Feeding n=3
par(G_in=15, Gn_in=4.0)
par(t0=0, F0=0, t1=52, F1=0.002, t2=74, F2=0.0045, t3=98.0, F3=0.010)
par(t4=99.0, F4=0.010, t5=106, F5=0.010, t6=150, F6=0.010)

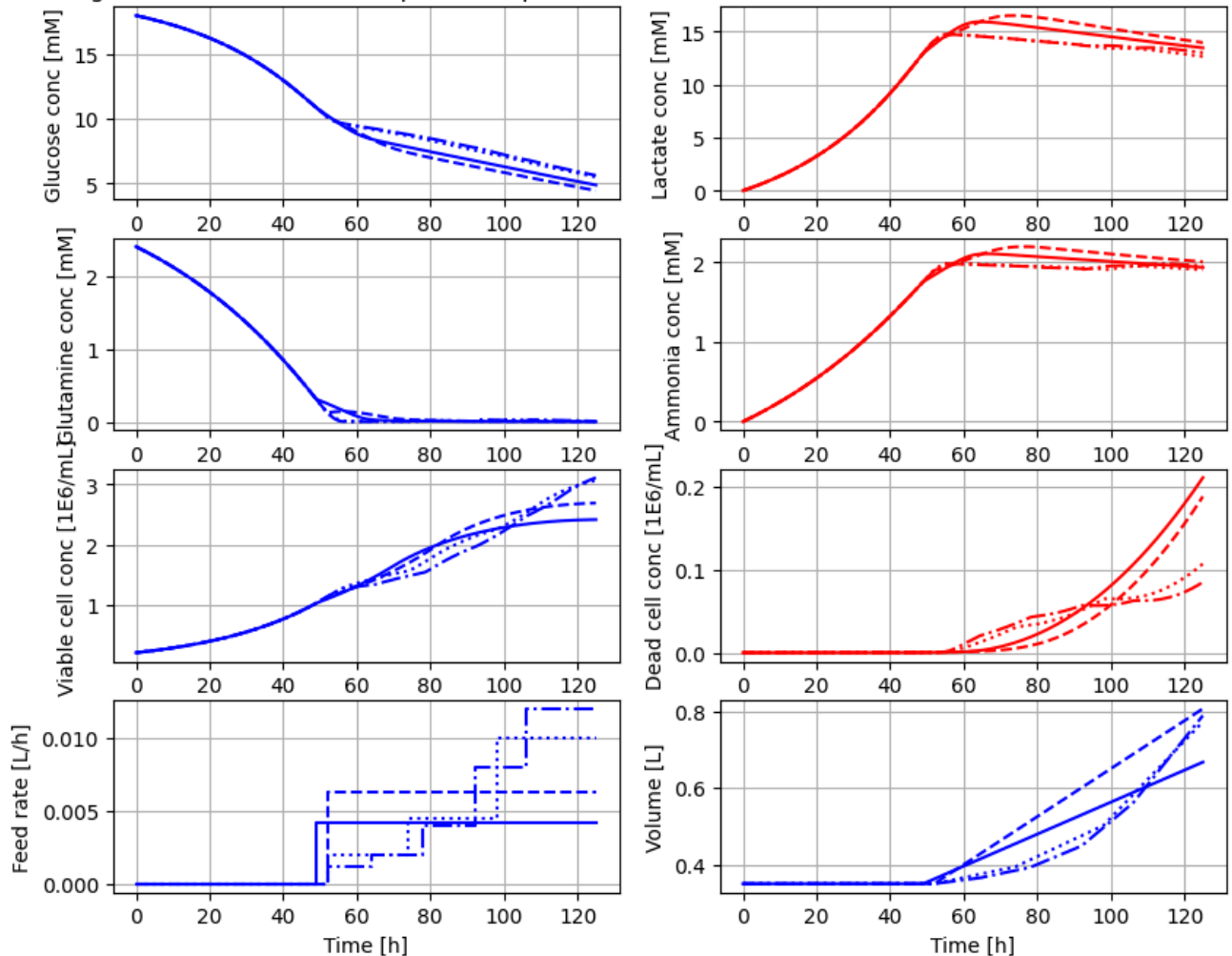
# Simulation
simu(125)

# Feeding n=5
par(G_in=15, Gn_in=4.0)
par(t0=0, F0=0, t1=52, F1=0.0012, t2=64, F2=0.0020, t3=78.0, F3=0.0040)
par(t4=92.0, F4=0.0080, t5=106, F5=0.012, t6=150, F6=0.012)

# Simulation
simu(125)

# Reset feeding parameters since the table need time in strict increasing value
par(t3=1004, t4=1005, t5=1005, t6=1006)
```

Figure 12 - Fedbatch with optimal step-wise feed



Comment: We see that that already the better tuned constant feed rate (dashed) compared to the experimental (solid) gives higher final cell concentration.

Breaking up the constant feed rate in three (dotted) and five (dash-dotted) steps with a more gradual increase of the feed rate gives even higher final cell concentration. The difference between $n=3$ and $n=5$ is small. The change to continuous exponential feed is even smaller and not shown here.

The results shown here are similar to what is presented in Table 7 in [1] but our simulation are slightly longer and here are small differences in the final cell concentration too. The qualitative result is the same though. The difference we see to the result in the original paper is most likely due to the fact that we here use the full model with 17 parameters while in the paper they have reduced the model to 15 parameters for the optimization work.

✓ 5 Simulation of different feed profiles to increase recombinant protein production

In this section we take a closer look at recombinant protein production. The original model is extended with the empirical model for specific protein production, see chapter 5 in [4]

$$q_P = \alpha \cdot \mu + \beta$$

Here we choose a negative value of growth-associated protein production α while keeping the non-growth associated β positive. The culture produced recombinant protein in the form of monoclonal antibodies for a specific IgG1 molecule, see section 2 in [1]. However, no experimental results were given. The only information we have is that feed rate was kept constant at a low level during fedbatch production and this choice indicates that the growth-associated protein production is negative. The consequence of this observation for the feed profile we take a look at there by simulation.

```
# Slide 3
newplot('CHO fedbatch cultivation - protein expression', plotType='Textbook_3')

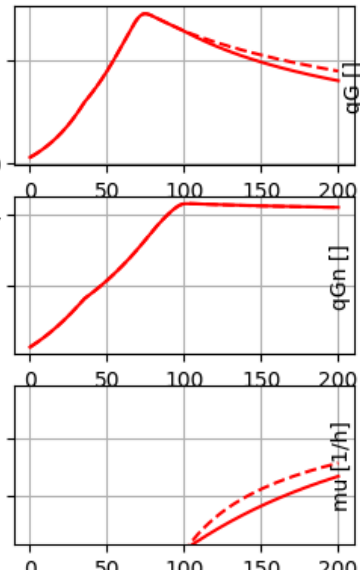
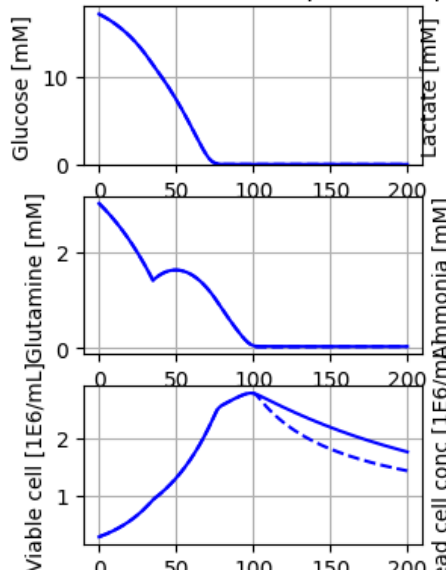
# Data from Table 1 and 2 for experiment 3
V_start=0.35
init(V_start=V_start, VXv_start=V_start*0.29, VXd_start=V_start*0.010)
init(VG_start=V_start*17.17, VGn_start=V_start*3.02, VL_start=V_start*1.12, VN_st

# Feeding
Feed=0.1/24
par(G_in=15, Gn_in=9.3)
par(t0=0, F0=0, t1=35, F1=Feed, t2=100, F2=Feed, t3=300, F3=Feed)

# Culture parameters
par(alpha=-1.0, beta=0.01)

# Simulation
simu(200)
par(t2=100, F2=0.7*Feed, t3=300, F3=0.7*Feed); simu(200)
par(F2=Feed, F3=Feed)
```

CHO fedbatch cultivation - protein expression



- cell specific rates

