

1 **Analysis and Optimal Design of Batch and Two-Column Continuous**  
2 **Chromatographic Frontal Processes for Monoclonal Antibody**  
3 **Purification**

4  
5 **Ce Shi<sup>a</sup>, Sebastian Vogg<sup>b</sup>, Dong-Qiang Lin<sup>a</sup>, Mattia Sponchioni<sup>c</sup>,**  
6 **Massimo Morbidelli<sup>d\*</sup>**

7  
8  
9 a. Key Laboratory of Biomass Chemical Engineering of Ministry of Education,  
10 College of Chemical and Biological Engineering, Zhejiang University, Hangzhou  
11 310027, China

12 b. YMC ChromaCon, Technoparkstrasse 1, 8005 Zürich, Switzerland

13 c. Department of Chemistry, Materials and Chemical Engineering “Giulio Natta”,  
14 Politecnico di Milano, Via Mancinelli 7, 20131 Milano, Italy

15 d. Institute for Chemical and Bioengineering, Department of Chemistry and Applied  
16 Biosciences, ETH 11 Zurich, Vladimir-Prelog-Weg 1-5/10, 8093 Zürich, Switzerland

17

18 **1. Introduction**

19 The increasing market share of monoclonal antibodies (mAbs), with 10% annual  
20 growth and more than 70 formulations approved in the last decade, makes mAbs one  
21 of the most important classes of biopharmaceuticals today<sup>[1-5]</sup>. The increasing number  
22 of therapeutic indications and the emerging of biosimilars contribute to strengthen the

23 demand for safe, efficient and cost effective manufacturing processes<sup>[6,7]</sup>. Continuous  
24 integrated bioprocessing indeed goes in this direction<sup>[8-10]</sup> and it is therefore encouraged  
25 by regulatory authorities <sup>[11,12]</sup>.

26 Frontal chromatography has seen increased interest for protein purification, in  
27 particular as a polishing step in downstream processes for therapeutic proteins  
28 production, as for example in the purification of monoclonal antibodies (mAbs) from  
29 high molecular weight impurities, e.g., aggregates, using cation exchange resins<sup>[13-17]</sup>.  
30 The schematic diagram of frontal chromatography operated on a single (batch) column  
31 is shown in Figure 1a. Here, the eluate from the capture step (feed), containing both the  
32 monomer and the aggregates, is first loaded into the column. The impurity (aggregates)  
33 binds stronger to the cation exchange resin and displaces the weaker binding product  
34 (monomer), which thus elutes first and is collected in the product pool. Loading is  
35 continued until reaching, in general, sufficiently high purity in the pool and relatively  
36 high recovery (yield). Next, a washing step is applied to recover the residual monomer  
37 still present in the column into the product pool, so as to further increase the yield, but  
38 being careful not to elute also the aggregates, which would spoil the purity below  
39 specifications. Finally, regeneration and re-equilibration (RR) are carried out to elute  
40 all the impurities (and remaining product) into the waste and prepare the column for the  
41 next loading step.

42 In such a batch operation, the loading time and linear velocity have to be properly  
43 selected so as to process the largest amount of material, without letting too much  
44 aggregate into the product pool, so as to preserve purity. In the following washing step,

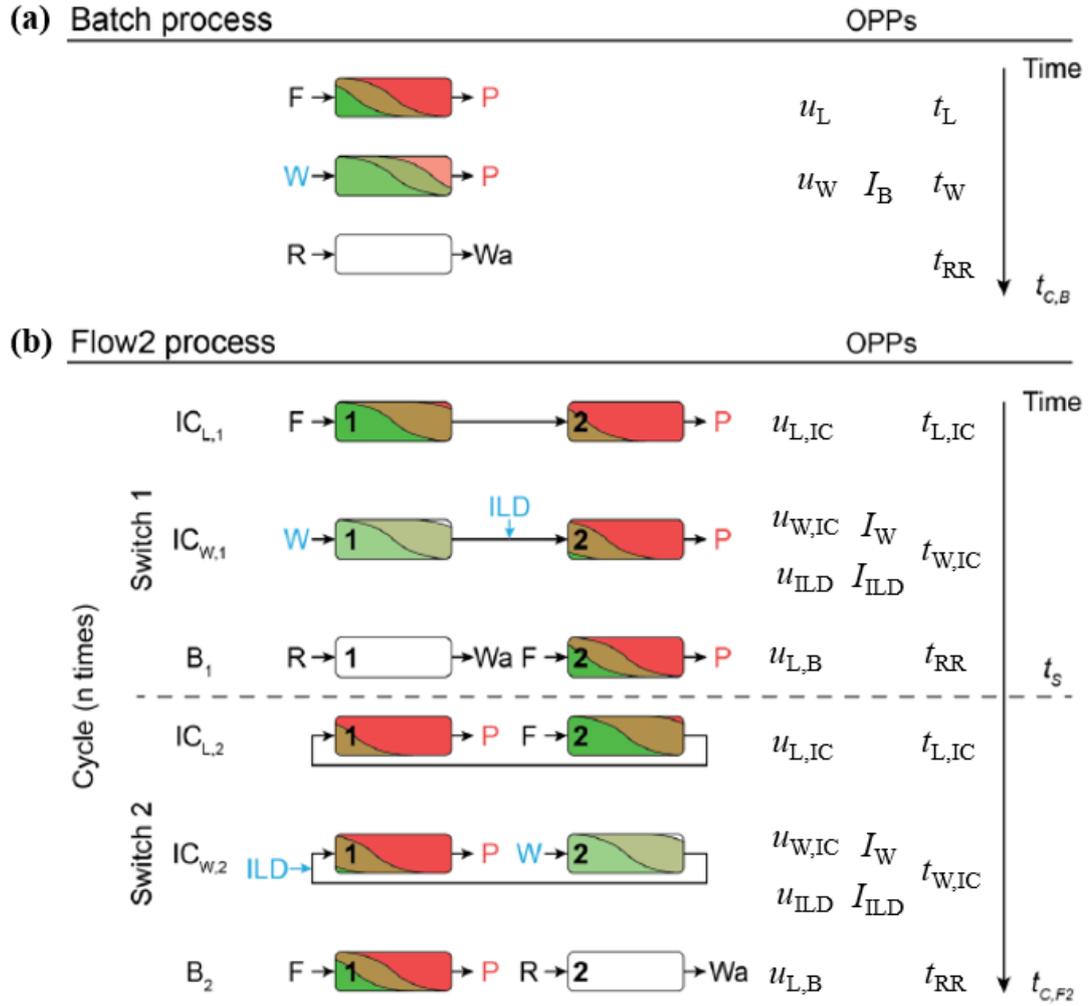
45 the linear velocity and duration should be carefully chosen to elute as much as possible  
46 of the remaining product, thus maximizing the yield, while not desorbing the impurity  
47 beyond the purity specification <sup>[18]</sup>. Therefore, batch frontal chromatography suffers  
48 from an intrinsic purity-yield tradeoff. High loadings and harsh washing conditions  
49 enable the recovery of much of the product, and thus an improved monomer yield, but  
50 an overall low purity. On the other hand, low loadings and too mild washing conditions  
51 enable high purity of the pool but prevent full recovery of the product, at the expense  
52 of the process yield.

53 In order to alleviate this purity-yield tradeoff, a novel cyclic two column  
54 continuous chromatographic process (referred to as Flow2) has been developed <sup>[18]</sup>. The  
55 schematic diagram is illustrated in Figure 1b. This is a periodic process, where each  
56 switch is constituted of three steps, after which the two columns exchange their role. In  
57 the first step, the two columns are fed while being interconnected, so that the  
58 breakthrough of the aggregates from the first column is captured by the second column.  
59 In the next interconnected washing step, with inline dilution between the two columns,  
60 both the product and the unbound impurity left in the first column are eluted into the  
61 second column. With the proper inline dilution, both of them are bound in the second  
62 column. Finally, in the third step, the two columns are disconnected. The first one  
63 undergoes the RR process while the second one is loaded with the fresh feed.

64 With two columns interconnected during loading and the following washing with  
65 inline dilution, aggregates are prevented from eluting from the second column into the  
66 product pool and more monomer can be eluted from the first column, thus improving

67 the tradeoff between purity and yield. In addition, the washing conditions (buffer and  
68 duration) do not need to be carefully designed as in the case of batch operation, thus  
69 increasing the process robustness. However, the design of this cyclic process needs to  
70 account for the increased number of operational parameters and complexity of the  
71 process dynamics, which can be best achieved using model-based approaches [19-24].

72 In this work, the fundamental aspects of batch and continuous frontal  
73 chromatography are analyzed. A model-based optimal design procedure, valid for both  
74 batch and Flow2 processes, is developed with reference to three process performance  
75 parameters: yield (recovery), purity and productivity. In particular, Pareto Fronts of  
76 productivity and yield, with purity fixed at given specification values ( $P_{\text{spec}}$ ), computed  
77 based on reliable chromatographic models of the two processes, are discussed. Next,  
78 the two processes, each operated at its own optimal conditions, are compared. This  
79 analysis is conducted with reference to the polishing of a mAb of industrial relevance  
80 and accounts, in addition to yield, purity and productivity [25], also for the important  
81 concept of process robustness, which is a major concern particularly in  
82 biopharmaceutical applications [26,27]. This has been quantified using a rigorous model-  
83 based sensitivity analysis of the process performance with respect to its operating  
84 process parameters.



85

86 *Figure 1. Schematic diagram of batch frontal chromatography (a) and continuous*

87 *Flow2 processes (b)<sup>[18]</sup>.*

88

## 89 2. Model-Based Optimal Design Methods

### 90 2.1 The Chromatographic Model

91 The chromatographic lumped kinetic model with linear driving force

92 approximation has been used in all simulations <sup>[16,28,29]</sup>:

$$93 \quad \frac{\partial c_i}{\partial t} = -\frac{u_{sf}}{\varepsilon_{t,i}} \frac{\partial c_i}{\partial x} + \frac{u_{sf}}{\varepsilon_{t,i}} d_{ax,i} \frac{\partial^2 c_i}{\partial x^2} - \frac{1 - \varepsilon_{t,i}}{\varepsilon_{t,i}} \frac{\partial q_i}{\partial t} \quad (1)$$

$$94 \quad \frac{\partial q_i}{\partial t} = k_{m,i} (q_i^{eq} - q_i) \quad (2)$$

95 with  $i = M, A$  and the boundary conditions:

96  $c_i(x, t = 0) = 0$

97  $c_I(x, t = 0) = I_0$

98  $c_{pH}(x, t = 0) = pH_0$

99  $c_i(x, t = 0) = c_{i,in}(t) + d_{ax,i} \left. \frac{\partial c_i}{\partial x} \right|_{x=0}$

100  $\left. \frac{\partial c_i}{\partial x} \right|_{x=L_{col}} = 0$

101 The mixing node in the continuous process has been simulated as follows:

102 
$$c_{i,in,col2} = \frac{C_{i,in,col1}u_{W,IC} + C_{i,ILD}u_{ILD}}{u_{W,IC} + u_{ILD}} \quad (3)$$

103 The adsorption equilibrium has been described through a surrogate model, which

104 mimics the behavior of the DLVO-derived model, based on the competitive Langmuir

105 isotherm and appropriate empirical correlations <sup>[18,30]</sup> as follows:

106 
$$q_i^{eq} = \frac{H_i c_i}{1 + \sum_j \frac{H_j c_j}{q_j^{sat}}} \quad (4)$$

107 
$$q_i^{sat} = a_i^{sat} pH + b_i^{sat} \quad (5)$$

108 
$$H_i = \alpha_i I^{-\beta_i} \quad (6)$$

109 
$$\log_{10} \alpha_i = a_i^\alpha pH + b_i^\alpha \quad (7)$$

110 
$$\beta_i = a_i^\beta pH + b_i^\beta \quad (8)$$

111 The meaning of all variables and parameters is explained in the notation section,

112 while the parameter values adopted in the simulations are listed in Table 1.

113

114

115

Table 1. Values of the chromatographic model parameters <sup>[18]</sup>

	Parameter	Unit	Salt	Monomer	HMW
$d_{col}$	Column diameter	cm	-----0.5-----		
$L_{col}$	Bed height	cm	-----5-----		
$\varepsilon_b$	Bed porosity	-	-----0.39-----		
$\varepsilon_{t,i}$	(Accessible) total porosity	-	0.95	0.65	0.65
$\varepsilon_{p,i}$	(Accessible) particle porosity	-	0.93	0.43	0.43
$a_i^{Sat}$	Slope of $q_i^{Sat}$ vs. pH	-	n/a	0	0
$b_i^{Sat}$	Intercept of $q_i^{Sat}$ vs. pH	-	n/a	212	106
$a_i^\alpha$	Slope of $\log_{10}\alpha$ vs. pH	-	n/a	-1.270	-3.090
$b_i^\alpha$	Intercept of $\log_{10}\alpha$ vs. pH	-	n/a	31.22	46.90
$a_i^\beta$	Slope of $\beta$ vs. pH	-	n/a	1.128	0.676
$b_i^\beta$	Intercept of $\beta$ vs. pH	-	n/a	5.227	9.870
$d_{ax,i}$	Axial dispersion coefficient	cm	0.034	37	98
$k_{m,i}$	Mass transfer coefficient	1/min	170	1.3	0.53

## 117 2.2 Process performance parameters

118 As mentioned above, the process performance is quantified in the following using  
 119 three process performance parameters: the productivity,  $Pr$  of the target species, i.e.,  
 120 mAb, defined as:

$$121 \quad Pr = \frac{m}{n_{col} V_{col} t_C} \quad (9)$$

122 where  $m$  is the mass of target recovered in the product pool in one cycle of duration  $t_C$

123 using  $n_{\text{col}}$  columns, each with volume  $V_{\text{col}}$ , the yield,  $Y$  of the target protein defined as:

$$124 \quad Y_i = \frac{m}{m_{\text{load}}} \quad (10)$$

125 where  $m_{\text{load}}$  is the amount of target protein loaded on the column in one cycle, and the  
126 purity,  $P$  defined as:

$$127 \quad P = \frac{m}{\sum_i m_i} \quad (11)$$

128 where the sum at the denominator is extended to the mass  $m_i$  of all proteins present in  
129 the product pool.

### 130 **2.3 Optimization methods**

131 The optimal design of frontal chromatographic processes can be complex. For this,  
132 a specific procedure has been devised, based on a series of suitable steps, and referred  
133 to as the *design procedure* (DP) in the following. This allows to facilitate and guarantee  
134 the identification of the optimal operating conditions, for a given set of performance  
135 parameters. The obtained results are compared with corresponding results obtained by  
136 a multi-objective optimization procedure based on Genetic Algorithms <sup>[31]</sup>.

137 The general concept of the design procedure is based on the evaluation of the  
138 loading and washing times (see Figure 1), which describe the Pareto Front of  
139 productivity and yield at a given purity equal to the specification value,  $P_{\text{spec}}$ . The  
140 regeneration and re-equilibration time,  $t_{\text{RR}}$  (Figure 1) is expected to derive from a  
141 specifically designed experimental study conducted on a single column and is therefore  
142 considered as a given value in this work. The basic idea is to first compute, all the other  
143 parameters and operating conditions being fixed, the loading times leading to purity

144 values at the end of the first loading step,  $P_1$  ranging from 100% to  $P_{\text{spec}}$ . In the  
145 following washing step, the process purity can only decrease and the corresponding  
146 duration is computed such that, for each one of the previous  $P_1$  values, it leads to the  
147 required purity  $P_{\text{spec}}$ . For each pair of loading and washing time values, we then  
148 compute the corresponding productivity and yield values, being in all cases the purity  
149 equal to  $P_{\text{spec}}$ . At this point, we can order all the obtained values in a productivity versus  
150 yield plot and obtain the desired Pareto Front at fixed purity. This procedure can be  
151 repeated by changing any other of the relevant parameters, like the buffer compositions  
152 or the column or particle size, and compute the new Pareto Front. This approach is  
153 useful not only to find the optimal operating conditions of the process, but also to  
154 quantify the robustness of a given process design, as well as the economic impact of  
155 the different operating conditions.

156 Alternatively, the optimization problem can be approached as a whole, without  
157 attempting any problem decomposition, using a fully general multi-objective  
158 optimization algorithm. The function ‘Gamultiobj’ of the MATLAB library <sup>[32]</sup>, based  
159 on a Genetic Algorithm, has been used in this work and the obtained results are  
160 compared with those of the *ad-hoc* design procedure.

161 In the next section, we describe in detail the algorithm to compute the optimal  
162 loading and washing times described above for both the batch and the Flow2 processes.

163

### 164 **3. Optimal Design of Frontal Chromatography Processes**

#### 165 **3.1. The Batch Process**

166 The Pareto Front of productivity and yield with constant fixed  $P_{\text{spec}}$ , computed

167 with both methods, are compared first in the case of a batch process. All parameters,  
 168 unless otherwise specified, are kept constant at the values summarized in Table 2.

169

170

*Table 2. Batch Operating Conditions*

Parameters	Unit	Value
$c_{L, mono}$	g/L	4.5
$c_{L, agg}$	g/L	0.5
$I_L$	mM	80
$I_W$	mM	120
$I_{RR}$	mM	1000
$pH_L$	-	5
$pH_W$	-	5
$pH_{RR}$	-	5
$u_L$	cm/hr	300
$u_W$	cm/hr	300
$u_{RR}$	cm/hr	300
$t_{RR}$	min	15

171

172 With illustrative purposes, the requested purity the value was set as  $P_{spec} = 99\%$ . The  
 173 procedure develops according to the following three steps:

174 *Step 1: Compute the purity values at the column outlet,  $P_1$  during the loading phase*  
 175 *(Figure 1a) for increasing loading time values,  $t_L$ .*

176

As  $t_L$  increases, first the product breaks through from the outlet of the column into

177 the product pool, followed by the impurity at longer times, thus reducing the purity in  
178 the product pool,  $P_1$ , as shown in Figure 2a. As the loading proceeds the purity  
179 decreases from 100% until  $P_1 = P_{spec}$ , which indicates the maximum acceptable value  
180 of  $t_L$ . In this conditions, in fact, the washing time in the next step should be set to zero  
181 to avoid any further decrease in purity below specification, but of course this would not  
182 allow for any improvement in the process yield. Accordingly, at optimal operation, the  
183 value of  $t_L$  should be shorter than 72 min, which corresponds to  $P_1$  values ranging from  
184 100% to the  $P_{spec} = 99\%$  value.

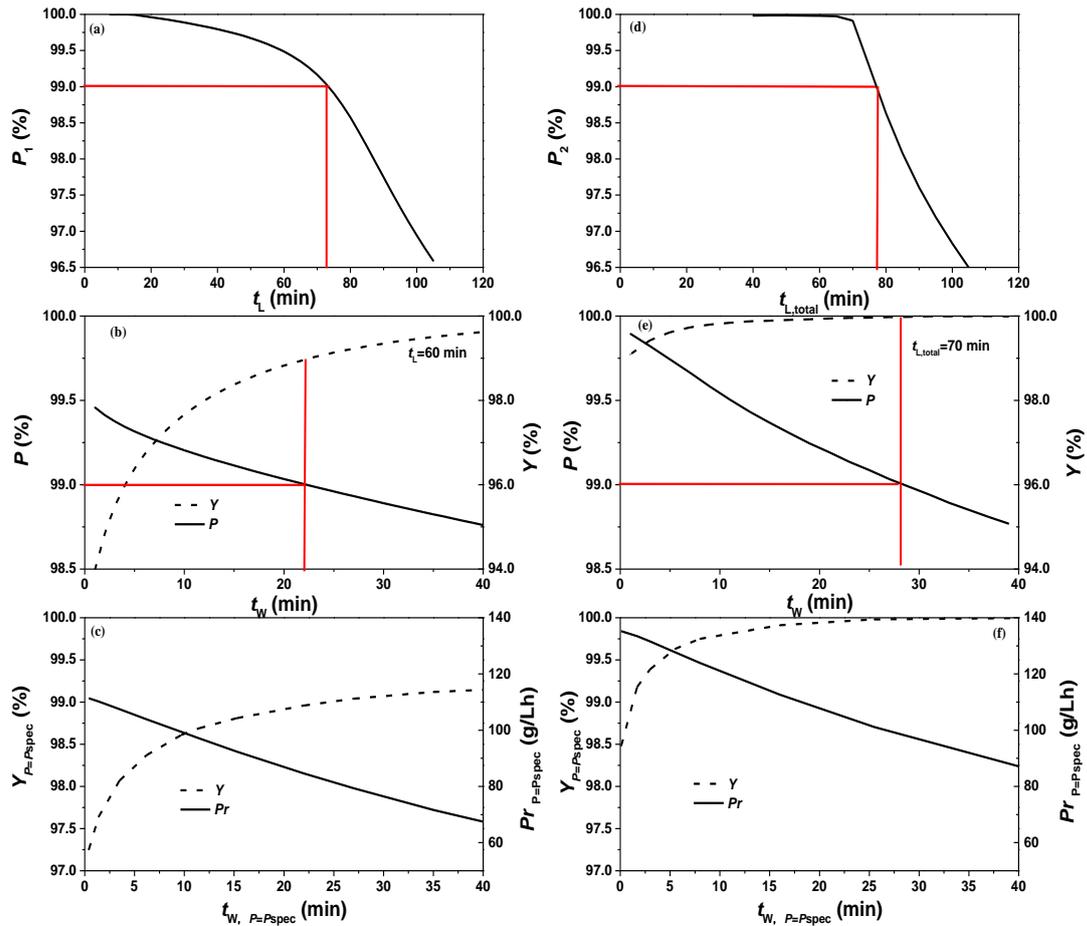
185 *Step 2: For each of these pairs of values  $t_L$  and  $P_1$ , compute the corresponding washing*  
186 *time,  $t_w$ , which, starting from  $P_1$ , leads to a final purity,  $P$  equal to  $P_{spec}$ .*

187 The obtained process yield and purity values are shown in Figure 2b as a function  
188 of the washing time,  $t_w$ , as an example for the case of  $t_L=60$  min and  $P_1=99.5\%$ . It is  
189 seen that the process purity,  $P$  decreases while  $Y$  increases for increasing washing times.  
190 The decrease in the process purity is because more eluate, including both product and  
191 impurity, is washed out into the product pool. On the other hand, the yield increases  
192 when increasing  $t_w$  since more product is recovered. By selecting the purity value equal  
193 to  $P_{spec}$ , the corresponding values of the yield,  $Y_{P=P_{spec}}$  and the washing time,  $t_{W,P=P_{spec}}$   
194 are found.

195 *Step 3: Repeat the procedure above to calculate productivity,  $Pr$  and yield,  $Y$  for each*  
196 *of the pairs of values  $t_L$  and  $P_1$  in Figure 2a and derive the corresponding Pareto Front*  
197 *at fixed purity equal to  $P_{spec}$ .*

198 Using the  $t_L$  and  $P_1$  values in Figure 2a, the curve shown in Figure 2c is obtained,

199 representing the yield as a function of the washing time leading to process purity,  $P =$   
 200 99%. On the other hand, it is seen that the corresponding productivity values, computed  
 201 through equation (19), decrease with  $t_{wash}$ , leading to the trade-off between  $Pr$  and  $Y$   
 202 illustrated by the Pareto Front, with fixed purity  $P_{spec}$ , in Figure 3.



203  
 204 *Figure 2. The design procedure for the batch and Flow2 processes. (a) Batch  $P_1$  as a*  
 205 *function of the loading time; the bar indicates  $P_{spec}$  (b) Batch  $P$  and  $Y$  as a function of*  
 206 *the washing time at  $t_L=60$  min and  $P_1=99.5\%$  (c) The relationship between  $Y_{P=P_{spec}}$*   
 207 *and  $Pr_{P=P_{spec}}$  as a function of  $t_{W, P=P_{spec}}$  for a batch process. (d) Flow2  $P_2$  as a function*  
 208 *of the loading time,  $t_{L,total}$ ; the bar indicates  $P_{spec}$  (e) Flow2  $P$  and  $Y$  as a function of the*  
 209 *washing time at  $t_{L,total} = 70$  min and  $P_2=99.8\%$  (f) The relationship between  $Y_{P=P_{spec}}$*

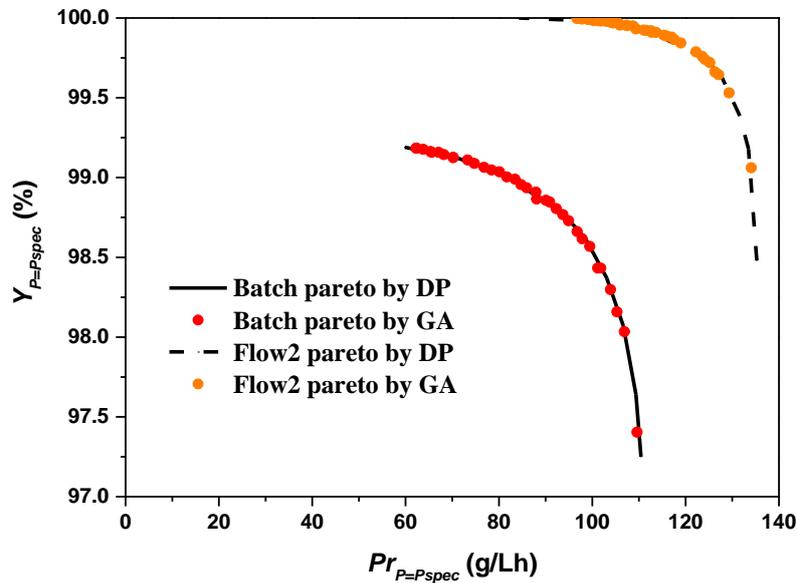
210 and  $Pr_{P=P_{spec}}$  as a function of  $t_{W,P=P_{spec}}$  for a Flow2 process.

211

212 The results of the *ad-hoc developed design procedure* (DP) are compared with  
213 those of a general multiobject Genetic Algorithm (GA), using 50 individuals per  
214 generation and a maximum of 200 generations. The purity constraint has been  
215 introduced by imposing heavy penalties on purity values smaller than  $P_{spec}$ . At each  
216 iteration, the 35 fittest individuals are selected to plot the Pareto Front and produce the  
217 next generation. The GA optimization is terminated when the 200<sup>th</sup> generation is  
218 reached or when the average relative change in the best fitness function value, with  
219 respect to the previous generation, is less than or equal to the function tolerance ( $10^{-4}$ ).  
220 The performance values corresponding to the best 35 individuals in the last generation  
221 are compared with the Pareto Front computed through the design procedure in Figure  
222 3. It is seen that all the points corresponding to the GA optimization are on or slightly  
223 below the curve generated by the design procedure, indicating that the two methods  
224 provide essentially the same result. In addition, it is found that all the points obtained  
225 through the GA method exhibit a purity value equal to the constrain value of 99% with  
226 a maximum 1 % relative deviation.

227 It is worth noticing that, although the two methods give equivalent results, the  
228 associated computational effort is quite different. In the *design procedure*, only 35\*10  
229 objective functions are calculated: 35 for getting the Pareto Front, and 10 each for  
230 determining the  $t_W$  values corresponding to 99% purity. On the other hand, in the multi-  
231 objects GA optimization, 50\*200 functions are calculated: one each for the 50

232 individuals constituting each of the 200 generations.



233

234 *Figure 3. Pareto Front of  $Pr$  and  $Y$  computed with the design procedure (DP)*  
 235 *compared with the results of the global optimization based on genetic algorithm (GA),*  
 236 *for  $P_{spec} = 99\%$  and other parameter values as in Tables 1, 2 and 3.*

237

### 238 3.2 The Continuous Flow2 Process

239 The two optimization methods considered above have been developed and  
 240 compared also for the Flow2 process. In particular, we optimize the interconnected  
 241 loading and washing times,  $t_{L,IC}$  and  $t_{w,IC}$  (Figure 1b) in order to obtain the Pareto Front  
 242 of productivity,  $Pr$  and  $Y$  with fixed purity equal to  $P_{spec}$ . Note that in this process, the  
 243 batch loading time is fixed and equal to the regeneration and re-equilibration time,  $t_{RR}$ ,  
 244 which is considered as a given constant in this analysis (Figure 1b). Accordingly, the  
 245 total loading time given by  $t_{L,total} = t_{RR} + t_{L,IC}$ , can actually be changed only through the  
 246 interconnected loading time,  $t_{L,IC}$ . All remaining parameters are kept constant and equal

247 to the values summarized in Tables 1 and 3. It is to be noted that all the simulation  
 248 results reported for the continuous Flow2 process refer to steady state conditions. These  
 249 are obtained by simulating the entire dynamics of the process and considering the  
 250 transient behavior completed when the mass flow of each protein entering and leaving  
 251 differ for no more than 1.0 % , which means that no protein is accumulated or lost in  
 252 the system during every switch.

253 *Table 3. Flow2 Operating Conditions*

Parameters	Unit	Value
$c_{L, mono}$	g/L	4.5
$c_{L, agg}$	g/L	0.5
$I_{IC}$	mM	80
$I_W$	mM	120
$I_{ILD}$	mM	10
$I_{RR}$	mM	1000
$pH_{L,IC}$	-	5
$pH_{W,IC}$	-	5
$pH_{ILD}$	-	5
$pH_{RR}$	-	5
$u_{L,IC}$	cm/hr	300
$u_W$	cm/hr	300
$u_{ILD}$	cm/hr	300
$u_{RR}$	cm/hr	300

254

255 As mentioned above, differently from the batch process, the Flow2 process has two  
256 loading phases within one switch: interconnected and batch loading. In the following,  
257 we consider these two steps together with a total duration,  $t_{L,total} = t_{RR} + t_{L,IC}$ , with a  
258 purity value  $P_2$ , which is analogous to the purity  $P_1$  in the batch process. After the  
259 washing step, the product purity is indicated as  $P$  which represents the final product  
260 purity at the end of the switch as indicated in Figure 1b.

261 The design procedure in this case is organized as follows:

262 *Step 1: Simulate the process for changing total loading times,  $t_{L,total}$  so as to obtain*  
263 *purity values,  $P_2$  ranging from 100% to the requested  $P_{spec}=99\%$ .*

264 As shown in Figure 2d, the obtained  $P_2$  values decrease as a function of the loading  
265 time,  $t_{L,total}$ : starting from 100% to values below the imposed process purity  
266 specification,  $P_{spec}$ , which is reached at  $t_{L,total} = 78$  min.

267 *Step 2: For each pairs of values  $t_{L,total}$  and  $P_2$  in Figure 2d, with  $P_2 > P_{spec}$ , compute the*  
268 *interconnected washing time ( $t_{W,IC}$  in Figure 1b) leading to a product purity,  $P$  at the*  
269 *end of the switch equal to the requested  $P_{spec}$ .*

270 As an example, Figure 2e shows the results obtained for the pair of values  $t_{L,total} = 70$   
271 min and  $P_2 = 99.8\%$ . As expected, it is seen that as the washing time increases, the purity  
272 decreases while the yield increases. The values  $Y_{P=P_{spec}}$  and  $t_{W,P=P_{spec}}$ , corresponding to  
273 the requested purity value  $P_{spec}$ , can be obtained.

274 *Step 3: Repeat the previous step for each of the pairs of values  $P_2$  and  $t_{L,total}$  in Figure*  
275 *2d and with the corresponding productivity,  $Pr$  and yield,  $Y$  values derive the*

276 *corresponding Pareto Front, at fixed purity equal to  $P_{spec}$ .*

277 Repeating the step above for all the pairs of values  $P_2$  and  $t_{L,total}$  in Figure 2d, the  
278 maximum yield values for each washing time,  $t_w$ , compatible with the fixed purity,  $P_{spec}$   
279 can be computed as shown in Figure 2f. From these, and the corresponding productivity  
280 values,  $Pr$  computed through Equation 9, the Pareto Front for productivity and yield at  
281 fixed purity equal to  $P_{spec}$  in Figure 3 is obtained.

282 The latter is compared in the same figure with the corresponding Pareto Front for  
283 the batch frontal chromatography process, obtained as discussed above. The higher  
284 efficiency of the Flow2 process, which will be discussed later in more detail, is clearly  
285 indicated by the movement of the Pareto Front to the upper right corner of the figure.

286 As mentioned above, the multi-object global optimization of the Flow 2 process  
287 has also been performed based on a genetic algorithm, using 50 individuals per  
288 generation and a maximum of 300 generations. The obtained results, corresponding to  
289 the 35 best individuals in the last generation, are shown by the points shown in Figure  
290 3 and compared with the results of the ad-hoc design procedure. It is seen that the two  
291 methods provide equivalent results, although the GA approach requires a significantly  
292 larger computational effort, as already discussed in the context of the batch process.

293

#### 294 **4. Analysis and Comparison of Optimized Batch and Flow 2 Process Performance**

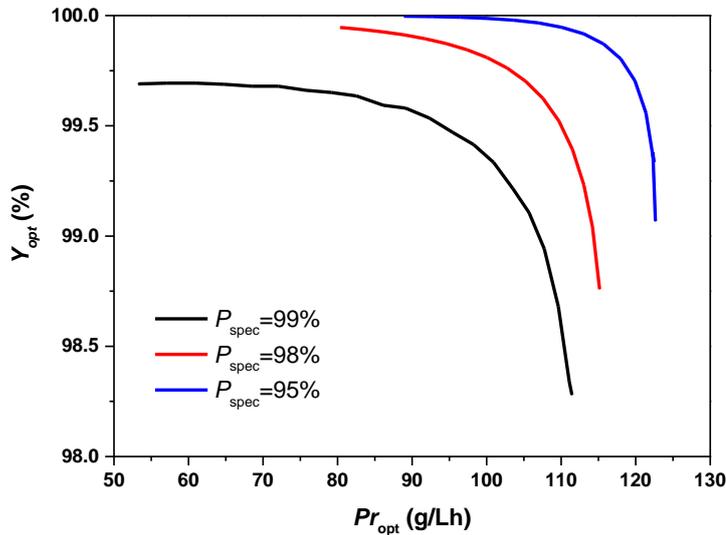
295 A general difficulty when comparing different processes, and not only in  
296 chromatography, is to select “fair” conditions for the comparison, that is operating  
297 conditions that do not favor one or the other. In this work, we consider each process

298 under independently optimized operating conditions. In particular, we are going to  
299 analyze the behavior of batch and Flow 2 processes as a function of operating  
300 parameters which are known to be most relevant in chromatography, such as linear  
301 velocities in the columns and composition of the loading and washing buffers. In all  
302 cases, we consider for each process the optimal Pareto yield-productivity (with fixed  
303 purity,  $P_{spec}$ ) obtained by optimizing the durations of both the loading and washing steps.  
304 In the following, the design procedure developed in this work will be used, since we  
305 have shown that this provides the same results as a general multi-objective optimization,  
306 but with lower computational effort. The objective is to analyze and compare the  
307 behavior of each of such processes with respect to both process performance and  
308 robustness.

#### 309 **4.1 The relevant performance parameters**

310 Among the various chromatographic steps involved in the production of mAbs,  
311 frontal chromatography is a quite promising candidate for the polishing step after  
312 protein capture, where high purity, productivity and robustness are requested. For  
313 example, in the case of aggregate removal, mAb purity values well above 95% are  
314 typically needed. In Figure 4, the tradeoff between productivity and yield for optimal  
315 batch process operations at specification purities,  $P_{spec}$  equal to 95%, 98% and 99% is  
316 shown. It can be seen that more stringent purity constraints move the Pareto Front to  
317 the lower left corner with correspondingly lower values for both productivity and yield.  
318 It can also be seen that the yield is always higher than 98%, indicating that this is not  
319 the discriminating performance parameter in designing frontal chromatography

320 processes. Accordingly, in the following we will base the process comparison on the  
 321 tradeoff between yield and productivity as well as on the operation robustness, with a  
 322 stringent purity specification of  $P_{\text{spec}} = 99\%$ .



323  
 324 *Figure 4. Tradeoff between yield and productivity (Pareto Front) for the batch process*  
 325 *at various  $P_{\text{spec}}$  values. Operating conditions as in Tables 1 and 2.*

#### 327 4.2 Role of linear velocities in loading and washing

328 In this section, the effect of the liquid velocity during loading and washing is  
 329 analyzed in both Batch and Flow2 process. The values considered range from 300 cm/hr  
 330 to the value compatible with the maximum pressure drop tolerated by the stationary  
 331 phase as computed through the Blake-Kozeny equation <sup>[33]</sup>

$$332 \quad \frac{\Delta P}{L_{\text{col}}} = \frac{150\mu (1 - \varepsilon_b)^2}{d_p^2 \varepsilon_b^3} u_{\text{sf}} \quad (12)$$

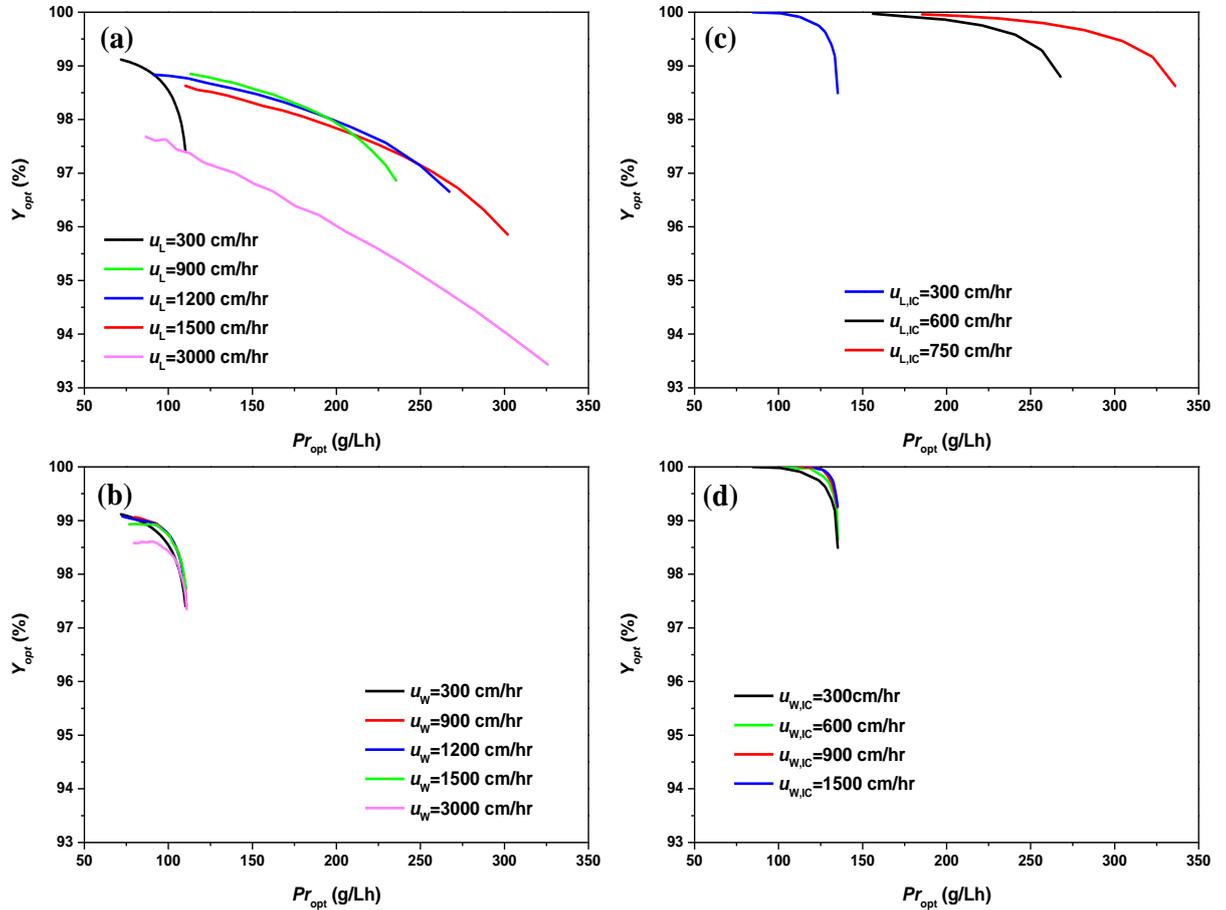
333 Considering the maximum pressure drop equal to 0.15 MPa<sup>[34]</sup>, the maximum linear  
 334 velocity of 3000 cm/hr is obtained for the 5 cm bed height and 50  $\mu\text{m}$  particle radius

335 considered in this work. The values of the remaining operating parameters used in all  
336 simulations considered in the following are listed in Tables 1 to 3.

#### 337 **4.2.1 Batch process**

338 The effect of loading and washing velocities is analyzed first with  $u_L$  changing  
339 from 300 to 3000 cm/hr with fixed  $u_W = 300$  cm/hr, and then with  $u_W$  changing from 1  
340 to 3000 cm/hr with fixed  $u_L = 300$  cm/hr. The Pareto fronts obtained for various  $u_L$   
341 values are shown in Figure 5a. Note that, in general, the Pareto fronts do not necessarily  
342 cover the entire range of possible yield and productivity values, since some portions of  
343 them may not be achievable with the considered operating conditions. In particular, it  
344 is seen that as the loading velocity increases, the process performance first improves,  
345 with the Pareto moving to the right of the plot, thus enabling higher productivity values  
346 for a given recovery value. This is because at higher loading velocity the loading time  
347 is shortened to the benefit of productivity. However, when further increasing the loading  
348 velocity, intraparticle mass transfer becomes more and more limiting [35,36], leading  
349 eventually to the earlier breakthrough of the impurities and then to lower purity values.  
350 This explains the worsening of the Pareto front at 3000 cm/hr with respect to lower  
351 loading velocities in Figure 5a. The effect of the washing velocity is showed in Figure  
352 5b. It is seen that as the washing velocity increases from 300 to 900 cm/hr, the Pareto  
353 front extends to higher productivities, but it decreases again for further increasing  $u_W$   
354 values. For the maximum allowable washing linear velocity of 3000 cm/hr, the process  
355 performance is in fact inferior to all the other washing velocities in almost the entire  
356 range of operating conditions. Limiting intraparticle mass transfer prevails at such

357 washing linear velocity, so that more target protein remains in the column, and both  
 358 yield and productivity decrease.



359  
 360 *Figure 5. Tradeoff (Pareto front) between yield and productivity of (a) batch process*  
 361 *under various loading velocities with  $u_w = 300$  cm/hr (b) batch process under various*  
 362 *washing velocities with  $u_L = 300$  cm/hr (c) Flow2 process under various interconnected*  
 363 *loading velocities with  $u_{w,IC} = 300$  cm/hr (d) Flow2 process under various*  
 364 *interconnected washing velocities with  $u_{L,IC} = 300$  cm/hr*

365 Thus summarizing, since the Pareto fronts in both Figures 5a and 5b tend to cross  
 366 each other, the best velocity values have to be defined depending on the specific  
 367 operating conditions. In particular, the idea of using the maximum possible velocity in

368 either loading or washing, corresponding in this case to 3000 cm/hr, is not  
369 recommended.

#### 370 **4.2.2 Continuous Flow2 process**

371 The analysis of the role of liquid velocities in this case is more complex than for  
372 batch processes because we now deal with four velocities: the interconnected loading  
373 velocity,  $u_{L,IC}$ , the interconnected washing velocity,  $u_{W,IC}$ , the inline dilution velocity,  
374  $u_{ILD}$  and the batch loading velocity,  $u_{L,B}$ . It appears reasonable to take equal the batch  
375 and interconnected loading velocities, i.e.  $u_{L,IC} = u_{L,B}$ , so as to apply in both the same  
376 residence time. In addition, the inline dilution velocity is taken equal to the  
377 interconnected washing velocity, i.e.  $u_{W,IC} = u_{ILD}$  as the resulting buffer composition for  
378 the downstream column remains constant independent of the linear velocity applied,  
379 thereby reducing the number of varied operating variables. Accordingly, in the  
380 following we analyze the effect of two velocities:  $u_{L,IC}$  and  $u_{W,IC}$ . These will be changed  
381 independently, one at a time, in the range 300 cm/hr to 1500 cm/hr. The latter  
382 corresponds to the largest velocity compatible with the considered maximum pressure  
383 drop of 0.15 MPa, and it is half of the one considered in the case of the batch process  
384 because two columns are operated in series in the interconnected step. The simulation  
385 results are shown in Figure 5c and 5d.

386 In Figure 5c it is seen that larger values of the loading velocity,  $u_{L,IC}$  improve  
387 significantly the tradeoff between yield and productivity of the Flow2 process. However,  
388 no Pareto Front could be calculated for loading velocities larger than 750 cm/hr, since  
389 it was not possible to achieve the requested purity of 99%. For such values of  $u_{L,IC}$  (and

390 of  $u_{L,B}$ ), together with the fact that the batch loading time must be fixed to match the R-  
391 R time, too many aggregates breakthrough into the product pool. Nevertheless, it is  
392 found that, although the loading velocity is constrained by time scheduling, the Flow2  
393 process can offer better performances than the batch operation. In particular, it can  
394 approach productivities larger than 300 g/L/h while keeping the yield in the order of  
395 99%, which for the batch process (Figure 5a) can only be achieved by decreasing the  
396 productivity by at least three times in the order of 100 g/L/h.

397 Also in the case of the washing step, the process performance improves for  
398 increasing linear velocity values,  $u_{W,IC}$  as shown in Figure 5d. This is because in the  
399 Flow2 process, the inline dilution allows all proteins washed out from the first column  
400 to be captured by the second column, regardless of the more or less harsh washing  
401 conditions in the first column. Better performance can be achieved compared to the  
402 batch process in terms of both yield and productivity.

403 Thus concluding, for the Flow2 process we can recommend the higher loading and  
404 washing velocities compatible with the pressure drop constraint, provided that the  $P_{spec}$   
405 is obtained (750 cm/hr and 1500 cm/hr, respectively in this work). This is the main  
406 reason for the continuous process to exhibit better productivities than the corresponding  
407 batch operation, thus over compensating for the increased column volume utilized.

### 408 **4.3 Role of buffer composition in loading and washing**

409 In this section, the effect of the ionic strength of the loading and washing buffers  
410 is investigated. Also in this case, we analyze the effect of each one separately, by  
411 keeping the other fixed. In particular, we consider the ionic strengths of the loading

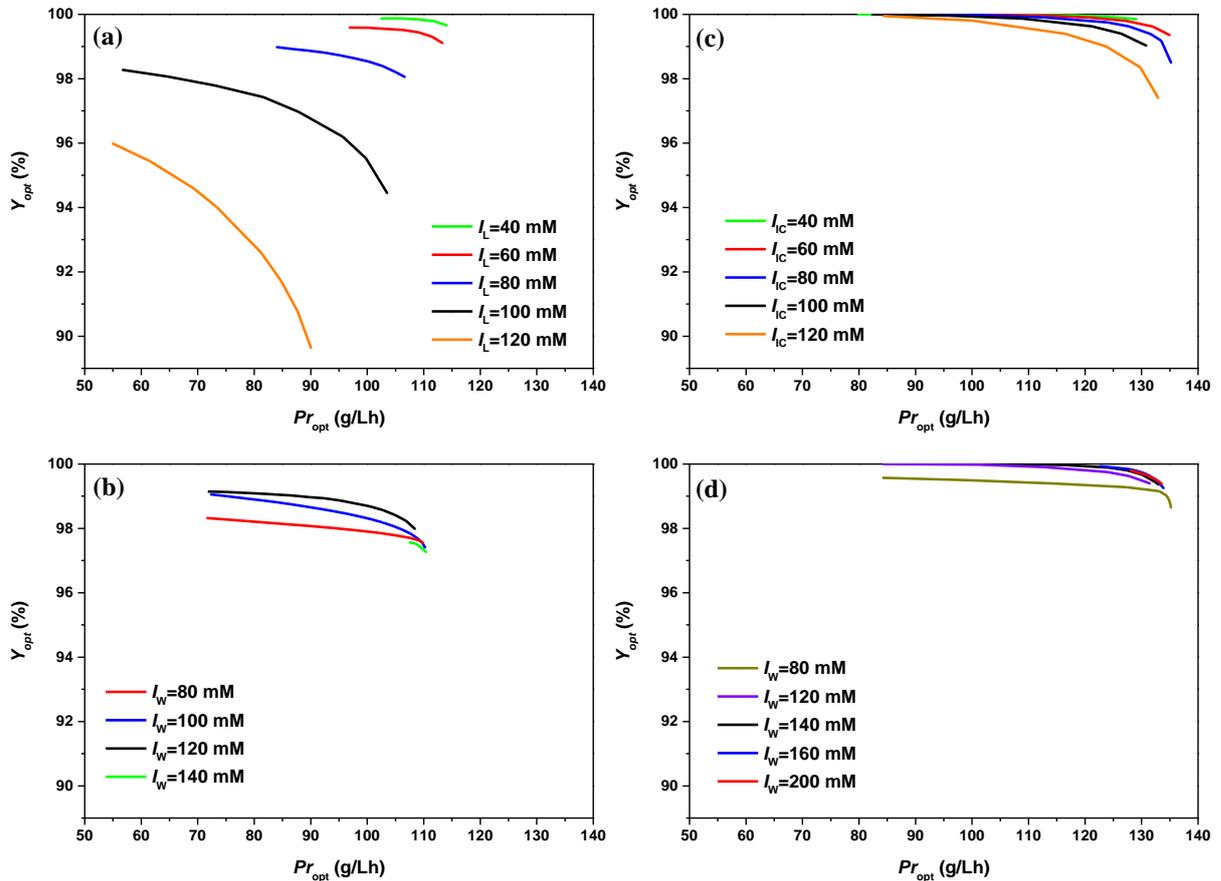
412 buffer,  $I_L$  ranging from 40 mM to 120 mM, and for the washing buffer higher values,  
413 with  $I_W$  ranging from 80 mM to 200 mM. The values of the remaining operating  
414 parameters are summarized in Tables 1 to 3, and in particular the ionic strength for  
415 inline dilution buffer is kept constant at  $I_{ILD} = 10$  mM.

#### 416 **4.3.1 Batch process**

417 The Pareto fronts computed for various values of the ionic strength of the loading  
418 buffer,  $I_L$  and at fixed ionic strength of the washing buffer,  $I_W$  equal to 120 mM, are  
419 shown in Figure 6a. It is seen that the process performance improves as  $I_L$  decreases.  
420 Lower ionic strength values, in fact, facilitate the displacement of the monomer by the  
421 aggregates by enlarging the difference of adsorptivity between aggregates and monomer.  
422 Using equations 6, 7 and 8, it can be seen that the ratio of the Henry coefficients of  
423 aggregates and monomer ( $H_{agg}/H_{mono}$ ) increases from about 40 to 600, as  $I_L$  decreases  
424 from 120 to 40 mM. Therefore, lower ionic strengths of the loading buffer can increase  
425 the monomer content and decrease the aggregate content in the product pool of the  
426 loading step. This comes of course in addition to the fact that using lower  $I_L$  typically  
427 implies also higher feed dilution and therefore lower protein concentration in the feed.

428 With respect to the washing conditions, a non-monotonous behavior is observed  
429 in Figure 6b: the process performance initially improves with increasing the wash  
430 buffer ionic strength, but then deteriorates at higher values. In particular, at  $I_W = 140$   
431 mM the Pareto becomes minute, indicating that the specified purity value can be  
432 achieved only for a restricted range of yield and productivity values. The reason is that  
433 in the batch process, the washing buffer has to be carefully tuned in order to elute the

434 remaining monomer inside the column without eluting also the aggregates. Too low  $I_w$   
 435 lead to too much monomer left in the column, thus decreasing yield and productivity,  
 436 while too high  $I_w$  increase the aggregate leakage, thus leading to lower product purities.



437  
 438 *Figure 6. Tradeoff (Pareto Front) between yield and productivity of (a) Batch process*  
 439 *for various ionic strengths of the interconnected loading buffer,  $I_L$ , with  $I_w = 120$  mM.*  
 440 *(b) Batch process for various ionic strengths of the interconnected washing buffer,  $I_w$ ,*  
 441 *with  $I_L = 80$  mM. (c) Flow2 process for various ionic strengths of the interconnected*  
 442 *loading buffer,  $I_{IC}$ , with  $I_w = 120$  mM. (d) Flow2 process for various ionic strengths*  
 443 *of the interconnected washing buffer,  $I_w$ , with  $I_{IC} = 80$  mM.*

444 The conclusion of this analysis is that, for batch processes, while for the loading

445 buffer lower ionic strength values (40 mM in this work) are recommended, for the  
446 washing buffer a detailed analysis is needed to identify the proper ionic strength (120  
447 mM in this work). The latter constitutes a delicate design problem, which obviously  
448 reflects at the manufacturing level in a control problem, which may have a strong  
449 influence on the performance of the entire process. This aspect will be discussed later  
450 in terms of process robustness.

### 451 **4.3.2 Continuous Flow2 process**

452 In the case of the Flow2 process we have four buffers involved and therefore four  
453 variables to be designed and optimized: the interconnected loading buffer ionic strength,  
454  $I_{L,IC}$ , the batch loading buffer ionic strength,  $I_{L,B}$ , the interconnected washing buffer  
455 ionic strength,  $I_{W,IC}$ , and the inline dilution washing buffer ionic strength,  $I_{ILD}$ . In the  
456 following,  $I_B$  is set to be equal to  $I_{IC}$ , since, for practical reasons, it is convenient to use  
457 in both steps the same feedstock, coming from the protein A eluate and corrected to this  
458 ionic strength value. In addition, the  $I_{ILD}$  is set to be fixed at 10 mM, so that the Pareto  
459 optimization can be limited only to the interconnected loading buffer ionic strength,  
460  $I_{L,IC}$  and the interconnected washing buffer ionic strength,  $I_{W,IC}$ . Similarly as for the  
461 batch process, we investigate the process performance first for  $I_{IC}$  ranging from 40 to  
462 120 mM at fixed  $I_W = 120$  mM, and then for  $I_W$  changing from 80 to 200 mM at fixed  
463  $I_{IC} = 80$  mM. The obtained results are shown in Figures 6c and 6d, respectively.

464 In Figure 6c it can be seen that, similarly to the batch process, also for the Flow2  
465 process the performance improves, that is the Pareto Front moves to the upper right  
466 corner of the plot, as  $I_{IC}$  decreases, although to a smaller extent. On the other hand, for

467  $I_w$ , the data in Figure 6d show that the process performance first improves as the  
468 washing buffer ionic strength increases, but then reaches a kind of plateau for  $I_w$  values  
469 in the order of 140 to 200 mM where the process performance remains substantially  
470 unchanged. Besides providing in general better performances than the batch process, it  
471 is remarkable that this behavior of the Flow2 process is qualitatively different from that  
472 of the batch process, which indicates a superior robustness to changes in the washing  
473 buffer. In Figure 6b it can be seen, in fact, that the batch process for the largest values  
474 of  $I_w$ , from around 100 to 140 mM, undergoes tremendous changes in its performance.  
475 This indicates that the Flow2 process can tolerate larger changes in the washing buffer  
476 ionic strength without compromising the process performance, which instead drops  
477 substantially for the batch process. This higher robustness of the Flow2 process clearly  
478 originates from the higher process flexibility, and in particular by the inline dilution,  
479 which allows for the re-adsorption in the downstream column of the impurities  
480 desorbed in the upstream column, therefore preventing product pool contamination  
481 even at strong washing conditions.

482 To conclude, for the Flow2 process, lower ionic strength for the loading buffer,  
483  $I_c$  (40 mM in this work) and higher ionic strength for the washing buffer,  $I_w$  (higher  
484 than 160 mM in this work) are generally recommended to obtain best process  
485 performance in terms of both yield and productivity.

486

## 487 **5 Process Robustness and Sensitivity Analysis**

488 Robustness is an important factor when evaluating the performance of a process.

489 This is relevant at the process development stage, since higher robustness makes it  
490 easier to identify operating conditions leading to optimal process performance, but it  
491 matters also at the manufacturing scale, by facilitating the design of the controller  
492 needed to reject possible disturbances and keep the process within specifications.

493 In this section, we address this issue through the process sensitivity analysis<sup>[37]</sup>.  
494 In particular, we define the normalized sensitivity,  $S(\psi;\varphi)$  of the generic output process  
495 parameter,  $\psi$  to small changes of the generic input process parameter,  $\varphi$  as follows:

$$496 \quad S(\psi;\varphi) = \frac{\partial\psi}{\partial\varphi} \left( \frac{\varphi}{\psi} \right) \quad (13)$$

497 The partial derivative quantifies the local change of  $\psi$  with respect to a small change  
498 of  $\varphi$ , *while keeping all remaining parameters constant*, and it is therefore appropriate  
499 to estimate the sensitivity of the output,  $\psi$  with respect to the input,  $\varphi$ . The ratio  $\varphi/\psi$   
500 is introduced to make the sensitivity dimensionless, that is independent of the units used  
501 in the evaluation of the input and output process parameters. However, it should be  
502 noted that the normalized sensitivity values alone do not represent the output variability  
503 due to a given input parameter, since this is also affected directly by the intrinsic  
504 variability of the input parameter.

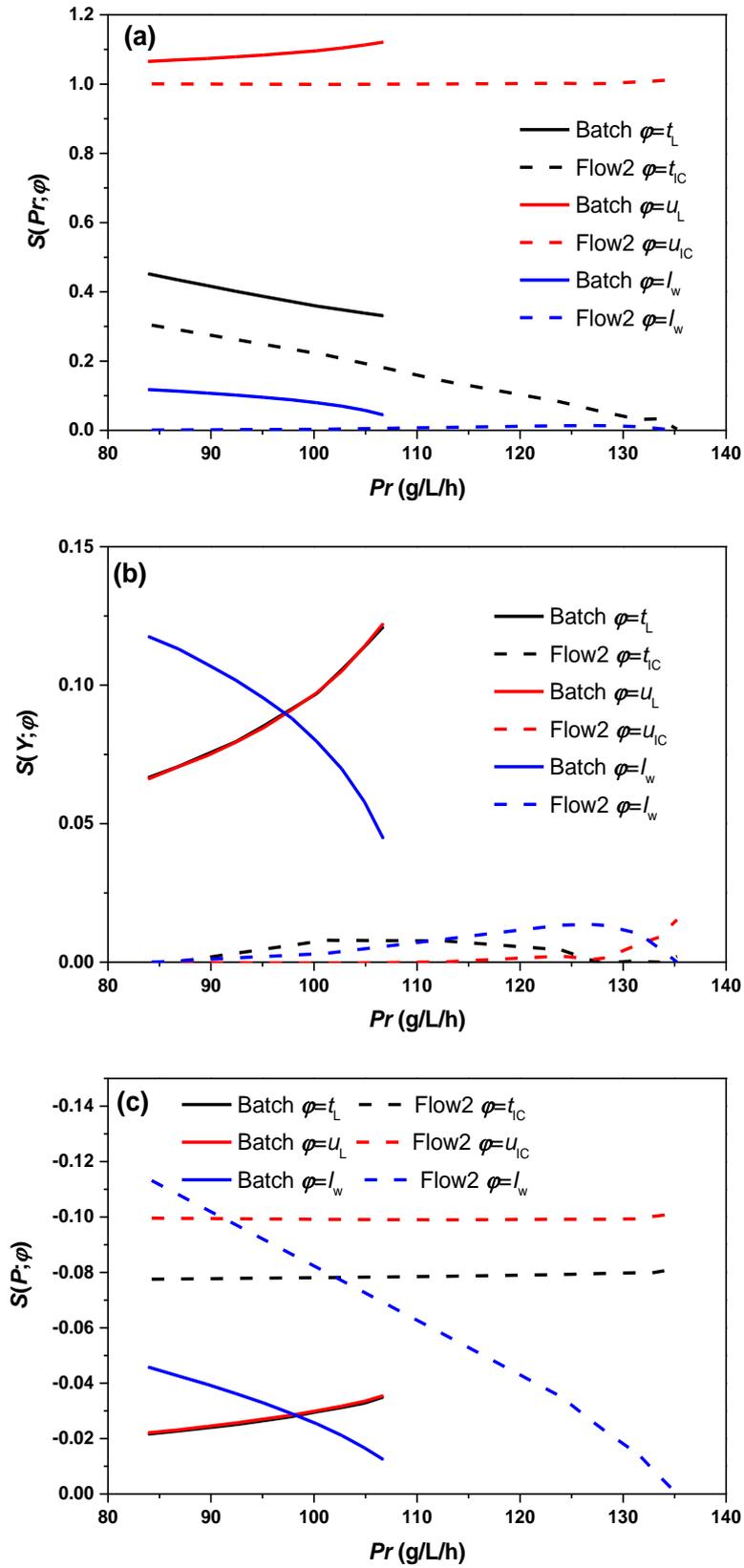
505 In the following, the sensitivity value is approximated through the incremental ratio  
506  $((\psi(\varphi + \Delta\varphi) - \psi(\varphi))/\Delta\varphi)$ , where the numerator represents the change in the  
507 output parameter corresponding to an imposed change of the input parameter, equal to  
508 +1% of the reference conditions considered in the sensitivity analysis. In particular, we  
509 consider, as output process parameters, the three parameters determining the process  
510 performance: productivity, yield and purity, that is  $\psi = Pr, Y$  and  $P$ , respectively. As

511 process input parameters we consider the loading time, the loading velocity and the  
512 washing buffer ionic strength, that is  $\varphi = t_L, u_L$  and  $I_w$ , respectively.

513 As reference conditions for the sensitivity analysis we select the optimised  
514 operating conditions along the Pareto fronts with  $P_{\text{spec}} = 99\%$  shown in Figure 3 for the  
515 batch and Flow2 process, respectively. Accordingly, for the various operating  
516 conditions along the Pareto Front, we compute, for each given change in the input  
517 parameter, the corresponding changes in the three performance parameters above, and  
518 from these the corresponding sensitivity values through equation (13). The obtained  
519 results, shown in Figure 7a to 7c, indicate that productivity and yield exhibit a *positive*  
520 sensitivity value, while the the purity sensitivity is *negative*. This is consistent with the  
521 fact that each of the considered operating conditions belong to the Pareto front at a fixed  
522 purity value equal to 99%. The perturbed operating parameters, in fact, although leading  
523 to improvements in productivity and yield (positive sensitivity value), lead to a lower,  
524 not acceptable, purity value (negative sensitivity value) and therefore cannot be part of  
525 the Paretoe Front. In the same Figure 7 it is also seen that the Flow 2 process, which  
526 can achieve larger productivity values because of its higher efficiency, also exhibits a  
527 generally better sensitivity behavior. More specifically, the very high sensitivity of the  
528 yield with respect to the washing buffer ionic strength,  $I_w$  exhibited by the batch process  
529 is largely removed in the Flow2 process.

530 In particular, Figure 7a shows that productivity is the most sensitive of all  
531 considered output parameters, and the corresponding sensitivity values are substantially  
532 equivalent for the two processes. Significantly lower sensitivity of the Flow2 process

533 is observed only for the washing buffer ionic strength,  $I_w$  and for the larger productivity  
534 values. The strong reduction of the yield sensitivity with respect to  $I_w$ , mentioned above,  
535 is illustrated in Figure 7b: The sensitivity values for the Flow2 process are less than  
536 0.015, compared to values about ten times larger, in the order of 0.1, for the batch  
537 process. This is a consequence of the stabilizing effect of the inline dilution process  
538 discussed above in the context of Figures 6b and 6d. It is worth noting that, in Figure  
539 7b, the yield sensitivities with respect to  $t_L$  and  $u_L$  for the batch process are almost  
540 coincident. This is because these two parameters have the same effect on the loading  
541 amount, which is in fact defined by their product,  $(t_L * u_L)$ , which in turns leads to the  
542 same change in the yield value. The same observation applies to the purity sensitivities,  
543 as it can be seen in Figure 7c. On the other hand, in Figure 7c, the batch process shows  
544 lower purity sensitivities than the Flow2 process, with respect to any of the input  
545 process parameters considered. However, the sensitivities with respect to the loading  
546 time and velocity are less critical in the context of process control (switching times and  
547 flow rates are typically well controlled), and the observed differences are lower than in  
548 the case above. On the other hand, the most critical sensitivity, with respect to  $I_w$ , can  
549 be substantially decreased when operating at high productivity values.



550

551 *Figure 7. Normalized sensitivity of productivity (a), yield (b) and purity (b) with respect*

552 *to  $t_L$ ,  $u_L$  and  $I_W$  for the batch process and to  $t_{IC}$ ,  $u_{IC}$  and  $I_W$  for the Flow2 process, along*  
553 *the corresponding Pareto fronts shown in Figure 3.*

554

## 555 **6 Conclusion**

556 Frontal chromatography has been analyzed with respect to two alternative  
557 implementations: a single column, batch process and a two-column, continuous process,  
558 referred to as Flow2. In particular, its application in the polishing step of the processes  
559 for mAb manufacturing, where the immunogenic high molecular weight species are  
560 removed from the target protein, is investigated with reference to a case of industrial  
561 relevance. An ad-hoc procedure for process optimization has been developed and  
562 validated through a general multiobjective optimization procedure, in terms of the  
563 Pareto Front of yield and productivity at a given purity, for both processes. The derived  
564 procedure allowed a thorough comparison of the two processes at their corresponding  
565 optimal operating conditions and not only in terms of the performance parameters, such  
566 as yield, purity and productivity, but also with respect to process robustness through a  
567 proper local sensitivity analysis.

568 The obtained results indicate that, although column interconnection puts  
569 constraints on the linear velocities of the Flow2 process, this in general achieves better  
570 performance in terms of both yield and productivity at a given purity, compared to the  
571 batch process. An important component of this improvement is the higher flexibility  
572 provided by the inline dilution process, which allows the Flow2 to better tolerate higher,  
573 and therefore more advantageous, ionic strength values in the washing step. The

574 comparison of the normalized sensitivities computed for the two processes shows that  
575 the Flow2 process exhibits much smaller yield sensitivities than the batch one. Even  
576 more importantly, it is shown that for the Flow2 process, optimal operating conditions  
577 can be found, where the process performance is not very sensitive to the washing  
578 conditions and in particular to the buffer ionic strength. This is a very important result,  
579 since this high sensitivity represents one of the largest drawbacks of the frontal  
580 chromatography batch process, which is the reason for its lack of robustness and reflects  
581 in difficulties in determining washing conditions that can guarantee reliable operation  
582 particularly at the large scale.

583 The discussed robustness analysis is based on the study of the *local* sensitivity  
584 values defined by equation (13). These local values are relevant, for example, for  
585 determining the characteristics of the algorithm used to control a specific input variable,  
586 e.g. determine the largest deviations that can be allowed to the input variable. It is  
587 interesting to note that the above reached conclusion is in good agreement with the  
588 analysis reported by Vogg et al. <sup>[18]</sup> based on a *global* definition of robustness. In  
589 particular, they compared the robustness of the two processes by considering the  
590 amplitude of the range of operating conditions, which allow respecting specific  
591 requirements in terms of process performance parameters. While their results indicate  
592 that the Flow2 process is characterized by larger robust design spaces than the batch  
593 process, our results augment this behavior by showing decreased local sensitivity of the  
594 Flow2 process towards process parameter variations at given sets of process parameters.

595

596 **Notations**

597	$d_p$	Particle diameter (m)
598	$d_{ax,i}$	Axial dispersion coefficient of i component (m <sup>2</sup> /s)
599	$H_i$	Henry coefficient (atm*m <sup>2</sup> /mg)
600	$I_B$	Ionic strength of Batch loading buffer of Flow2 process (mM)
601	$I_C$	Ionic strength of Batch and Flow2 interconnected loading
602	buffer (mM)	
603	$I_L$	Ionic strength of Batch and Flow2 loading buffer (mM)
604	$I_W$	Ionic strength of Batch and Flow2 washing buffer (mM)
605	$I_{ILD}$	Ionic strength of Flow2 inline dilution buffer (mM)
606	$k_{m,i}$	Mass transfer coefficient of i component (m <sup>2</sup> /s)
607	$L_{col}$	Column length (m)
608	$Pr$	Process Productivity (g/Lh)
609	$P_i$	Purity for i component
610	$P_{spec}$	Specification value for purity
611	$u_L$	Batch loading linear velocity (mL/min)
612	$u_w$	Batch washing linear velocity (mL/min)
613	$u_{L,IC}$	Flow2 interconnected loading linear velocity (cm/hr)
614	$u_{W,IC}$	Flow2 interconnected washing linear velocity (cm/hr)
615	$u_{ILD}$	Flow2 inline dilution linear velocity (cm/hr)
616	$u_{L,B}$	Flow2 disconnected loading linear velocity (cm/hr)
617	$q_i$	Concentration of i component in solid phase (mg/mL)

618	$q_i^{eq}$	Equilibrium concentration of i component in solid phase
619	(mg/mL)	
620	$q_i^{sat}$	Saturation binding capacity of i component in solid phase
621	(mg/mL)	
622	$t_L$	Batch loading time (min)
623	$t_w$	Batch washing time (min)
624	$t_{RR}$	R-R time for batch and Flow2 process (min)
625	$t_{L,IC}$	Flow2 interconnected loading time (min)
626	$u_{sf}$	Superficial velocity (m/s)
627	$Y_i$	Yield for i component
628	$\varepsilon_{t,i}$	Total accessible porosity of I component
629	$\mu$	Mobile phase dynamic viscosity (1.0 mPas)

630

## 631 **References:**

- 632 [1] H. L. Levine, J. E. Lilja, R. Stock, H. Hummel, S. D. Jones, *BioProcess Int* **2012**, *10*, 20.
- 633 [2] D. M. Ecker, S. D. Jones, H. L. Levine, *MAbs*, **2015**, *9*.
- 634 [3] S. Singh, N. K. Tank, P. Dwiwedi, J. Charan, R. Kaur, P. Sidhu, V. K. Chugh, *Current clinical*
- 635 *pharmacology* **2018**, *13*, 85.
- 636 [4] H. Kaplon, J. M. Reichert, *MAbs*, Taylor & Francis **2019**, 219.
- 637 [5] A. L. Grilo, A. Mantalaris, *Trends Biotechnol.* **2019**, *37*, 9.
- 638 [6] S. S. Farid, J. Washbrook, N. J. Titchener Hooker, *Biotechnol. Progr.* **2005**, *21*, 486.
- 639 [7] C. A. Challener, *Biopharm Int.* **2014**, *27*, 20.
- 640 [8] S. Vogg, T. Muller-Spath, M. Morbidelli, *Current opinion in chemical engineering* **2018**, *22*, 138
- 641 [9] F. Feidl, S. Vogg, M. Wolf, M. Podobnik, C. Ruggeri, N. Ulmer, R. Wälchli, J. Souquet, H. Broly,
- 642 A. Butté, *Biotechnol. Bioeng.* 2020, *117*, 1367.
- 643 [10] D. J. Karst, F. Steinebach, M. Morbidelli, *Curr. Opin. Biotech.* 2018, *53*, 76.
- 644 [11] FDA, Modernizing the way drugs are made: a transition to continuous manufacturing , **2017**.
- 645 [12] FDA, Quality considerations for continuous manufacturing-guidance for industry **2017**.
- 646 [13] G. Carta, A. Jungbauer, *Protein chromatography: process development and scale-up*, John Wiley
- 647 & Sons, **2020**.
- 648 [14] T. Ichihara, T. Ito, Y. Kurisu, K. Galipeau, C. Gillespie, *MAbs*, Taylor & Francis **2018**, 325.

- 649 [15] H. F. Liu, B. McCooey, T. Duarte, D. E. Myers, T. Hudson, A. Amanullah, R. van Reis, B. D. Kelley,  
650 *J. Chromatogr. A* **2011**, 1218, 6943.
- 651 [16] D. Pfister, L. Nicoud, M. Morbidelli, *Continuous Biopharmaceutical Processes: Chromatography,*  
652 *Bioconjugation, and Protein Stability*, Cambridge University Press **2018**.
- 653 [17] M. T. Stone, K. A. Cotoni, J. L. Stoner, *J. Chromatogr. A* **2019**, 1599, 152.
- 654 [18] S. Vogg, T. Müller-Späth, M. Morbidelli, *J. Chromatogr. A* **2020**, 460943.
- 655 [19] N. J. Titchener Hooker, P. Dunnill, M. Hoare, *Biotechnol. Bioeng.* **2008**, 100, 473.
- 656 [20] S. L. C. Ferreira, R. E. Bruns, E. G. P. Da Silva, W. N. L. Dos Santos, C. M. Quintella, J. M. David,  
657 J. B. de Andrade, M. C. Breikreitz, I. C. S. F. Jardim, B. B. Neto, *J. Chromatogr. A* **2007**, 1158, 2.
- 658 [21] C. Shi, Z. Gao, Q. Zhang, S. Yao, N. K. Slater, D. Lin, *J. Chromatogr. A* **2020**, 460936.
- 659 [22] N. Andersson, H. Knutson, M. Max-Hansen, N. Borg, B. Nilsson, *Ind. Eng. Chem. Res.* **2014**, 53,  
660 16485.
- 661 [23] T. Müller-Späth, G. Ströhlein, L. Aumann, H. Kornmann, P. Valax, L. Delegrange, E. Charbaut, G.  
662 Baer, A. Lamproye, M. Jöhnck, *J. Chromatogr. A* **2011**, 1218, 5195.
- 663 [24] D. Baur, M. Angarita, T. Müller Späth, M. Morbidelli, *Biotechnol J.* **2016**, 11, 135.
- 664 [25] S. M. Pirrung, M. Ottens, *Preparative Chromatography for Separation of Proteins* **2017**, 269.
- 665 [26] T. Müller Späth, M. Krättli, L. Aumann, G. Ströhlein, M. Morbidelli, *Biotechnol. Bioeng.* **2010**, 107,  
666 652.
- 667 [27] J. Siitonen, M. Mänttari, A. Seidel-Morgenstern, T. Sainio, *J. Chromatogr. A* **2015**, 1391, 31.
- 668 [28] G. Guiochon, A. Felinger, D. G. Shirazi, *Fundamentals of preparative and nonlinear*  
669 *chromatography*, Elsevier, **2006**.
- 670 [29] G. Carta, A. Jungbauer, Wiley-VCH Verlag GmbH, **2010**.
- 671 [30] B. Guélat, R. Khalaf, M. Lattuada, M. Costioli, M. Morbidelli, *J. Chromatogr. A* **2016**, 1447, 82.
- 672 [31] G. Zames, N. M. Ajlouni, N. M. Ajlouni, N. M. Ajlouni, J. H. Holland, W. D. Hills, D. E. Goldberg,  
673 *Information Technology Journal* **1981**, 3, 301.
- 674 [32] <https://it.mathworks.com/help/gads/gamultiobj.html>, **2020**
- 675 [33] J. P. Abulencia, L. Theodore, *Fluid flow for the practicing chemical engineer*, Wiley Online Library,  
676 **2009**.
- 677 [34] [https://www.merckmillipore.com/Web-CH-site/de\\_DE/-/CHF/ShowDocument-](https://www.merckmillipore.com/Web-CH-site/de_DE/-/CHF/ShowDocument-Pronet?id=201806.078)  
678 [Pronet?id=201806.078](https://www.merckmillipore.com/Web-CH-site/de_DE/-/CHF/ShowDocument-Pronet?id=201806.078), **2018**
- 679 [35] D. Farnan, D. D. Frey, C. Horváth, *Biotechnol. Progr.* **1997**, 13, 429.
- 680 [36] G. Gotmar, T. Fornstedt, G. Guiochon, *J. Chromatogr. A* **1999**, 831, 17.
- 681 [37] A. Varma, M. Morbidelli, *Parametric sensitivity in chemical systems*, Cambridge University Press,  
682 **2005**.
- 683 [38] D. J. Downing, R. H. Gardner, F. O. Hoffman, *Technometrics* **1985**, 27, 151.
- 684 [39] T. J. Krieger, C. Durston, D. C. Albright, *Transactions of the American Nuclear Society* **1978**, 28.