

✓ BPL_IEC_operation script with PyFMI

The key library PyFMI is installed.

After the installation a small application BPL_IEC_operation 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.sh
```

```
!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/')
```

```
➦ --2024-05-23 11:50:06-- https://repo.anaconda.com/miniconda/Miniconda3-py310_23.1.0-1-Linu
  Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.32.241, 104.16.191.158, 2606:4700:
  Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.32.241|:443... connected.
  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 176MB/s in 0.4s
```

```
2024-05-23 11:50:07 (176 MB/s) - 'Miniconda3-py310_23.1.0-1-Linux-x86_64.sh' saved [74403966]
```

```
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 3.10.14
```

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

```
⇒
```

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

✓ Preparation of BPL_IEC_operation

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

- FMU - BPL_IEC_Column_system_linux_om_me
- Setup-file - BPL_IEC_explore

```
%%bash  
git clone https://github.com/janpeter19/BPL_IEC_operation
```

```
📁 Cloning into 'BPL_IEC_operation'...
```

```
%cd BPL_IEC_operation
```

```
📁 /content/BPL_IEC_operation
```


✓ 1 Typical parameters for a pilot scale ion exchange chromatography column process setup

```
# From given column height (h) diameter (d) and linear flow rate (lfr)
# actual column volume (V) and volume flow rate (VFR) are calculated below.
```

```
from numpy import pi
h = 20.0
d = 1.261
a = pi*(d/2)**2
V = h*a
print('V =', np.round(V,1), '[mL]')
```

```
lfr = 48
VFR = a*lfr/60
print('VFR =', np.round(VFR,1), '[mL/min]')
```

Pump schedule par

```
→ V = 25.0 [mL]
   VFR = 1.0 [mL/min]
```

```
# Sample concentration product P_in and antagonist A_in
par(P_in = 1.0)
par(A_in = 1.0)
par(E_in = 0.0)
```

```
# Column properties are described by the size and binding capacity of the resin Q_av
par(height = h)
par(diameter = d)
par(Q_av = 6.0)
```

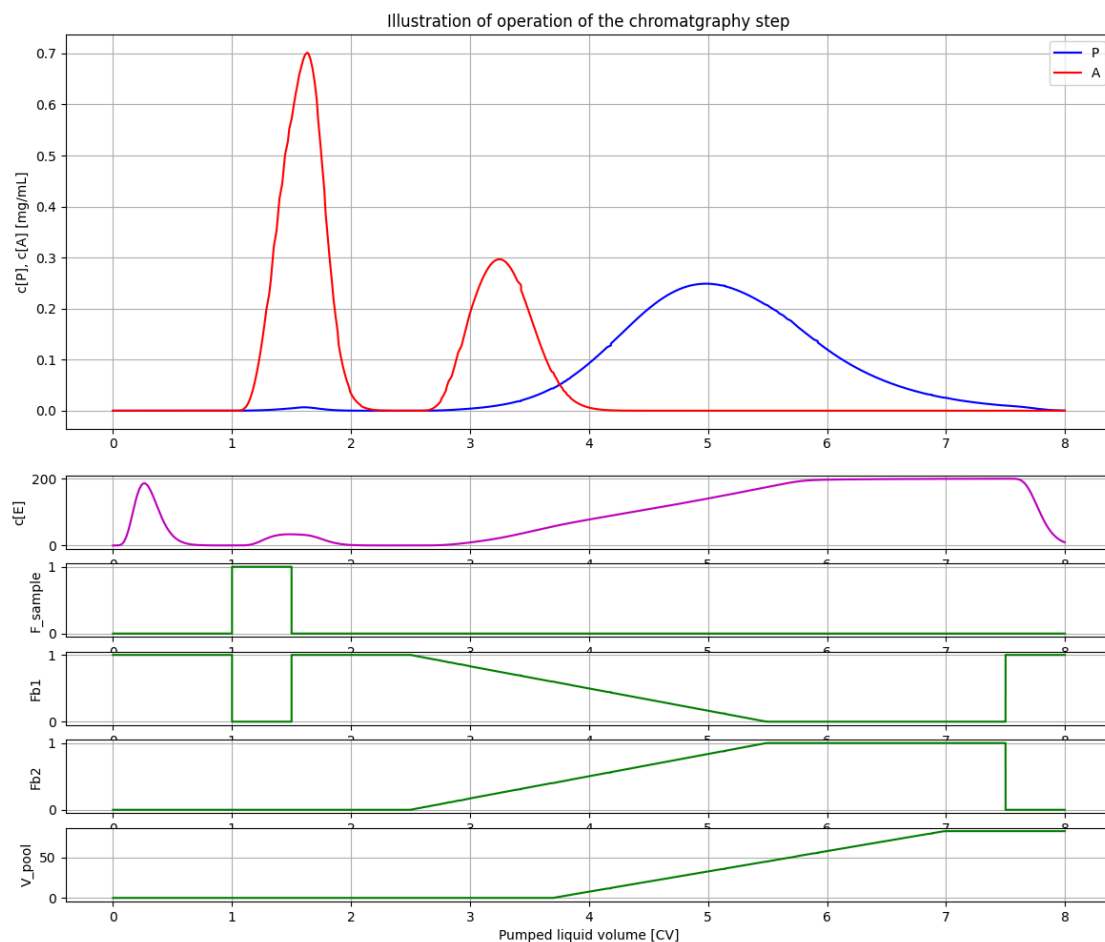
```
# Remaining salt koncentration in the column from prvious batch and eliminated during the initial
init(E_start = 50)
```

```
# Salt koncentration of the desorption buffer
par(E_in_desorption_buffer = 8.0)
```

```
# Flow rate rate through the
par(LFR=lfr)
```

```
# Switching points during operation are conveniently described in terms of multiples of the column
CV_ekv = 1.0
CV_ads = 0.5
CV_wash = 1.0
CV_desorb = 3.0
CV_start_pool = 1.2
CV_stop_pool = 4.5
CV_ekv2 = 2.5
par(scale_volume=True, start_adsorption=CV_ekv*V, stop_adsorption=(CV_ekv+CV_ads)*V)
par(start_desorption=(CV_ekv+CV_ads+CV_wash)*V, stationary_desorption=(CV_ekv+CV_ads+CV_wash+CV_c
par(stop_desorption=7.5*V)
par(start_pooling=(CV_ekv+CV_ads+CV_wash+CV_start_pool)*V, stop_pooling=(CV_ekv+CV_ads+CV_wash+CV
```

```
# Simulation and plot of results
newplot(title='Illustration of operation of the chromatgraphy step', plotType='Elution-conductivi
simu((CV_ekv+CV_ads+CV_wash+CV_desorb+CV_ekv2)*V/VFR)
```



Comments of steps of operations:

- 1) Time: 0-1 hours - equilibration. Just to illustrate the equilibration process the first part of the column is given an initial value of salt concentration.
- 2) Time: 1-1.5 hours - sample is loaded on the column. The product P is adsorbed to the column and just a small amount passes through and goes to the waste. The antagonist A is much less adsorbed.
- 3) Time: 1.5-2.5 hours - washing 1. The column comes to equilibrium and both antagonist and product comes down to low levels.
- 4) Time: 2.5-5.5 hours - desorption. A linear gradient of increasing salt concentration is applied. First the antagonist and later the product comes out.
- 5) Time: 5.5-7.5 hours - washing 2. The column has constant salt concentration and stationary desorption.
- 6) Time: 3.7-7.0 hours - pooling of product. The start- and stop of pooling are chosen with trade-off between maximizing the product pooled and minimize the amount of antagonist in the pooling.
- 7) Time: 7.5-8.0 hours - desorption stopped and salt is washed out and preparation of the next batch to come.

Note that step 4 and 5 is parallel to step 6.

```
# Check mass-balance of P and A
P_mass = model.get('tank_harvest.m[1]') + model.get('tank_waste.m[1]')
A_mass = model.get('tank_harvest.m[2]') + model.get('tank_waste.m[2]')
print('P_mass [mg] =', P_mass)
print('A_mass [mg] =', A_mass)

↩ P_mass [mg] = [12.42212163]
  A_mass [mg] = [12.48878113]
```

These values should be compared with the expected value 12.5 mg, i.e. half a column volume with sample concentration 1 mg/L. The difference is due to numerical errors during simulation.

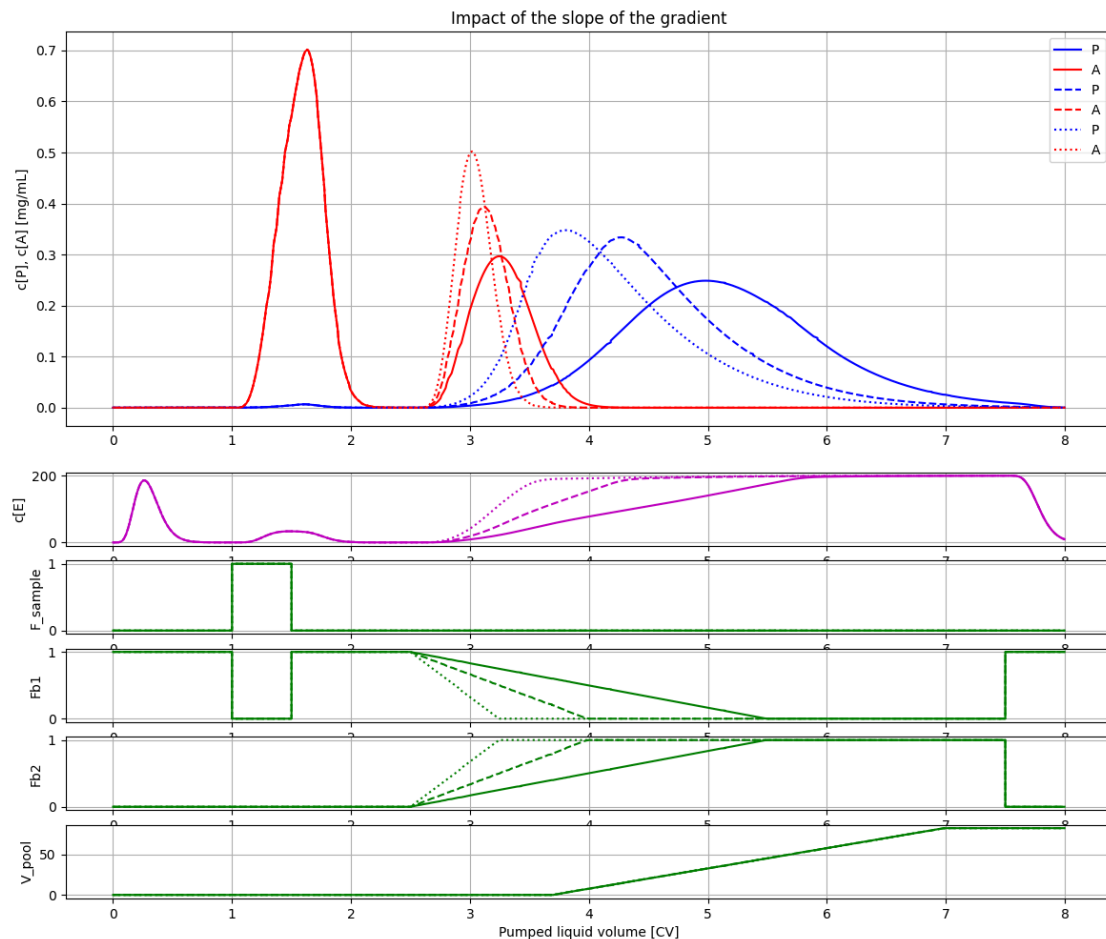
✓ 2 The impact of the slope of the desorption gradient

```
# Simulations showing the impact of change of slope of the desorption gradient
newplot(title='Impact of the slope of the gradient', plotType='Elution-conductivity-vs-CV-combi')

# Same gradient as before
par(start_desorption=(CV_ekv+CV_ads+CV_wash)*V, stationary_desorption=(CV_ekv+ CV_ads+CV_wash+C
par(stop_desorption=7.5*V)
simu((CV_ekv+CV_ads+CV_wash+CV_desorb+CV_ekv2)*V/VFR)

# Gradient finishes after 0.5 of the volume
par(stationary_desorption = (CV_ekv + CV_ads + CV_wash + 0.5*CV_desorb)*V )
simu((CV_ekv+CV_ads+CV_wash+CV_desorb+CV_ekv2)*V/VFR)

# Gradient finishes after 0.25 of the volume
par(stationary_desorption = (CV_ekv + CV_ads + CV_wash + 0.25*CV_desorb)*V )
simu((CV_ekv+CV_ads+CV_wash+CV_desorb+CV_ekv2)*V/VFR)
```



Note the pens shift style for each simulation in the order: solid, dashed, dotted, dash-dotted. The actual simulations done you see in the preceeding cell.

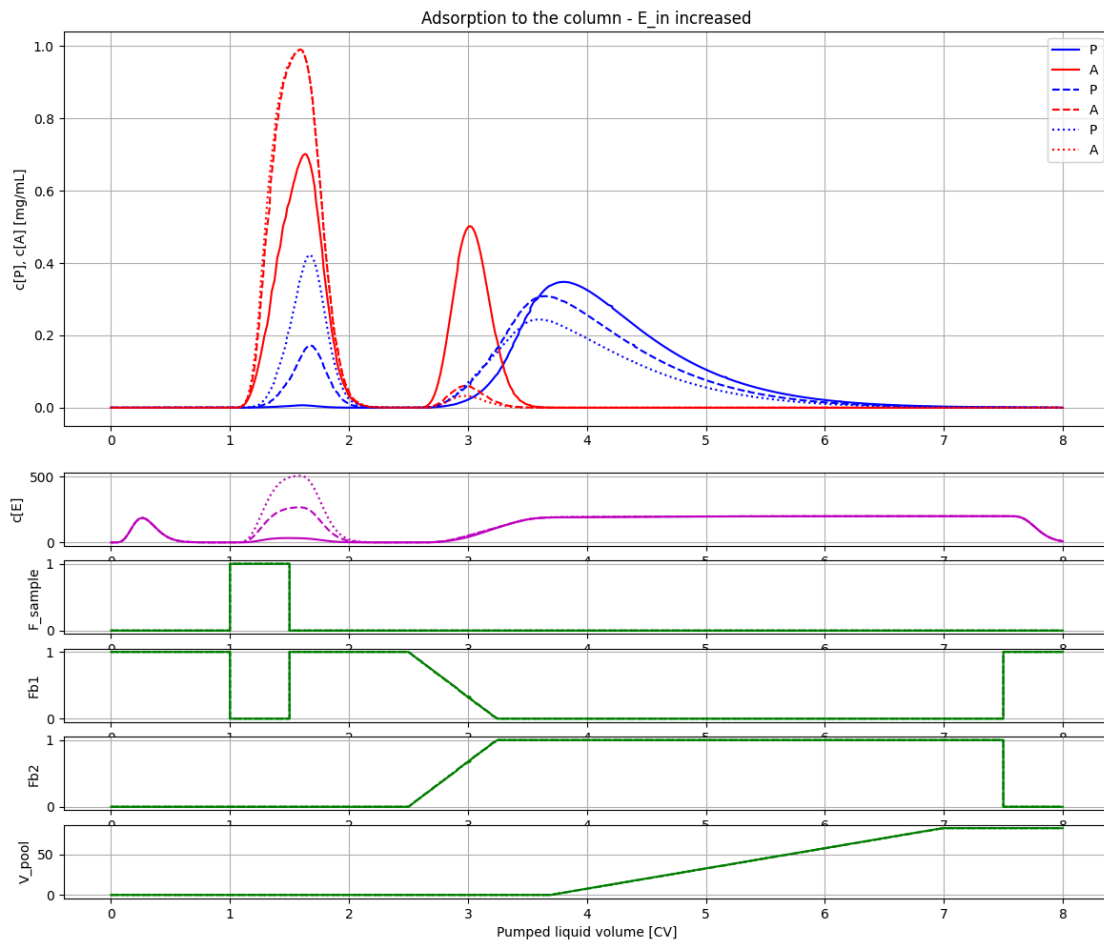
3 The impact of salt concentration in the sample

```
# Let us investigate the impact of increasing salt concetration in the sample E_in

# Simulate and plot the results
newplot(title='Adsorption to the column - E_in increased', plotType='Elution-conductivity-vs-CV'

for value in [0, 10, 20]:
    par(E_in=value)
    simu((CV_ekv+CV_ads+CV_wash+CV_desorb+CV_ekv2)*V/VFR)

# Restore default values
par(k2=0.05, k4=0.3, E_in=0)
```

Note, that increased salt concentration in the sample affect binding of both proteins. During adsorption less is bound. During desorption less product P can be harvested but the fraction of antagonist A may be lowered. Thus, some product is lost but the quality in terms of purity is improved.

✓ 4 The impact of change of binding strength due to pH

There are many factors that contribute to the binding strength. A most important factor is the pH-value of the resin and the characteristic iso-electric point of the protein. The binding strenght can be seen as proportional to the difference.

The binding strength of the resin is described by the quotient $K_P = k_1/k_2$ for the protein P and similarly $K_A = k_3/k_4$ for the protein A.

Below a few help-functions that describe this idea of the pH difference and its impact on binding strength in terms of the parameters k_1 , k_2 , k_3 , and k_4 of the protein-resin interaction.

```

# Define function that describe the proportionality of binding strength of
# the pH difference of the iso-electric point and the resin

def KP_pH_sensitivity(pI_P=8.0, pH_resin=7.0):
    coeff_pH = 6.0
    return coeff_pH*(pI_P-pH_resin)

def KA_pH_sensitivity(pI_A=7.1667, pH_resin=7.0):
    coeff_pH = 1.0
    return coeff_pH*(pI_A-pH_resin)

def par_pH(pI_P=8.0, pI_A=7.1667, pH_resin=7.0, TP=3.33, TA=20.0):
    if (pI_P > pH_resin) & (pI_A > pH_resin):
        par(k2 = 1/(TP*KP_pH_sensitivity(pI_P=pI_P, pH_resin=pH_resin)))
        par(k4 = 1/(TA*KA_pH_sensitivity(pI_A=pI_A, pH_resin=pH_resin)))
    else:
        print('Both pI_P > pH_resin and pI_A > pH_resin must hold - no parameter change made')

# The default parameters of the column
disp('column')

⇨ diameter : 1.261
height : 20.0
x_m : 0.3
k1 : 0.3
k2 : 0.05
k3 : 0.05
k4 : 0.3
Q_av : 6.0
E_start : 50.0

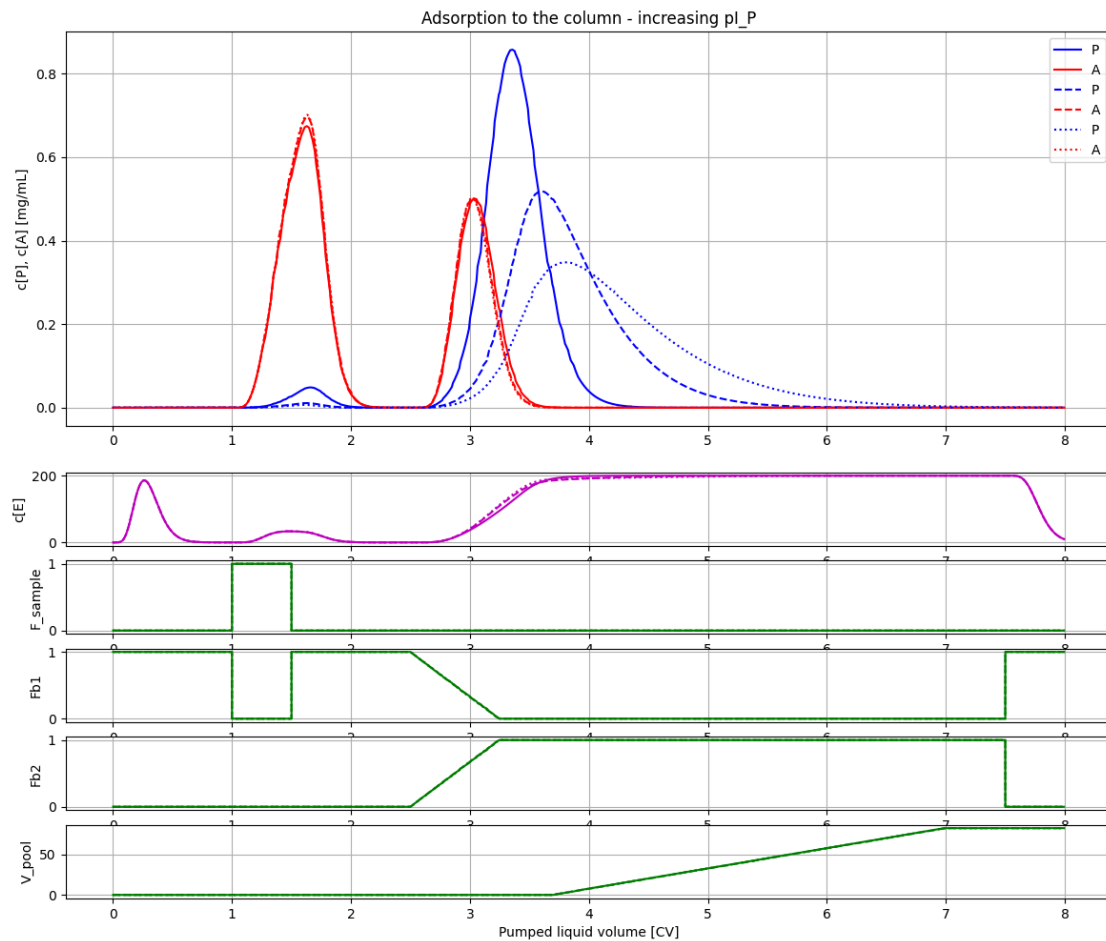
# Let us investigate the impact of change of the iso-electric pH for protein P

# Simulate and plot the results
newplot(title='Adsorption to the column - increasing pI_P', plotType='Elution-conductivity-vs-C'

for value in [7.2, 7.6, 8.0]:
    par_pH(pI_P=value, pI_A=7.1667, pH_resin=7.0)
    simu((CV_ekv+CV_ads+CV_wash+CV_desorb+CV_ekv2)*V/VFR)

# Restore default values
par(k2 = 0.05, k4 = 0.3)

```



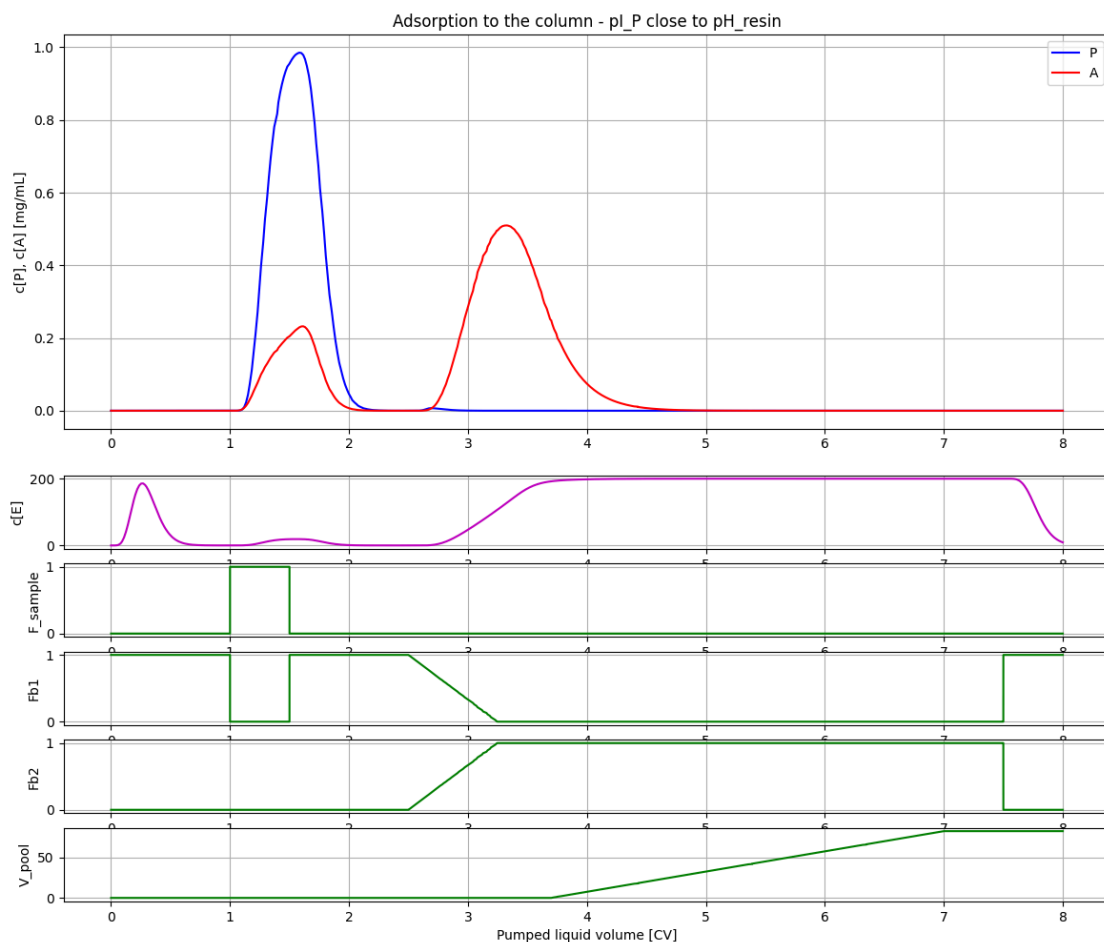
Note, with increasing pI_P the binding of P increase which leads less loss of product during adsorption. During desorption the peak height is lower with increasing binding strenght, but the total amoiunt of product P that can be harvested is higher, due to the smaller loss during adsorption.

```
# Let us investigate the impact of pI_P close to pH_resin

# Simulate and plot the results
newplot(title='Adsorption to the column - pI_P close to pH_resin', plotType='Elution-conductivi'

for value in [7.0001]:
    par_pH(pI_P=value, pI_A=8)
    simu((CV_ekv+CV_ads+CV_wash+CV_desorb+CV_ekv2)*V/VFR)

# Restore default values
par(k2=0.05, k4=0.3)
```



```
# Let us investigate the impact of pI_A close to pH_resin
```

```
# Simulate and plot the results
```

```
newplot(title='Adsorption to the column - pI_A close to pH_resin', plotType='Elution-conductivity')
```

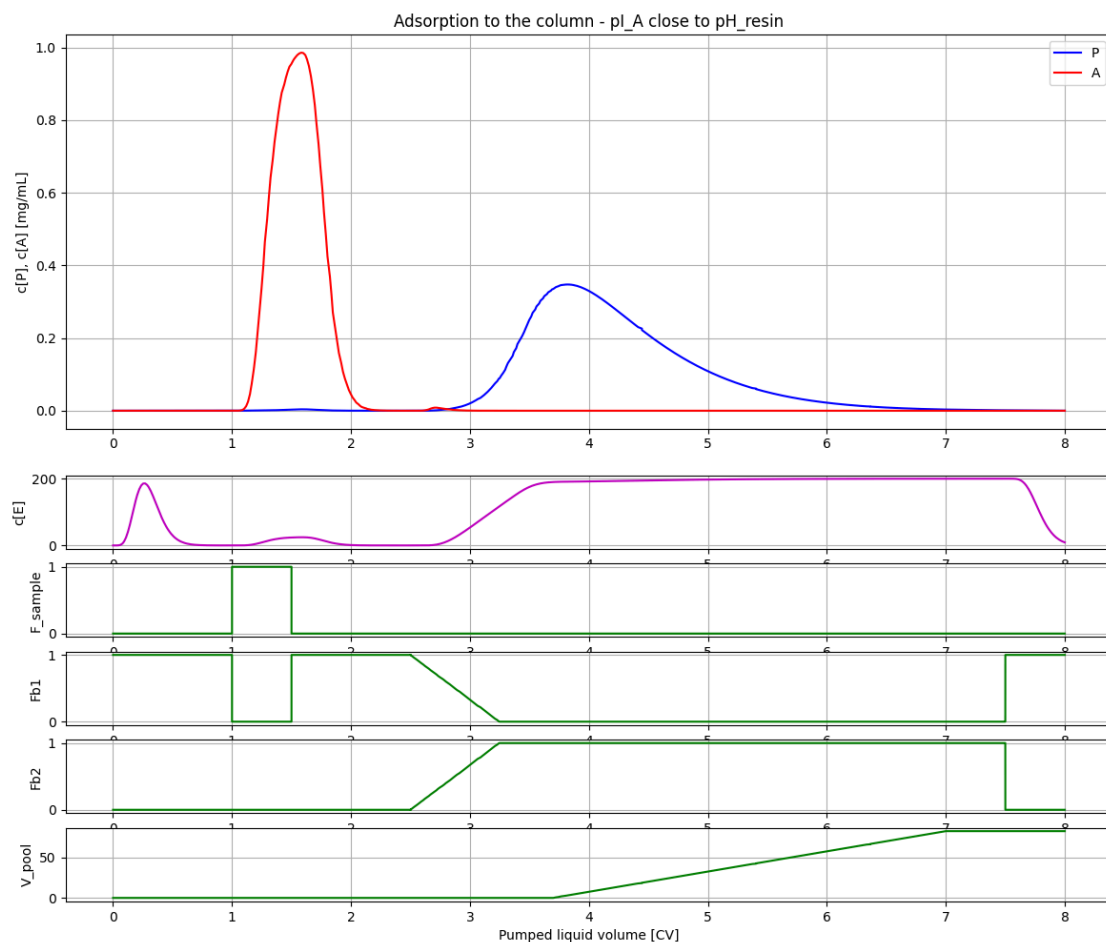
```
for value in [7.001]:
```

```
    par_pH(pI_P=8.0, pI_A=value)
```

```
    simu((CV_ekv+CV_ads+CV_wash+CV_desorb+CV_ekv2)*V/VFR)
```

```
# Restore default values
```

```
par(k2=0.05, k4=0.3)
```



```
# Let us also investigate the impact of salt concentration of the desorptions buffer
```

```
# Simulate and plot the results
```

```
newplot(title='Adsorption to the column - desorption buffer salt conc varied', plotType='Elutio
```

```
for value in [8.0, 16.0]:
```

```
    par(E_in_desorption_buffer=value)
```

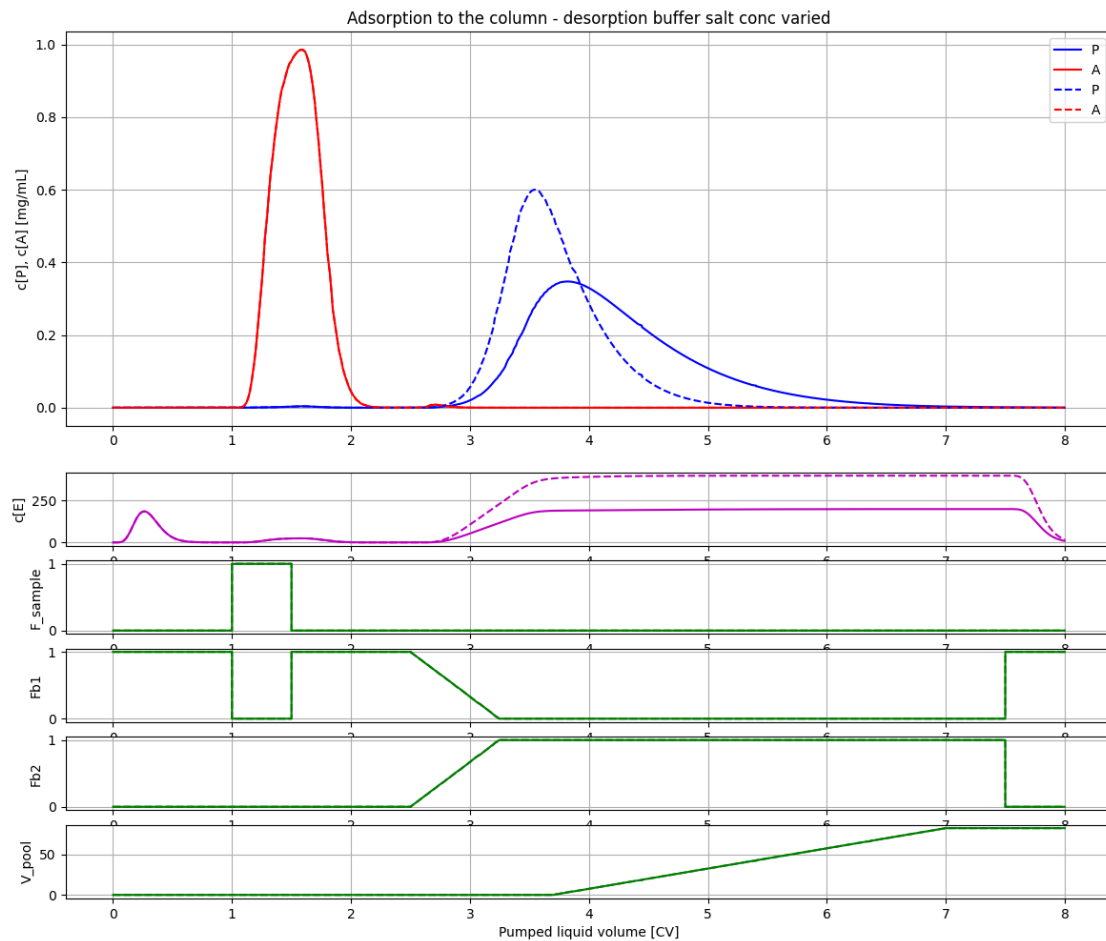
```
    par_pH(pI_P=8.0, pI_A=7.001, pH_resin=7.0)
```

```
    simu((CV_ekv+CV_ads+CV_wash+CV_desorb+CV_ekv2)*V/VFR)
```

```
# Restore default values
```

```
par(E_in_desorption_buffer=8.0)
```

```
par(k2=0.05, k4=0.3)
```



✓ 5 Breakthrough curve often used during process development

Experiment to check column capacity Q_{av} often called breakthrough curve

```
par(P_in=1, A_in=0, E_in=0)
```

```
init(E_start = 0)
```

```
par(Q_av=6.0)
```

```
par(scale_volume=True, start_adsorption=1*V, stop_adsorption=4.01*V)
```

```
par(start_desorption=10*V, stationary_desorption=10.5*V, stop_desorption=11*V)
```

```
par(start_pooling=11*V, stop_pooling=12*V)
```

```
newplot(title='Impact of variation in column capacity  $Q_{av}$ ', plotType='Elution-conductivity-vs-  
for value in [1, 2, 3, 6]: par(Q_av=value); simu(4.0*V/VFR)
```

```
# Linje för 10% UV
```

```
ax1.plot([0,4], [0.1,0.1], 'k--')
```

```
# Restore default parameters
```

```
par(Q_av=6.0, A_in=1.0)
```

