



Opportunities and challenges for model utilization in the biopharmaceutical industry: current versus future state

Deenesh K Babi¹, Jan Griesbach², Stephen Hunt³,
Francis Insaiddo⁴, David Roush⁴, Robert Todd⁵,
Arne Staby¹, John Welsh⁴ and Felix Wittkopp⁶

Processes and manufacturing in the biopharmaceutical industry are mainly based on experimental data and statistical approaches, however, regulatory expectations of increasing understanding and insights into methods behind medicinal products have paved the way for employment of more mechanistic and first principle modeling tools and concepts. Current, advanced modeling tools can basically be divided into four groups: biophysical modeling, mechanistic modeling, computational fluid dynamics, and plant modeling. Although very useful in themselves, the first three modeling concepts may also be used to establish better plant models, where digital twins of manufacturing plants are pursued broadly in the industry. This review presents the current development stage, opportunities, and challenges of the four modeling tools, and activities needed to reach future state of modeling or ‘*in silico* CMC’ (Chemistry, Manufacturing and Controls), a state where modeling, based either on first principles or hybrid approaches combining both empirical and mechanistic approaches, can be routinely employed in lieu of solely empirical or experimental approaches. It builds largely on presentations and discussions at the recent 4th Mini Modeling Workshop from May 25, 2021.

Addresses

¹ Novo Nordisk A/S, CMC Development and API Manufacturing Development, Novo Alle 1, 2880 Bagsværd, Denmark

² F. Hoffmann-La Roche Ltd., Grenzacherstrasse 124, 4070 Basel, Switzerland

³ Allogene Therapeutics, Inc., 210 E. Grand Avenue, South San Francisco, CA 94080, USA

⁴ Merck & Co., Inc., 2000 Galloping Hill Rd, Kenilworth, NJ 07033, USA

⁵ KBI Biopharma, 2500 Central Ave, Boulder, CO 80301, USA

⁶ Pharma Research and Early Development (pRED), Roche Innovation Center Munich, Roche Diagnostics GmbH, Nonnenwald 2, 82377 Penzberg, Germany

Corresponding author: Staby, Arne (ast@novonordisk.com)

Current Opinion in Chemical Engineering 2022, 36:100813

This review comes from a themed issue on **Separations engineering (2021): downstream bioprocessing**

Edited by **Scott Husson** and **Abraham M Lenhoff**

For complete overview of the section, please refer to the article collection, “[Separations engineering \(2021\): downstream bioprocessing](#)”

Available online 15th March 2022

<https://doi.org/10.1016/j.coche.2022.100813>

2211-3398/© 2022 Elsevier Ltd. All rights reserved.

Introduction

Modeling tools are increasingly employed in the biopharmaceutical industry to improve and control manufacturing processes with increasing application of chemical engineering approaches [1[•],2[•]]. The models and tools have been developed in academia over the last 100 years [3] and leverage significant advancements in other disciplines including computational chemistry [4] the utility of which is fully recognized (e.g. Nobel Prize for Computational Chemistry in 2013) with the application to complex biomolecular systems and biophysical interactions. Despite the specific investments by academic researchers who laid the first principles foundations for these efforts [5–8], the maturity of these tools have not until recently matched industry expectations/requirements for implementation. However, with the introduction of high-throughput screening (HTS) techniques, increased computational power, and sufficient understanding of the benefits provided by these modeling approaches, implementation has increased in the last decade. Part of the challenge in application of these tools was the perception that the systems were merely too complex. This paper shows, it should be feasible, although challenging, to derive and apply appropriate models for bioprocessing systems. We also list the gaps remaining to apply models to these systems. The adoption of modeling approaches; translated and referred to as digital twins; has increased due to industry 4.0. Emerging from this adoption is not a ‘one size fits all’ definition of a digital twin but rather a landscape view, product, process, production, and performance (Siemens Digital

Table 1

4th Mini Modeling Workshop**Biophysics session**

Chairs: Francis Insaioo, MSD; John Welsh, MSD
Sean Burgess, Genentech

David Saleh, BI

Using quantitative structure property relationships to predict monoclonal antibody binding properties

Modeling the impact of amino acid substitution in a monoclonal antibody on cation exchange chromatography

Armenio Barbosa, University NUOVA Lisbon

Molecular details of *de Novo* designed affinity-adsorbents

Biophysics breakout session

Moderators

John Welsh, MSD; Steve Cramer, RPI

Panelist

Lijuan Li, Takeda

Mechanistic modeling — downstream session

Chairs: Shuchi Yamamoto, Yamaguchi University; Felix Wittkopp, Roche

Giorgio Carta, University of Virginia

Modeling the chromatographic behavior of conformationally flexible

Multidomain proteins

Christian Frech, University of Applied Sciences
Mannheim

Modeling and simulation of antibody elution behavior under high load conditions in cation exchange chromatography by using a modified SMA isotherm

Yinying Tao, Eli Lilly & Company

Predictive modeling for TFF process development in high concentration self-buffering formulations

Mechanistic modeling — upstream session

Chairs: Arne Staby, Novo Nordisk; Jan Griesbach, Roche

Shantanu Banerjee, IIT Delhi

Mechanistic modeling of continuous clarification of Chinese Hamster Ovary (CHO) cells

Using Acoustic Wave Separation Technology

Katrin Paul, Novartis

FBA-Based Process Optimization by Decreasing Ammonia Accumulation

Thomas Wucherpfennig, BI

Computational models for bioreactors and cultivation processes in biologicals

Development: Stirred, not Shaken!

Mechanistic modeling — breakout session

Moderators

Felix Wittkopp, Roche; Jan Griesbach, Roche

Panelists

Isabell Hagemann, Bayer AG

Gang Wang, Boehringer-Ingelheim

Juliane Diedrich, Amgen Research

Emmanouil Papadakis, Novo Nordisk

Plant modeling session

Chairs: Deenesh Kavi Babi, Novo Nordisk; Bob Todd, KBI Biopharma

Christos T. Maravelias, Princeton University

Lijuan Li, Takeda

Batch production scheduling: methods and applications

Driving strategic decisions making for cost reduction and manufacturability through process economic modeling

Johann Kaiser, Novo Nordisk

A multi-scale approach for monoclonal antibody (mAb) process modeling

Plant modeling breakout session

Moderators

Suzanne Farid, University College London

Deenesh Kavi Babi, Novo Nordisk

Arne Staby, Novo Nordisk

Computational fluid dynamics section

Chair: Steven Hunt, Allogene

Ross Kenyon, Regeneron Pharmaceuticals

A combined computational and data-driven approach to accelerate drug

Product mixing parameter development

Abraham Lenhoff, University of Delaware

Scale-down of precipitation: CFD, population balance models and experiment

Ignacio Montes Serrano, Austrian Centre of
Biotechnology

CFD simulations for the hydrodynamic characterization of microtiter plates for the development of a scale-up strategy of downstream processes based on volumetric power input

Computational fluid dynamics breakout session

Chairs

Abraham Lenhoff, University of Delaware; Bob Todd, KBI Biopharma

Panelists

Eric von Lieres, Research Center Jülich

Andrew Zydny, Penn State University

Open challenges session

Chairs: David Roush, MSD; John Welsh, MSD

Maximilian Krippel, University of Natural Resources
and Life Sciences, Vienna

Increasing efficiencies in bioprocess development and manufacturing through digital process development

Johannes Schmölder, Research Center Jülich

Towards integrated process chain simulation in biotechnology

Sofia Nunes, University College London

A novel approach to quantify floc growth and strength for robust primary recovery operations

Open challenges breakout session

Moderators

David Roush, MSD; Giorgio Carta, University of Virginia

Panelists

Bernt Nilsson, Lund University

Todd Przybycien, Rensselaer Polytechnic Institute

Industries Software: Digital Twin. <https://www.plm.automation.siemens.com/global/en/our-story/glossary/digital-twin/24465>). Generically, a digital twin therefore can be defined as a virtual, cyber-physical system (product, process, production and/or performance) to be used for moving from a current to improved-optimized future state by testing ideas via modeling and simulation.

A thorough assessment of the current state of the broad range of modeling activities to support biologics development and production was obtained during Recovery of Biological Products 4th Mini Modeling Workshop (4MMW) held virtually on 25 May 2021. A total of 127 participants representing 58 diverse academic (21) and industrial (37) institutions contributed to the discussions. The workshop focused on key areas of modeling that have direct relevance to challenges faced in the industry and provided a forum for connecting leading academic researchers with industrial researchers and suppliers. The four main topics included Biophysics, Mechanistic Modeling (Upstream and Downstream), Plant Modeling, and Computational Fluid Dynamics provided in separate sections below, as well as a session for Open Challenges (key areas/technical challenges for future development). The workshop program, contributors and chairs are listed in Table 1. The publication from the 3rd Modeling Workshop [1**] was the substrate to initiate the discussions at 4MMW and to be used as a reference point for assessing progress in the modeling space combined with general trends and developments in the field. A summary of the current progress versus the gaps identified at the 3rd Modeling Workshop is presented in Figure 1. Advances in implementation over the last two years have mainly occurred within the biophysics, mechanistic, and plant modeling areas, and cover elements like, for example, candidate selection support, models for communication with health authorities, and commissioning of plant changes, respectively. Workshop participant survey results are provided in Figure 2. In general, survey respondents viewed later stages of development as requiring more significant research to implement although some are sufficiently mature for commercial use (e.g. Computational Fluid Dynamics, Plant Modeling, Downstream Mechanistic Modeling), whereas modeling in early stages is more ready for deployment. One interesting observation was that the most survey participants identified the red bar (gaps limiting deployment) as the main level of maturity.

The proposed and emerging viewpoint of digital twins for manufacturing development is presented in Figure 3a and b. These show how different scales are connected based on competing complexities and how these are selected based on three main properties, purpose, complexity, and maturity, respectively. One key point from the analyses summarized in Figure 3 is that the computational areas that are sufficiently mature for commercial

utilization which begs the question as to what are the impediments to overcome to achieve broad industry adoption? The figure provides an assessment of the current state of investment in the various modeling areas to address the required gaps and support broader implementation.

Model utilization in the biopharmaceutical industry

Biophysics

Biophysical modeling has the potential to utilize the biophysical properties of proteins and ligands to direct biologics design, development, and manufacturing. Currently, there are several tools commercially available that can be used to calculate biophysical properties of molecules, (CCG-MOE [9] and Schrödinger [10]). In the instance where no known homologous structure is available to be used as a template to build the structure of a new protein sequence, new tools are in development to build or predict atomic detailed structure of proteins using ML and AI, for example, AlphaFold from Google [11]. Novel molecular properties and descriptors are constantly in development in industry, academia, and other joint collaborations [12*]. Models exist that correlate these biophysical properties to process conditions [5,13]. However, these models tend to be limited in scope and are typically not broadly applicable. Linking molecular properties and descriptors to process related conditions in a way that is not therapeutic molecule specific and modality agnostic is an area that is currently underdeveloped (Figure 1).

An active area of research is the use of QSAR-based models to build predictive properties of monoclonal antibodies. The general assumption in these studies is to identify molecular properties that correlate to experimentally determined values [5,13]. A significant challenge in this approach is the type of structure properties used and how broadly applicable they are to other molecules that are not part of the training set. One practical way to correlate molecular properties to process outcome is to investigate the impact of amino acid substitution on process performance, for example, chromatographic separations. By perturbing the molecular properties of a given molecule and testing under standardized conditions, a better understanding of process development will emerge. However, if these activities are not coupled with a better understanding of ligand properties and effective ligand design, a comprehensive knowledge will not be attained. If a better understanding of ligand properties and linker chemistries is attained, predictive models can extend between chromatographic modalities.

A general limitation of a robust and broadly applicable biophysical model for biologics process development is the limited data set available for model building. A

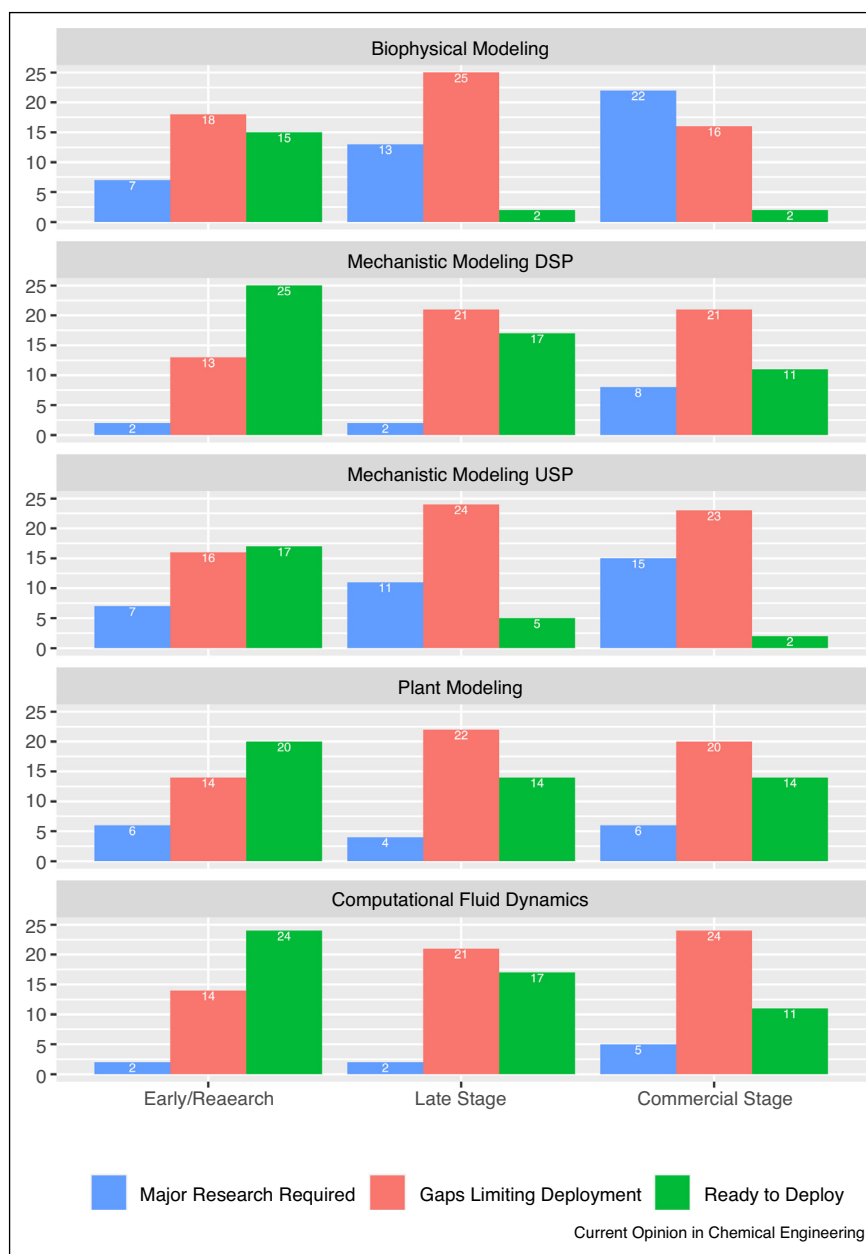
Figure 1

	Biophysics	Mechanistic	CFD/Mixing	Plant Model/Facility
Early Stage Process design qualitative models	<p>Models exist for candidate selection/liability ID and stability (aka <i>in silico</i> developability)</p> <p>Upstream</p> <ul style="list-style-type: none"> Limited ability to predict epitope binding/ molecular design via <i>in silico</i> screen (ability for relative rank ordering) <p>Downstream</p> <ul style="list-style-type: none"> Stability prediction of candidates Potential to screen modalities for purification <p>Gap</p> <ul style="list-style-type: none"> Standard system to predict stability, expression, and purification modality (eg, impact of subtle changes) Some limitations on prediction of specific PTM Large curated high-quality data sets (potentially via consortium) 	<p>Upstream</p> <ul style="list-style-type: none"> Mathematical or hybrid models primarily employed (e.g. scale-up/scale-down) and systems biology <p>Chromatography/Conjugation</p> <ul style="list-style-type: none"> Current state: Simplified/basic models and commercial tools exist to support PD (optimization, robustness, scale-up) Straightforward model calibration workflows are publicly available Surrogates for impurities, eg, HCP (lumped) Understanding limited to specific modalities (IEX) as opposed to mixed mode (RP and Protein A) <p>Gap</p> <ul style="list-style-type: none"> Modeling experiments exceed the number of potential experimental savings, preliminary analytical methods hinder the transferability of models to late stage, primarily applied to but not limited to Mab (applicable to other modalities) Opportunity to use QSAR models to select operating conditions (eg, resin, pH) to evaluate in HTS for entire process (orthogonal selectivity) 	<ul style="list-style-type: none"> Ability to predict power numbers computationally (more accurate than experiment) Facility fit – mapping required mixing conditions and vessels to process requirements (including engineering factors) Quantification of mixing – which model to apply? Confirmation of modeling results (feasible for PH) via multiple point sampling Multiphase modeling exists Limited use of bubble breakage and coalescence models (eg, population balance models) 	<p>Models are dependent on the complexity of the mechanistic models of unit operations since this understanding is translated into states and tasks per unit time</p> <p>Gap</p> <ul style="list-style-type: none"> If mechanistic understanding is limited, the worst case model can only solve a purely planning-scheduling problem. However, this does not limit evaluation because the objective here is to minimize investment risk (= probability x consequence). Here probability is high and consequence is low
Late Stage Characterization validation and quantitative models	<p>Opportunity to use QSAR models to select operating conditions to evaluate in HTS</p> <p>Upstream</p> <ul style="list-style-type: none"> Limited ability to predict epitope binding/molecular design via <i>in silico</i> screen for developability and manufacturability evaluation (ability for relative rank ordering) <p>Downstream</p> <ul style="list-style-type: none"> Utilize biophysics to address PC-related question (eg, parametric understanding) Potential to utilize models to support process parameter classification Potential to predict aggregation/deamidation (limited examples) <p>Gap</p> <ul style="list-style-type: none"> Missing link from biophysics parameters to process and stability (in lieu of experiments) Biophysics to supplement mechanistic model Mapping/characterization of process and product-related impurities on chromatographic performance Incorporating dynamics into predictive tool development – explore multiple scales from atomic to coarse grain at different time scales Expand the scope from antibodies/proteins to include other modalities, eg, DNA, RNA, viral vector, etc 	<p>Upstream</p> <ul style="list-style-type: none"> TBD <p>Chromatography</p> <ul style="list-style-type: none"> Current state: Sophisticated models for single process steps (IEX) exist to support PD and communication with health authorities Surrogates for impurities, eg, HCP, charge variants (lumped) Mixed Mode isotherms are available but rarely applied Initial models for scale-down/HTS <p>Gap</p> <ul style="list-style-type: none"> Mechanistic understanding of all modes of chromatography Standardization (including reference data sets) for modeling tools does not exist Combination of homology models and mechanistic DSP modeling for knowledge transfer Streamlined model calibration with simple and modular isotherms Intelligent strategies to combine model applications such as modeling of all CQAs, ie, DNA, HCP, resin fouling, temperature, etc Detailed understanding of non-standard protein separation effects like protein-protein interactions, dimerization, or changes in protein conformation 	<ul style="list-style-type: none"> Initial models established (including multiphase), eg, ambr scale-down Predictive models do not necessarily exist (confirmation of experimental results feasible) Modeling not yet fully quantitative (eg, aggregate formation, discrete particles, bubble size distribution/ coalescence) Directional/semi-quantitative effects of shear are feasible (experimental confirmation is challenging) <p>Chromatography</p> <ul style="list-style-type: none"> Heterogeneity of packing, flow distribution Experimental confirmation of chromatography flow distribution established and general collaboration with experimentalists to validate CFD models Value maximized by implementing CFD upstream in equipment or during process development 	<p>Same as Early Stage</p> <p>Gap</p> <ul style="list-style-type: none"> Additionally, having material flow mapped, sustainability among selected alternatives using process mass intensity (PMI) can be evaluated for selection of the best process
Commercial Scale-up, transfer, plant simulation	<p>Same as late Stage</p> <p>Mixed Mode Isotherms QSPR-Tools</p>	<p>Upstream</p> <ul style="list-style-type: none"> Limited understanding of process variability, scale-up/scale-down <p>Chromatography</p> <ul style="list-style-type: none"> Current State: Simplified/basic models exist to support PD surrogates for impurities (lumped) Understanding limited to specific modalities (IEX) as opposed to mixed mode <p>Gaps</p> <p>Upstream</p> <ul style="list-style-type: none"> Combination of biological models and mixing models <p>Downstream</p> <ul style="list-style-type: none"> Mechanistic understanding of all modes of chromatography Limited isotherms Standardization (including reference data sets) for modeling tools does not exist Smart analytical strategies for challenging molecules like complex protein formats, which create a strong database for pure mechanistic models <p>Scale-down for HTS systems</p>	<ul style="list-style-type: none"> Quantitative assessment of facility fit to potentially support PPQ Utilized to support deviation management Unknown credibility of existing CFD models – establishment of industry best practices lacking 	<p>Same as early stage and additionally, this is the best approach for understanding the process to be built. Model frameworks and solution strategies independently exist for solving the plant simulation problem</p> <p>Plant model also helps with commissioning; planning IQ, OQ, PPQ, etc, and characterization of short (mid-long) term changes</p> <p>Gap</p> <ul style="list-style-type: none"> As the previous two stages, complexity of the models used here are dependent on the mechanistic models and as they improve, the plant simulation improves

Current Opinion in Chemical Engineering

Current state and gaps to achieve future state of *in silico* application of modeling concepts in industry. Green: models are sufficiently developed to support implementation now. Yellow: gaps identified that require modest investments to address before implementation (2–5 years). Gray: opportunities for exploration or significant gaps required to achieve realization (5–10 years) or may not be scientifically feasible (initial assessment required). Early stage indicates models appropriate for supporting first-in-human studies or developmental studies. Late stage indicates quantitative models potentially applicable for licensing applications. Blue text indicates advances in modeling implementation in the last two years [1**].

Figure 2

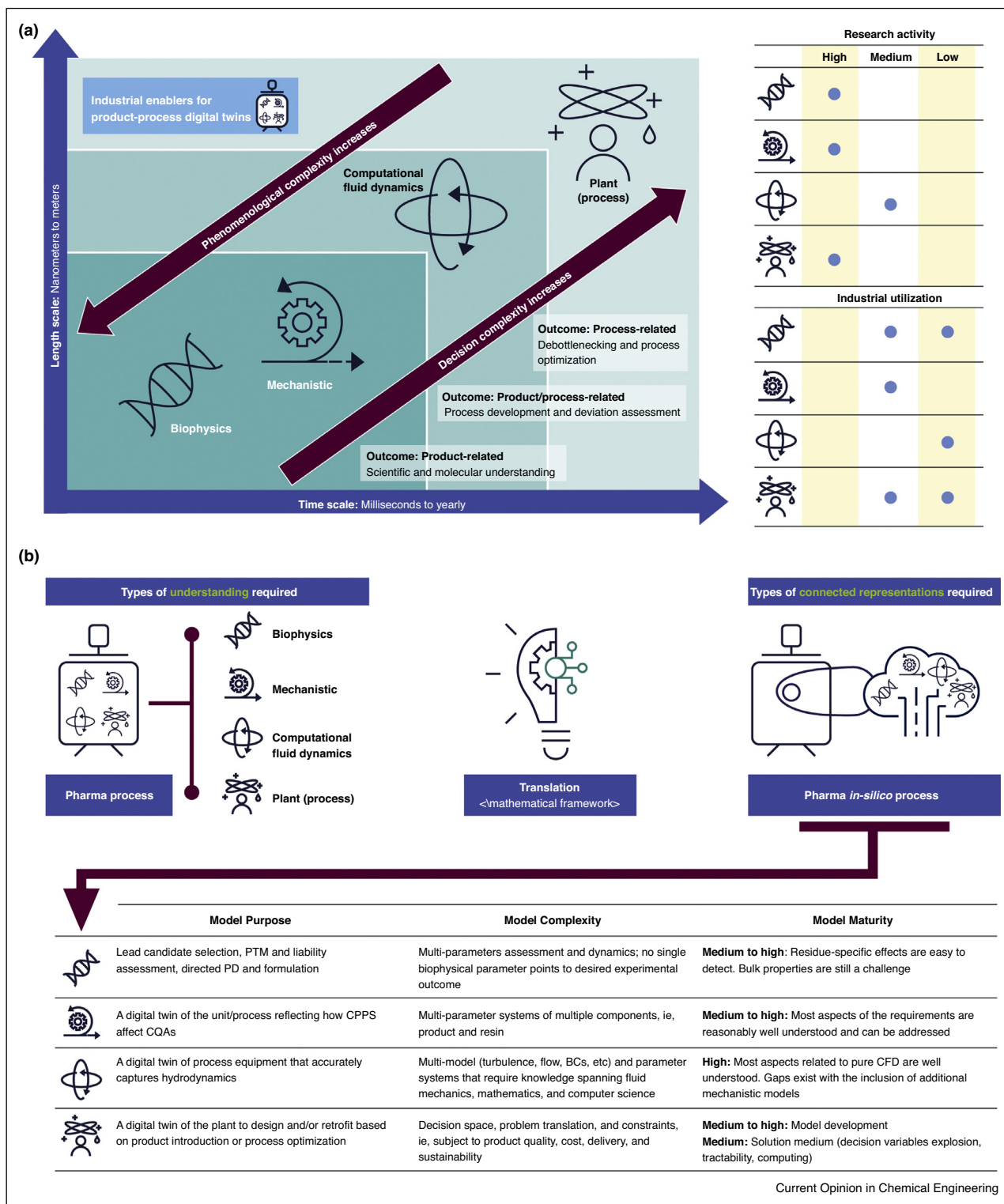


Workshop participant survey indicating the current maturity level of Biophysical Modeling, Mechanistic Modeling (USP and DSP), Plant Modeling, and Computational Fluid Dynamics for Research/Early Stage Development, Late Stage Development, and Commercial Stage. Maturity level is scored by three levels: Major Research Required (5–10 years), Gaps Limiting Deployment (2–5 years), or Ready to Deploy. The y-axis depicts the number of survey respondents that indicated the given stage of deployment in each category.

general rule of thumb is to ensure that the training set should be as diverse as the potential application space. Another layer of complexity is the types of molecular descriptors and how accurately they describe the molecules and processes to be predicted. A more informative set of descriptors emerge as the number of experimental observations increase. Novel concepts like protein and

ligand dewetting coupled with molecular dynamics hold the potential to accurately describe most chromatographic systems. These types of molecular dynamics simulations are very computationally expensive to fully sample conformational space. As computational power increases, increased use and applicability of these types of simulations will be very valuable.

Figure 3



(a) Modeling Trajectory across different model modalities (multiscale) for enabling Product-Process Digital Twins categorized by research effort and industrial usage (2019–2021), and **(b)** Modeling Connectivity across the multiscale highlighting key properties: purpose, complexity, maturity, for selecting the appropriate model based on industrial requirements.

Top challenges

- 1) Design accurate molecular descriptors for predictive modeling — artificial intelligence (AI), machine learning (ML), quantitative structure property relationship (QSAR)
- 2) Incorporate dynamics into predictive tool development — explore multiple scales from atomic to coarse grain at different timescales
- 3) Predict optimal process conditions from structure and biophysical properties — developability, formulation and manufacturability
- 4) Predict chromatographic changes from molecular properties and accurately map out the experimental design space
- 5) Expand the scope from antibodies/proteins to include other modalities, for example, DNA, RNA, viral vector, and so on

If some of these gaps and challenges can be overcome, there are two-specific areas where biophysical modeling could have broad applicability: ‘developability’ assessments during candidate selection and formulation development, and prediction of bioseparations (Figure 2). Developability assessments are a common way to predict molecular liabilities such as aggregation, fragmentation, and deamidation propensity before costly development and clinical investments are made [14–16]. While some of these assessments already include sequence and some structural information, better biophysical information and descriptors could lead to significantly better predictions and formulations. A recent study and workshop presentation from Saleh *et al.*, has also begun to look at the impact of sequence modifications on chromatographic performance, see Ref. [17] and Table 1.

For bioseparations, typical processes rely on filtration or chromatography unit operations for impurity removal. Previous studies have demonstrated QSAR to be useful for chromatographic predictions of model proteins [5,13]. More recent work has looked to create *in silico* heat maps as reported by Burgess at the workshop (see Table 1) that are similarly predictive to high throughput screening tools [18–20]. Another impactful application to bioseparations currently under investigation, as suggested by Armenio Barbosa in the workshop (see Table 1), would be to use biophysical structures to design novel ligands, thereby creating customized and highly specific separation mechanisms.

Mechanistic modeling

The term mechanistic modeling describes the mathematical description of data applying physical fundamentals. In contrast to empiric approaches, the degrees of freedom of mechanistic models are restricted by considering key mechanisms like for instance kinetics or mass balances. Mechanistic modeling approaches of chromatography

build on the work done by Irving Langmuir on gas–solid phase equilibria [21], Tiselius on different modalities of chromatography [22] and many subsequent authors. The most common isotherm for ion-exchange is the steric mass-action (SMA) isotherm, which has been established in the 1990s [6^{*}] and is still the foundation of a lot of chromatography modeling, but many other approaches do also apply [23,24].

Top challenges

- 1) Combination of homology models and mechanistic downstream processing (DSP) modeling to enable transfer of existing models and process knowledge to upcoming projects
- 2) Streamlined model calibration with simple and modular isotherms
- 3) Intelligent strategies to overcome existing gaps in current industrial model applications such as modeling of all critical quality attributes (CQA) parameters such as DNA, host cell proteins (HCPs), resin fouling, temperature and so on and enable full mechanistic filings
- 4) Detailed understanding of non-standard protein separation effects like protein-protein interactions, dimerization, or changes in protein conformation. Collaborations with academia might be a good way forward.
- 5) High throughput, high resolution, and orthogonal analytical strategies for challenging molecules like complex protein formats, which create a strong database for pure mechanistic models

Yet, it has taken the pharmaceutical industry quite some time to adopt this technology due to lack of coding ability and rigorous experimental requirements. Software Tools for mechanistic modeling (ChromX®/DSPX®, CADET, ChromWorks®, a.o.) are, however, now available and reduce the entry barrier to chromatography modeling and in some cases even other unit operations. Workflows for model calibration have been standardized and work in many cases [25,26]. Even less common processes using membrane adsorbers have been successfully modeled by companies and used in their process development/characterization efforts. More and more companies are taking the final step and are discussing modeling approaches in downstream processing with the regulatory agencies and in particular the US FDA. Even frameworks that govern the quality assurance paradigms and lifecycle of a certain model are now being presented to the agencies and, as discussed at the workshop, are generally well received by authorities (Good modeling practice for industrial chromatography [27^{*},28^{*},29^{*}]). In addition, companies make use of modeling data, albeit only to some extent, in their regulatory filings. Although the submission of modeling data to the regulatory agencies is seen as the pinnacle of modeling, most workshop

participants see the value of using modeling to a large extent for better process understanding during process development.

Tools for all unit operations to model the platform monoclonal antibody (mAb) process have been established, starting with Protein A chromatography [30], molecular modeling of affinity Chromatography [31], cation exchange (CEX) and anion exchange (AEX) chromatography, mixing and tangential flow filtration (TFF) models [32^{••},33]. Hence, a standard mAb process can have its digital twin demonstrating the maturity of the field.

However, the field has suffered several setbacks. For chromatography, the standard SMA isotherm does not accurately reflect the experimental behavior [34], that is, when the ligand density varies between lots [35], at high load densities or over wide pH ranges. Extensions are thus needed which derails the standard calibration workflow, some CQAs are inherently difficult to model (i.e. HCPs), and a lack of high throughput, high resolution and orthogonal analytical data is still limiting the field. Furthermore, there is a gap in data availability that could be used for training and validating the model, similarly as mentioned for Biophysics above. Within a single company where the transferability from lab data to process scale data is not possible, as they have been recorded with different systems or purposes, publicly available datasets are not available that would allow easy testing of new model isotherms and other approaches. Validating a new model often requires generating all the data needed from scratch for model development.

As is evident in the presentations by Prof. Carta on the influence of different conformations and binding configurations of a bispecific mAb on adsorption and Prof. Frech on the elution behavior at high load densities at the workshop, see Table 1, some of these issues are being efficiently addressed by the academic community, either alone or in industry-academic partnerships (NIIMBL). These academic-industry partnerships [36[•]] hold the promise to address some of the remaining theoretical gaps in downstream processing, which are robust isotherms for mixed-mode chromatography and/or HIC chromatography, functionalized depth filters which are in general not very well understood and frameworks on how to deal with diverse impurities such as HCPs. Lastly, the intersection of making use of biophysical parameters for a certain molecule to supplement the mechanistic model and reduce the initial investment in experimentation is an area that is being addressed by industry-academic collaborations [13,17].

It would be beneficial if the tools that are currently available for mechanistic modeling better support the user in selection of the appropriate isotherm and guide

the user through an efficient calibration workflow. A comprehensive review of downstream mechanistic modeling is provided in Ref. [37^{••}], and multiple examples of industrial application are presented in Ref. [2[•]].

The workshop also comprised a session on mechanistic modeling of upstream processes, however, this publication is focused on the downstream aspects of mechanistic modeling. The mechanistic modeling of upstream processes is somewhat more challenging than for downstream processes. The upstream process consists of at least three very different elements, the equipment and input materials, the biological system of the cell and the target output molecule, that is, the antibody and its various embodiments. The equipment is reasonably well understood as described in the computational fluid dynamics (CFD) section of this manuscript. The biological system of the Chinese hamster ovary (CHO) cell is sufficiently well understood and there are metabolic-flux-analysis models and other models that can well describe the growth behavior of the cells. In addition, the products such as antibodies are very well characterized. The challenge seems to lie in correlating changes in equipment or process parameters not to cell growth or behavior but on the output of the product. Further insights into the status of upstream modeling may be found in Refs. [38[•],39].

Plant modeling

Plant modeling (can also be referred to as flowsheet modeling), is the combination of complex causal relationships from the lower scales, see Figure 3 into interconnected unit operation models to study, analyze and evaluate the full decision space of a given end-to-end process. The benefit of developing and employing such a model (whether at steady state or dynamic) is having the opportunity for process design and idea testing (so called ‘what if analysis’) considering, where necessary, uncertainty (e.g. robustness analysis). Plant modeling activities range from research over research-industrial to industrial activities. There is a clear gap from participants on plant modeling, see Figure 2, on three main things, what is the objective, why such a problem is complex and how to navigate it, and what commercial tools exist that are ready to deploy.

Top challenges

- 1) Problem translation — formulation of challenges into explicit problem definitions that satisfy full scale manufacturing constraints
- 2) Technology/topologies — how to efficiently generate, screen and select appreciated technologies/topologies before large investments in dedicated, multi-product, multipurpose, mixed, and modular designs
- 3) Batch & Continuous evaluation — how to generate topological process alternatives either for batch or

continuous or in combination and selection of the best based on quality and manufacturing requirements

- 4) Solution methods — how to incorporate and handle decision variables (integer and continuous) in both deterministic and stochastic instances
- 5) Computer-aided tools — selection of the right tool for the right problem incorporating research and development methods for obtaining efficient solutions

The three gaps mentioned above will be addressed based on the three presentations and the Break-out session given at the workshop (see Table 1) and the current state in transitioning from academia to industry. In an industrial context, many different types of challenges exist, for example, what are the key design decisions for new processes, how to identify retrofit for increased capacity, how to introduce a new product into an existing process, and so on? To be able to navigate these and other challenges, there is a need to both categorize and define these challenges into clear problem definitions. Here, three problem definitions are defined as seen emerging from the industry thereby giving rise to different digital twins (Siemens Digital Industries Software: Digital Twin. <https://www.plm.automation.siemens.com/global/en/our-story/glossary/digital-twin/24465>). Problem 1, referred to as the design problem where for a new product with specified requirements (throughput, purity, yield etc.), designs a (core) process to achieve these requirements [40]. Problem 2, referred to as the retrofit problem where for an existing product and known achievable requirements, modifies an existing design of a (core) process to improve processing [41]. Problem 3 and often overlooked referred to as the incorporation problem where for a new product with specified requirements, retrofits an existing design of a (core) process to incorporate this new product. The three defined problems give rise to different, terminal process designs as follows: dedicated processes, multi-product processes, multi-purpose and modular processes [7]. Dedicated processes are defined by: as topology is fixed, product is fixed, and the mode of operation can either be batch or continuous. Multi-product processes are defined by: as topology is fixed, product is varying, and the mode of operation can either be batch or continuous. Multi-purpose processes are defined by: as topology is varying, product is varying, and the mode of operation can either be batch and/or continuous. Modular processes are defined by: how units, process sections and thereby, process are defined in terms of unit-unit connectivity and combination, if these are to generate modules that can be utilized in a plug and play fashion. This introduces both flexibility (e.g. increasing capacity) and agility (e.g. the rate at which capacity can be increased) [42,43].

Plant modeling is generally approached and solved as a multiscale problem where different scales of information must be analyzed, curated, and combined for

representation of system complexities both at the process and plant levels. The plant model is defined as the combination of the different processes (core, auxiliary or supporting) working in synchronicity to achieve product requirements. For plant modeling the multiscale, combinatorial abstraction of the problem can be explained by interlinked phenomena, that is, a unit operation coupled to the unit operation model, coupled to the process model (multiple unit operations connected), and coupled to the auxiliary model (e.g. raw material supply) and supporting systems (e.g. solvent systems), respectively. Therefore, the decision space is huge and gives rise to a mixed-integer non-linear (MINLP) problem [44,45].

At the plant scale, the product is produced at the required quantities based on the market demand. At this scale, for example, phase III clinical trials are also manufactured due to the amounts required. Based on both the regulatory environment for maintaining patient safety via product quality and documentation, changes to the process for phase III manufacturing are challenging and undesired. Therefore, a dilemma arises on how to a priori generate, screen, select and test ideas that can be implemented in new as well as existing plants in order to achieve product requirements both economically and sustainably.

Early stage techno-economical evaluation utilizing a modular analytical approach where bill of materials (BoM), overall (projected) process performance and realized efficiencies from known products can be combined and used to evaluate scenarios [46]. This allows the identification of where to focus, for example, should raw materials be replaced to improved sustainability or should the process be improved to enhance product economy and so on. Highlighted computer-aided tools that are available off-the-shelf for this type of early stage evaluation include BioSolve Process and the industrial-university consortium Techno-Economic Engine [47]. Next is screen and select, where detailed process models representing the existing plant virtually at both the unit operation and process level can be developed as a digital twin and used to perform 'what if analysis' to select the best, sustainable ideas for final implementation [42]. Computer-aided tools for this type of detailed material flow analyses include GAMS, PYOMO INOSIM, gPROMS, SuperPro Designer, and though less specific, Anylogic and ExtendSim. Finally, continuous improvement for process optimization [48**] can be performed for minimizing cost, maximizing sustainability, maximizing throughput and so on, and computer-aided tools are a combination of those aforementioned, subject to limitations of uncertainties and potential, known/expected sensitivities.

Computational Fluid Dynamics (CFD)

Computational Fluid Dynamics is a specific type of mechanistic modeling that refers to the numerical method of simulating steady and unsteady fluid motion

using numerical methods and has become a commonly applied engineering tool for simulating complex fluid flows involving solid interactions. The ever-growing availability of high-performance computing (thanks to Moore's law [49]) and development of numerous commercial codes has fueled the uptake in applying CFD modeling over the past two decades. In fact, most major biopharmaceutical companies have now established some internal CFD capability. It is now common to see CFD applied to systems involving agitated vessels (e.g. mixing tanks [50,51], bioreactors [8,52–54], and UFDF tanks), and increasingly common in its application to other biopharmaceutical unit operations, for example, chromatography [55–60] and for general validation [61–63]. The apparent maturity of CFD is presented in Figure 2.

Top challenges

- 1 Established industry best practices
 - a No best model for a given unit operation – need to balance complexity with requirements
 - b Most CFD models are a combination of CFD and other mechanistic models (turbulence, binding isotherm, porous media, population balance, etc.)
 - c There is still a need for collaboration and sharing of best practices / common tools
- 2 Collaboration between experimentalists is needed to develop and adequately validate CFD models
- 3 Value is maximized by doing CFD further upstream in equipment or process development

The broad expansion in application of CFD can be attributed to the development of additional mechanistic models (population balance, multiphase models, kinetic expressions, Darcy's law [64] etc.) that can be combined with CFD to extend its predictive capability. In fact, most CFD simulations are now a combination of CFD, and other models that enable capture of additional mechanistic phenomena like bubble breakage/coalescence, chemical reactions, filtration, and precipitation. With these developments arise a need to balance complexity with model requirements and ensure that a model is sufficiently fit for purpose. Depending on the questions being asked of a CFD model, there is often not a single best model for a given unit operation.

As previously discussed [1^{••}], CFD is still generally used to provide directional guidance in early stage activities or as supporting evidence despite its ability to provide high resolution results. The primary regulatory science gaps and challenges that have impeded the biopharmaceutical industry from reaching a future state of having digital twins for equipment are:

- Unknown credibility of existing CFD models: Most of the CFD models developed within the industry receive

little to no rigorous evaluation and therefore have unknown credibility. The fact that CFD models can often be predictive without estimating parameters has enabled the directional use of CFD without rigorous comparison to experimental data.

- Lack of experimental methods and data for comparing to CFD results: Accurately characterizing a flow field is complicated and an area where the industry has little experience beyond the use of aggregate measures like mixing time and outlet concentration profiles. Generating appropriate experimental datasets to evaluate up against the CFD and any other models is a critical part of establishing credibility of a model. Good collaboration between experimentalists and model developers is critical to generating the appropriate datasets.
- Lack of established best practices for CFD: These include pre-processing and CFD best practices, and full end to end case studies for common unit operations that include the entire credibility assessment process across a wide range of operating conditions. Limited knowledge exists in the public domain even for the simple case of establishing mixing times in an agitated vessel.

While there has been much, a lack of published industry-accepted approaches for model development and validation still prevents CFD from being used in later stage activities as primary data. This is not a problem specific to CFD but impedes development of improved work processes that use computational models to offset experimental work. Publication of case studies in a peer reviewed journal or establishment of industry wide standards for unit operations commonly modeled with CFD is a necessary first step toward the future state of using CFD models as a digital twin for common unit operations. CFD models should thus encompass computational grid requirements, domain decomposition, model setup, experimental requirements for generating datasets for validation, statistical approaches for validating CFD models, and defining boundaries for where CFD models are predictive.

Conclusion

In addition to the focused modeling areas covered in the 4MMW, a broader discussion of challenges associated with implementation of modeling in lieu of experimentation was discussed in the Open Challenges Session. A detailed summary of the trajectory and opportunities for the modeling field is presented in Figure 3. One of the key challenges is the ability to incorporate modeling into regulatory submissions, especially for biophysics and CFD, when a full mechanistic understanding is not available. Statistical methods like DoE are widely used and accepted in regulatory submissions, thus one potential approach is the utilization of hybrid models which combine mechanistic and empirical components with the general experiments, that needs to be performed anyway.

Experiments at different scales as a mandatory part of process development will complement the hybrid model to handle CQAs that may otherwise only be handled empirically, and the model will thus improve the experimental protocol leading to a better process and/or less experiments.

A key consideration to significantly advance the state of modeling is the various ways that models can be employed to: guide experimentation, control processes, evaluate value proposition for new products (manufacturability). A near term objective is the development of approaches to predict impending failure (e.g. loss of chromatographic column separation performance). Modeling can also be employed to describe and help understand secondary kinetics effects on surfaces such as unfolding and on-column aggregate formation. Although the quantitative requirements for a model may vary based on the application (e.g. directional to guide experimentation versus fully quantitative efficient models for feedback control in continuous processing) all modeling approaches need to be scientifically rigorous not merely abstract mathematical constructs — effectively, a transition from black-box to grey box to white box models [65,66].

One current challenge is the lack of standardization of the modeling tools and the ability to benchmark performance (efficiency and accuracy) versus a standard case. Availability of open-source modeling software that is standardized and useful as a benchmark with a standard experimental system (e.g. NIST mAb [67]) would alleviate this challenge. The linkage to an experimental dataset (or diverse datasets) for model verification coupled with a fundamental understanding of the underlying mechanisms for a specific system are important to avoid ‘misuse’, leading to incorrect or unphysical results. Perhaps the development and maintenance of this diverse dataset could be pursued by a consortium [1^{••}] or via a standardization organization (NIST). This proposed approach would ensure that modeling tools are mathematically convergent and physically realistic and will serve to continue to build confidence in the approach.

Publication of case studies and a benchmark comparison of hybrid versus mechanistic modeling would also be quite beneficial to further advance the state of modeling into machine learning models that do not stray into unphysical boundaries. Current gaps include Biophysical tools to measure and describe binding to custom affinity ligands.

This review presents the authors’ view of the current status of modeling tools in the biopharmaceutical industry, and the challenges to progress the field. The modeling workshop series was established by industry representatives to share knowledge and experiences to

advance implementation of advanced modeling tools in the biopharmaceutical processes. The tools will ensure better understanding and development of the processes and thus produce better products for patients, and the workshop series will continue to help advance the developments in the field. The next workshop is planned to occur in 2023.

Conflict of interest statement

Nothing declared.

Acknowledgements

Thank you to all who contributed to the workshop sessions, especially presenters and session chairs mentioned in Table 1, to continue to build a diverse community of modelers and to refine the vision of advancement of the field.

Declaration of Competing Interest

The authors report no declarations of interest.

References and recommended reading

Papers of particular interest, published within the period of review, have been highlighted as:

- of special interest
- of outstanding interest

1. Roush David, Asthagiri Dilip, Babi Deenesh K, Benner Steve, Bilodeau Camille, Carta Giorgio, Ernst Philipp, Fedesco Mark, Fitzgibbon Sean, Flamm Matthew et al.: **Toward in silico CMC: an industrial collaborative approach to model-based process development.** *Biotechnol Bioeng* 2020, **117**:3986-4000 <http://dx.doi.org/10.1002/bit.27520>
- Fundamental description and discussion of modeling topics and approaches used in the biopharmaceutical industry, and review of Modeling Workshop 3 cases.
2. Staby n, Rathore Anurag Sua ., Ahuja tne (Eds): *Preparative Chromatography for Separation of Proteins*. John Wiley & Sons, Inc. 9781119031109; 2017 <http://dx.doi.org/10.1002/9781119031116>
- Whole book relevant with numerous good chapters about industrial and academic modeling in chromatography, simulation and biophysics.
3. Dirac PAM: **Quantum mechanics of many-electron systems.** *Proc R Soc Lond Ser A* 1929, **123**:714-733 <http://dx.doi.org/10.1098/rspa.1929.0094>.
4. Karplus M: **Development of multiscale models for complex chemical systems: from H+H2 to biomolecules (Nobel lecture).** *Angew Chem Int Ed* 2014, **53**:9992-10005 <http://dx.doi.org/10.1002/anie.201403924>.
5. Ladiwala Asif, Rege Kaushal, Breneman Curtis M, Cramer Steven M: **A priori prediction of adsorption isotherm parameters and chromatographic behavior in ion-exchange systems.** *Proc Natl Acad Sci U S A* 2005, **102**:11710-11715 <http://dx.doi.org/10.1073/pnas.0408769102>.
6. Brooks Clayton A, Cramer Steven M: **Steric mass-action ion exchange: displacement profiles and induced salt gradients.** *AIChE J* 1992, **38** <http://dx.doi.org/10.1002/aic.690381212>
- One of the most seminal papers in the field that most other publications are based on.
7. Cybulski A, Moulijn JA, Sharma MM, Sheldon RA: In *Production Plants, Chapter 7 in "Fine Chemicals Manufacture - Technology and Engineering"*. Edited by Cybulski A, Moulijn JA, Sharma MM, Sheldon RA. Elsevier; 2001 <http://dx.doi.org/10.1016/B978-044482202-4/50007-9>.
8. Dhanasekharan Kumar M, Sanyal Jay, Haidari Ahmad: **A generalized approach to model oxygen transfer in bioreactors using population balances and computational fluid dynamics.** *Chem Eng Sci* 2005, **60**:213-218 <http://dx.doi.org/10.1016/j.ces.2004.07.118>.

9. Molecular Operating Environment (MOE): 2019.01; *Chemical Computing Group ULC, 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7*. 2021 <https://www.chemcomp.com/Products.htm>.
 10. Zhu K, Day T, Warshaviak D, Murrett C, Friesner R, Pearlman D: **Antibody structure determination using a combination of homology modeling, energy-based refinement, and loop prediction**. *Proteins* 2014, **82**:1646-1655 <http://dx.doi.org/10.1002/prot.24551>.
 11. Jumper John, Evans Richard, Pritzel Alexander, Green Tim, Figurnov Michael, Ronneberger Olaf, Tunyasuvunakool Kathryn, Bates Russ, Židek Augustin, Potapenko Anna *et al.*: **Highly accurate protein structure prediction with AlphaFold**. *Nature* 2021, **596**:583-589 <http://dx.doi.org/10.1038/s41586-021-03819-2>.
 12. Coffman J, Marques B, Orozco R, Aswath M, Mohammad H, Zimmermann E, Khouri J, Griesbach J, Izadi S, Williams A *et al.*: **Highland games: a benchmarking exercise in predicting biophysical and drug properties of monoclonal antibodies from amino acid sequences**. *Biotechnol Bioeng* 2020, **117**:2100-2115 <http://dx.doi.org/10.1002/bit.27349>.
- Industrial case studies on prediction of mAb properties in downstream processing based on Highland Games at the Recovery of Biological Products XVIII conference.
13. Robinson Julie R, Karkov Hanne S, Woo James A, Krogh Berit O, Steven M: **Cramer "QSAR models for prediction of chromatographic behavior of homologous Fab variants"**. *Biotechnol Bioeng Symp* 2016, **12**:1231-1240 <http://dx.doi.org/10.1002/bit.26236>.
 14. Jain T, Sun T, Durand S, Hall A, Houston NR, Nett JH, Sharkey B, Bobrowicz B, Caffry I, Yu Y *et al.*: **Biophysical properties of the clinical-stage antibody landscape**. *Proc Natl Acad Sci U S A* 2017, **114**:944-949 <http://dx.doi.org/10.1073/pnas.1616408114>.
 15. Bailly M, Mieczkowski C, Juan V, Metwally E, Tomazela D, Baker J, Uchida M, Kofman E, Raoufi F, Motlagh S *et al.*: **Predicting antibody developability profiles through early stage discovery screening**. *MAbs* 2020, **12**:1743053 <http://dx.doi.org/10.1080/19420862.2020.1743053>.
 16. Lauer Timothy M, Agrawal Neeraj J, Chennamsetty Naresh, Egodage Kamal, Helk Bernhard, Trout Bernhardt L: **Developability index: a rapid in silico tool for the screening of antibody aggregation propensity**. *Biotechnology* 2012, **101**: P102-115 <http://dx.doi.org/10.1002/jps.22758>.
 17. Saleh D, Hess R, Ahlers-Hesse M, Beckert N, Schönberger M, Rischawy F, Wang G, Bauer J, Blech M, Kluters S *et al.*: **Modeling the impact of amino acid substitution in a monoclonal antibody on cation exchange chromatography**. *Biotechnol Bioeng* 2021, **118**:2923-2933 <http://dx.doi.org/10.1002/bit.27798>.
 18. McDonald P, Tran B, Williams CR, Wong M, Zhao T, Kelley BD, Lester P: **The rapid identification of elution conditions for therapeutic antibodies from cation-exchange chromatography resins using high-throughput screening**. *J Chromatogr A* 2016, **1433**:66-74 <http://dx.doi.org/10.1016/j.chroma.2015.12.071>.
 19. Coffman JL, Kramarczyk JF, Kelley BD: **High-throughput screening of chromatographic separations: I. Method development and column modeling**. *Biotechnol Bioeng* 2008, **100**:605-618 <http://dx.doi.org/10.1002/bit.21904>.
 20. Kelley BD, Tobler SA, Brown P, Coffman JL, Godavarti R, Iskra T, Switzer M, Vunnum S: **Weak partitioning chromatography for anion exchange purification of monoclonal antibodies**. *Biotechnol Bioeng* 2008, **101**:553-566 <http://dx.doi.org/10.1002/bit.21923>.
 21. Langmuir Irving: **The adsorption of gases on plane surface of glass, mica and platinum**. *J Am Chem Soc* 1918, **40**:1361-1402 <http://dx.doi.org/10.1021/ja02242a004>.
 22. Tiselius A: **Studien über adsorptionsanalyse, I**. *Kolloid-Zeitschrift* 1943, **105**:101-109 <http://dx.doi.org/10.1007/BF01520008>.
 23. Yamamoto S, Nakanishi K, Matsuno R: *Ion-Exchange Chromatography of Proteins*. New York: Marcel Dekker; 1988 <http://dx.doi.org/10.1002/aic.690350429>.
 24. Carta Giorgio, Jungbauer Alois: *Protein Chromatography: Process Development and Scale-Up*. Wiley-VCH Verlag GmbH & Co. KGaA; 2010. ISBN 9783527318193 <http://dx.doi.org/10.1002/978352763015>.
 25. Saleh David, Wang Gang, Müller Benedict, Rischawy Federico, Kluters Simon, Studts Joey, Hubbuch Jürgen: **Straightforward method for calibration of mechanistic cation exchange chromatography models for industrial applications**. *Biotechnol Progress* 2020, **36**:e2984 <http://dx.doi.org/10.1002/btpr.2984>.
- Good reading to understand what is required for calibration of a mechanistic model.
26. Pirrung Silvia M, van der Wielen Luuk AM, van Beckhoven Ruud FWC, van de Sandt Emile JAX, Eppink Michel HM, Ottens Marcel: **Optimization of biopharmaceutical downstream processes supported by mechanistic models and artificial neural networks**. *Biotechnol Progress* 2020, **33**:696-707 <http://dx.doi.org/10.1002/btpr.2435>.
 27. Rischawy Federico, Saleh David, Hahn Tobias, Oelmeier Stefan, Spitz Julia, Kluters Simon: **Good modeling practice for industrial chromatography: mechanistic modeling of ion exchange chromatography of a bispecific antibody**. *Comput Chem Eng* 2019, **130**:106532 <http://dx.doi.org/10.1016/j.compchemeng.2019.106532>.
- Worth reading if interested in what it means to use a digital in the context of GMP production of pharmaceuticals.
28. Saleh David, Wang Gang, Rischawy Federico, Kluters Simon, Studts Joey, Hubbuch Jürgen: **In silico process characterization for biopharmaceutical development following the quality by design concept**. *Biotechnol Progress* 2021, **37**:1-13 <http://dx.doi.org/10.1002/btpr.3196> e3196.
- Good read for those interested in the aspects of using models in a regulated environment.
29. Briskot Till, Stückler Ferdinand, Wittkopp Felix, Williams Christopher, Yang Jessica, Konrad Susanne, Doninger Katharina, Griesbach Jan, Bennecke Moritz, Hepbildikler Stefan, Hubbuch Jürgen: **Prediction uncertainty assessment of chromatography models using Bayesian inference**. *J Chromatogr A* 2019, **1587**:101-110 <http://dx.doi.org/10.1016/j.chroma.2018.11.076>.
- Nice publication on how to deal with uncertainty inherent to all modeling aspects.
30. Benner SW, Welsh JP, Rauscher MA, Pollard JM: **Prediction of lab and manufacturing scale chromatography performance using mini-columns and mechanistic modeling**. *J Chromatogr A* 2019, **1593**:54-62 <http://dx.doi.org/10.1016/j.chroma.2019.01.063>.
 31. Paloni M, Cavallotti C: **Molecular modeling of the affinity chromatography of monoclonal antibodies**. *Methods Mol Biol* 2015, **1286**:321-335 http://dx.doi.org/10.1007/978-1-4939-2447-9_25.
 32. Pirrung Silvia M, Berends Carmen, Backx Antoon H, van Beckhoven Ruud FWC, Eppink Michel HM, Ottens Marcel: **Model-based optimization of integrated purification sequences for biopharmaceuticals**. *Chem Eng Sci X* 2019, **3**:100025 <http://dx.doi.org/10.1016/j.cesx.2019.100025>.
- Good read about the integration of modeling through various unit operations.
33. Creasy A, Reck J, Pabst T, Hunter A, Barker G, Carta G: **Systematic interpolation method predicts antibody monomer-dimer separation by gradient elution chromatography at high protein loads**. *Biotechnol J* 2019, **14**:e1800132 <http://dx.doi.org/10.1002/biot.201800132>.
 34. Diedrich Juliane, Heymann William, Leweke Samuel, Hunt Stephen, Todd Robert, Kunert Christian, Johnson Will, Lieres Ericvon: **Multi-state steric mass action model and case study on complex high loading behavior of mAb on ion exchange tentacle resin**. *J Chromatogr A* 2017, **1525**:60-70 <http://dx.doi.org/10.1016/j.chroma.2017.09.039>.
 35. Sanchez-Reyes Gabriela, Graafls Heiner, Hafner Mathias, Frech Christian: **Mechanistic modeling of ligand density variations on anion exchange chromatography**. *J Sep Sci* 2021, **44**:805-821 <http://dx.doi.org/10.1002/jssc.202001077>.
 36. Briskot Till, Hahn Tobias, Huuk Thiemo, Wang Gang, Kluters Simon, Studts Joey, Wittkopp Felix, Winderl Johannes,

- Schwan Peter, Hagemann Isabell et al.: **Analysis of complex protein elution behavior in preparative ion exchange processes using a colloidal particle adsorption model.** *J Chromatogr A* 2021, **1654**:462439 <http://dx.doi.org/10.1016/j.chroma.2021.462439>
- Good publication that is addressing some of the more challenging behaviours of protein elution seen in industrial applications. Very good example of industry-academic-partnerships.
37. Kumar Vijesh, Lenhoff Abraham M: **Mechanistic modeling of preparative column chromatography for biotherapeutics.** *Annu Rev Chem Biomol Eng* 2020, **11**:235-255 <http://dx.doi.org/10.1146/annurev-chembioeng-102419-125430>
 - Very comprehensive and recent review of the field of mechanistic modeling in chromatography.
 38. Tsopanog Apostolos, Jiménez del Val Iou Ioscani: **Moving towards an era of hybrid modeling: advantages and challenges of coupling mechanistic and data-driven models for upstream pharmaceutical bioprocesses.** *Curr Opin Chem Eng* 2021, **32**:100691 <http://dx.doi.org/10.1016/j.coche.2021.100691>.
 39. Mears Lisa, Stocks Stuart M, Albaek Mads O, Sin Gürkan, Gernaey Krist V: **Mechanistic fermentation models for process design, monitoring, and control.** *Trends Biotechnol* 2017, **35**:914-924 <http://dx.doi.org/10.1016/j.tibtech.2017.07.002>.
 40. Bertran Maria-Ona, Frauzem Rebecca, Sanchez-Arcilla Ana-Sofia, Zhang Lei, Woodley John M, Gani Rafiqul: **A generic methodology for processing route synthesis and design based on superstructure optimization.** *Comput Chem Eng* 2017, **106**:892-910 <http://dx.doi.org/10.1016/j.compchemeng.2017.01.030>.
 41. Paula Barbosa-Póvoa Ana: **A critical review on the design and retrofit of batch plants.** *Comput Chem Eng* 2007, **31**:833-855 <http://dx.doi.org/10.1016/j.compchemeng.2006.08.003>.
 42. Efstratios N, Pistikopoulos Yuhe, Tian Rahul, Bindlish: **Operability and control in process intensification and modular design: challenges and opportunities.** *AIChE J* 2021, **67**:e17204 <http://dx.doi.org/10.1002/aic.17204>.
 43. Bhosekar Atharv, Ierapetritou Maranthi: **A framework for supply chain optimization for modular manufacturing with production feasibility analysis.** *Comput Chem Eng* 2021, **145**:107175 <http://dx.doi.org/10.1016/j.compchemeng.2020.107175>.
 44. Ryu Joonjae, Kong Lingxun, Pastore de Lima Arthur E, Maravelias Christos T: **A generalized superstructure-based framework for process synthesis.** *Comput Chem Eng* 2020, **133**:106653 <http://dx.doi.org/10.1016/j.compchemeng.2019.106653>.
 45. Anjan K, Tula Mario R, Eden Rafiqul, Gani: **Hybrid method and associated tools for synthesis of sustainable process flowsheets.** *Comput Chem Eng* 2019, **131**:106572 <http://dx.doi.org/10.1016/j.compchemeng.2019.106572>.
 46. Stamatis Christos, Farid Suzanne S: **Process economics evaluation of cell-free synthesis for the commercial manufacture of antibody drug conjugates.** *Biotechnol J* 2021, **16**:2000238 <http://dx.doi.org/10.1002/biot.202000238>.
 47. Guillén-Gosálbez Gonzalo, You Fengqi, Galán-Martín Ángel, Pozo Carlos, Grossmann Ignacio E: **Process systems engineering thinking and tools applied to sustainability problems: current landscape and future opportunities.** *Curr Opin Chem Eng* 2019, **26**:170-179 <http://dx.doi.org/10.1016/j.coche.2019.11.002>.
 48. Maravelias Christos T: *Chemical Production Scheduling - Mixed-Integer Programming Models and Methods.* Cambridge University Press; 2021:9781107154759 <https://www.cambridge.org/dk/academic/subjects/engineering/chemical-engineering/chemical-production-scheduling-mixed-integer-programming-models-and-methods?format=HB>
 - Fundamental reading on plant and facility modeling.
 49. Moore Gordon E: **Cramming more components onto integrated circuits.** *Electronics*, **38**, 1965, pp.114 ff. *IEEE Solid-State Circuits Newslett* 2006, **11**:33-35 <http://dx.doi.org/10.1109/N-SSC.2006.4785860>.
 50. Kabra Aakash, Nema Archana, Karvinkoppa Mathew, Nema Anurag, Thorat Sandeep: **Computational fluid dynamics used by mixing vessels for predicting hydrodynamic behaviour of mixture: an overview.** *Mater Today Proc* 2021, **47**:2305-2309 <http://dx.doi.org/10.1016/j.matpr.2021.04.292>.
 51. Pohar Andrej, Naneh Omar, Bajec David, Likozar Blaž: **Chemical reactor/compounding vessel fingerprinting: scale-up/down considerations for homogeneous and heterogeneous mixing using computational fluid dynamics.** *Chem Eng Res Des* 2020, **163**:125-137 <http://dx.doi.org/10.1016/j.cherd.2020.08.024>.
 52. Rahimi Mohammad J, Sitaraman Hariswaran, Humbird David, Stickel Jonathan J: **Computational fluid dynamics study of full-scale aerobic bioreactors: evaluation of gas-liquid mass transfer, oxygen uptake, and dynamic oxygen distribution.** *Chem Eng Res Des* 2018, **139**:283-295 <http://dx.doi.org/10.1016/j.cherd.2018.08.033>.
 53. Huttmacher Dietmar W, Singh Harmeet: **Computational fluid dynamics for improved bioreactor design and 3D culture.** *Trends Biotechnol* 2008, **26**:166-172 <http://dx.doi.org/10.1016/j.tibtech.2007.11.012>.
 54. McClure Dale D, Kavanagh John M, Fletcher David F, Barton Geoffrey W: **Characterizing bubble column bioreactor performance using computational fluid dynamics.** *Chem Eng Sci* 2016, **144**:58-74 <http://dx.doi.org/10.1016/j.ces.2016.01.016>.
 55. Subraveti Sai Gokul, Nikrityuk Petr, Rajendran Arvind: **Computational fluid dynamics study of viscous fingering in supercritical fluid chromatography.** *J Chromatogr A* 2018, **1534**:150-160 <http://dx.doi.org/10.1016/j.chroma.2017.12.057>.
 56. Teepakorn Chalore, Grenier Denis, Fiati Koffi, Charcosset Catherine: **Characterization of hydrodynamics in membrane chromatography devices using magnetic resonance imaging and computational fluid dynamics.** *Chem Eng Res Des* 2016, **113**:61-73 <http://dx.doi.org/10.1016/j.cherd.2016.06.027>.
 57. Ghosh Pranay, Vahedipour Kaveh, Lin Min, Vogel Jens H, Haynes Charles, Lieres Ericvon: **Computational fluid dynamic simulation of axial and radial flow membrane chromatography: mechanisms of non-ideality and validation of the zonal rate model.** *J Chromatogr A* 2013, **1305**:114-122 <http://dx.doi.org/10.1016/j.chroma.2013.07.004>.
 58. Smits Wim, Nakanishi Kazuki, Desmet Gert: **The chromatographic performance of flow-through particles: a computational fluid dynamics study.** *J Chromatogr A* 2016, **1429**:166-174 <http://dx.doi.org/10.1016/j.chroma.2015.12.019>.
 59. Smits Wim, Deridder Sander, Desmet Gert: **The impact of flow distribution on column performance: a computational fluid dynamics study.** *J Chromatogr A* 2014, **1369**:125-130 <http://dx.doi.org/10.1016/j.chroma.2014.10.024>.
 60. Wang Guan, Haringa Cees, Noorman Henk, Chu Ju, Zhuang Yingping: **Developing a computational framework to advance bioprocess scale-up.** *Trends Biotechnol* 2020, **38**:846-856 <http://dx.doi.org/10.1016/j.tibtech.2020.01.009>.
 61. Barresi Antonello A, Rasetto Valeria, Marchisio Daniele L: **Use of computational fluid dynamics for improving freeze-dryers design and process understanding. Part 1: modeling the lyophilisation chamber.** *Eur J Pharm Biopharm* 2018, **129**:30-44 <http://dx.doi.org/10.1016/j.ejpb.2018.05.008>.
 62. Lucas D, Rzehak R, Krepper E, Ziegenhein Th, Liao Y, Kriebitzsch S, Apanasevich P: **A strategy for the qualification of multi-fluid approaches for nuclear reactor safety.** *Nucl Eng Des* 2016, **299**:2-11 <http://dx.doi.org/10.1016/j.nucengdes.2015.07.007>.
 63. Oberkampf William L, Trucano Timothy G: **Verification and validation in computational fluid dynamics.** *Prog Aerosp Sci* 2002, **38**:209-272 [http://dx.doi.org/10.1016/S0376-0421\(02\)00005-2](http://dx.doi.org/10.1016/S0376-0421(02)00005-2).
 64. Darcy Henry: *Les Fontaines Publiques de la Ville de Dijon.* Paris: Dalmont; 1856. gallica.bnf.fr.
 65. Khan Mohd Ehmer, Khan Farmeena: **A comparative study of white Box, black Box and grey Box testing techniques.** *Int J*

- Adv Comput Sci Appl* 2012, **3**:12-15 <https://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.261.1758&rep=rep1&type=pdf>.
66. Pintelas Emmanuel, Livieris Ioannis E, Pintelas Panagiotis: **A grey-box ensemble model exploiting black-box accuracy and white-box intrinsic interpretability**. *Algorithms* 2020, **17** <http://dx.doi.org/10.3390/a13010017>.
67. Chen Chien-Hsun, Feng Huatao, Guo Rui, Li Pingjing, Laserna Anna Karen C, Ji Ya, Ng Bao Hui, Li Sam Fong Yau, Khan Shaheer H, Paulus Aran *et al.*: **Intact NIST monoclonal antibody characterization—proteoforms, glycoforms—using CE-MS and CE-LIF**. *Cogent Chem* 2018, **4**:1480455 <http://dx.doi.org/10.1080/23312009.2018.1480455>.