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REVIEW



# Progress and challenges for the machine learning-based design of fit-for-purpose monoclonal antibodies

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## ABSTRACT

Although the therapeutic efficacy and commercial success of monoclonal antibodies (mAbs) are tremendous, the design and discovery of new candidates remain a time and cost-intensive endeavor. In this regard, progress in the generation of data describing antigen binding and developability, computational methodology, and artificial intelligence may pave the way for a new era of *in silico* on-demand immunotherapeutics design and discovery. Here, we argue that the main necessary machine learning (ML) components for an *in silico* mAb sequence generator are: understanding of the rules of mAb-antigen binding, capacity to modularly combine mAb design parameters, and algorithms for unconstrained parameter-driven *in silico* mAb sequence synthesis. We review the current progress toward the realization of these necessary components and discuss the challenges that must be overcome to allow the on-demand ML-based discovery and design of fit-for-purpose mAb therapeutic candidates.

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## 1. Introduction

### 1.1. mAb discovery remains anchored to legacy technologies

Monoclonal antibody (mAb) based therapeutics continue to top the chart for best-selling drugs worldwide. In 2021, the sales figures for the top 10 antibody therapeutics are forecasted to reach more than \$110 billion and almost double in 2024.<sup>1,2</sup> Despite the major commercial success, antibody discovery has remained anchored to time- and cost-intensive legacy technologies, namely display libraries, animal immunization,<sup>3,4</sup> and comparatively low-throughput antibody modeling.<sup>5–10</sup> Indeed, although effective, monoclonal antibody therapies cost up to 100,000 USD per year.<sup>11</sup> As such, there is a critical need for developing novel *in silico*, and specifically ML-based, antibody discovery tools, to achieve fast, inexpensive, and on-demand generation of fit-for-purpose antibodies.

### 1.2. Three technological pillars for ML-based on-demand generation of mAbs: learnability, modularity, and unconstrained generation of novel sequences

In recent years, ML has taken the center stage in various fields due to its ability to recognize latent patterns in data, allowing a constructive extrapolation of such

patterns to unseen new data.<sup>5,7,12–16</sup> A particularly potent type of ML is deep learning where layers of interconnected computing units (neurons) work in tandem to detect signals in the data, enabling the model to discriminate between groups (classification) or to synthesize new data points that share particular traits with the original data (generation).<sup>17–19</sup>

Based on current literature, we identify and review recent progress and challenges in the three pillars that are instrumental to a successful realization of the long-sought immunobiotechnological vision of on-demand antigen-specific antibody generation (Figure 1): 1) the presence of rules underlying antibody-antigen interactions and developability (**learnability**),<sup>20,21</sup> 2) the capacity for the modular and non-linear optimization of interdependent antibody design parameters, e.g., plasma half-life, is affected by multiple regions of the antibody interdependently (**modularity**),<sup>22–24</sup> and 3) the capability to synthesize a virtually limitless quantity of new antibodies that are distinct from the training data yet possess affinity and developability parameters (feature-controlled) that match, exceed, or extend those of the training dataset (**unconstrained generation**).<sup>25–27</sup>

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### 1.3. Learning from nature: considering biological complexity in computational antibody design

Although antibody-antigen binding is a subset of protein-protein interactions, several important differences exist that render the prediction and design of antibody-antigen binding even more challenging than the prediction of typical protein-protein interaction. These differences are: 1) the immense diversity of antibody sequences, 2) many-to-many binding due to the high extent of non-linear sequence dependencies, and 3) inter-dependence of affinity and pharmacokinetic parameters. These specific characteristics need to be considered in antibody design and inform computational design constraints.

**Diversity:** V(D)J recombination and somatic hypermutation jointly create a potential immunoglobulin (Ig) diversity of  $>10^{14}$ ,<sup>28,29</sup> as compared to a non-immune protein diversity of  $10^5$ – $10^6$ .<sup>30</sup> Although there exists antigen-driven (or functional) repertoire convergence (formation of similar antibodies in different individuals undergoing an identical antigen challenge),<sup>28,31,32</sup> the extent of antigen-specific convergence is antigen-dependent<sup>33</sup> and overall comparatively low (on average,  $<10\%$  pairwise overlap of antigen-specific Ig sequences).<sup>34</sup> Thus, the vast observed diversity of (antigen-specific) antibodies implies that the discovery space for target-specific mAbs is rather large and amenable to constraint-based sequence design approaches.

**Additional mechanisms to diversify antibody repertoires** include insertion and deletion of amino acid (AA) sequences into the V region, the use of non-protein cofactor molecules, and post-translational modifications.<sup>35</sup> On the one hand, the insertion, and deletion of AAs and the use of non-protein cofactors (e.g., metal ion or haem) are suggested to be strategies toward diversifying specificity against pathogens.<sup>35–37</sup> On the other hand, post-translational modifications, such as O- and N-glycosylation, phosphorylation, and oxidation in the antibody structure may affect the pharmacokinetics, solubility, stability, modulation of effector functions as well as receptor-binding properties.<sup>38–42</sup> These modes of antibody diversification are not fully understood and require further investigations to enable favorable *in vivo* binding and transport properties as well as optimal manufacturability and storage formulations.

**Many-to-many binding:** Antibody-antigen binding is mediated by the interaction of AAs at the paratope-epitope interface of the complex. Antibody binding to the epitope is mainly formed by the three hypervariable regions termed complementarity-determining regions (CDRs) situated in each of the antibody heavy and light chains.<sup>43</sup> The CDR3 on the heavy chain (CDR3H) is obligate for epitope binding and is on average 15–17 AAs long.<sup>44,45</sup> Given that the diversity of antigens is even larger, the recognition of the majority of antigens encountered is ensured by antibody cross-reactivity, which means they may bind multiple epitopes on different proteins with high affinity.<sup>46</sup> Epitope binding is therefore encoded in higher-order complex dependencies (correlations between spatially distant AAs in the CDRH3 enabling the binding of conformational epitopes, allowing a higher combination of binding motifs) in the low dimensionality of the antibody sequence space. These strong dependencies reflect 3D binding, where residues that are distant along the sequence can be close in the folded 3D structure. Indeed, the majority of antibody epitopes are thought to be conformational<sup>47</sup> – although 85%

of epitopes contain one or several contiguous (linear) epitope stretches.<sup>45,48</sup> Therefore, to learn the rules of antibody-antigen binding, approaches need to be developed that untangle the non-linear sequence dependencies that govern the antibody, antigen, and antibody-antigen structures in both bound<sup>49,50</sup> and unbound<sup>51</sup> states.

**Interdependence of antibody design parameters:** Antibody design parameters can be broadly categorized into binding parameters (paratope, epitope, affinity) as well as developability parameters (e.g., plasma half-life, thermal stability, solubility, aggregation propensity, and immunogenicity). Traditionally, it was thought that antibody design categories may be optimized independently. However, recent reports suggest that, for example, the plasma half-life is not only a function of the antibody isotype and constant fragment crystallized (Fc) region, but also sequence variations in the CDRs.<sup>22–24</sup> Therefore, antibody design parameters are inter-dependent and thus require modular optimization and bioengineering techniques (Figure 1).

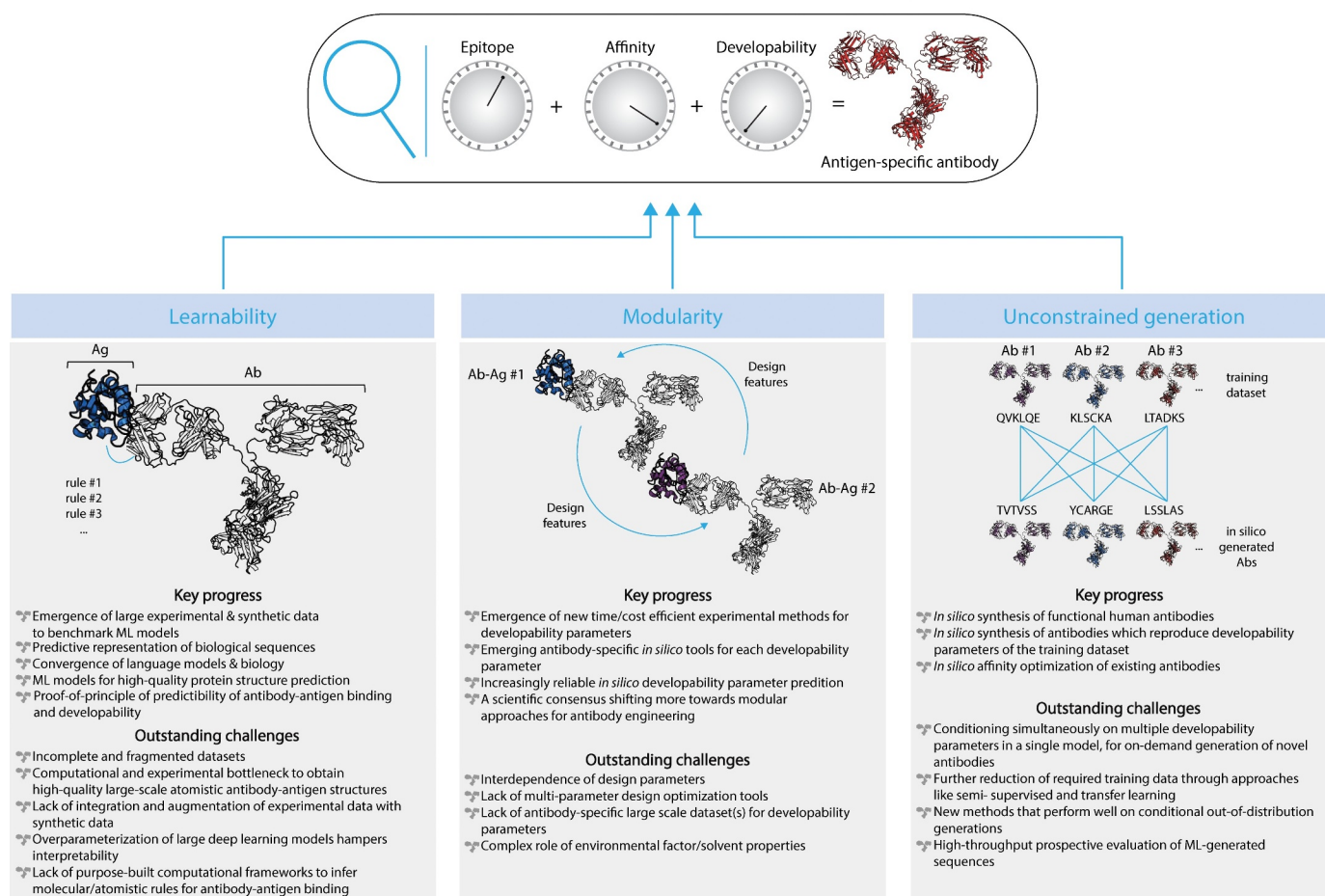
Taken together, nature succeeded in devising an extraordinary antibody repertoire that combines diversity, specificity, and modularity. Hence, leveraging data sources that combine these properties and developing computational models that can take advantage of multi-property optimization would be the key to define the fundamental principles that can guide tailored antibody design.

### 1.4. Augmenting scarce experimental data with simulated data that account for the biological complexity of antibody-antigen interaction

For the design and discovery of mAbs, available experimental datasets are particularly scarce in comparison to the biological complexity of antibody-antigen binding. To date, one of the largest developability studies on mAbs remains very restricted at 137 samples (Figure 2).<sup>52</sup> Similarly, 3D structures, which are useful in defining residues of the antibody (paratope) that engage the residues of the antigen (epitope) at the interaction interface, are limited to 1200 non-redundant antibody-(protein)antigen complexes.<sup>55</sup> Sequence data, however, can be produced at larger scales, higher efficiencies, and at markedly reduced costs, making it the leading choice to study antibody-antigen binding albeit at a reduced resolution where paratope-epitope information often is not available (Figure 2). At present, the Observed Antibody Space (OAS)<sup>57</sup> database contains over one billion antibody sequences curated from 79 studies, while the iReceptor database contains almost four billion sequences and 6013 repertoires from three remote repositories, 49 research labs, and 60 studies.<sup>53</sup> Such large sequence datasets have been used, for example, to generate latent representations of phenotypically similar antibodies,<sup>58,59</sup> prior to training ML models on small-scale structural datasets.

Recently, we presented our efforts to increase the amount of 3D-structure data by six orders of magnitude larger than the 1200 structures available experimentally (Figure 2)<sup>55</sup> via simulating virtual coarse-grained docking of billions of antibody-antigen pairs with several layers of biological complexity.<sup>54</sup> We complemented this data with *in silico* predicted developability parameters to create datasets that encompass the three aforementioned key design parameters: paratope-epitope binding,

## On-demand machine learning-based antibody design



**Figure 1.** Overview of progress and challenges within the three technological pillars for ML-based on-demand generation of mAb therapeutic candidates, namely learnability, modularity, and unconstrained generation. We highlight three key optimizable design parameters for *in silico* on-demand mAb design: (i) the AA residues at the surface of the antigen (epitope) that engage the antibody residues (paratope) at the interaction interface, (ii) the strength of an antibody–antigen interaction (affinity), and (iii) the extent to which the mAb successfully progresses from the discovery to the development phase (developability). We discuss these design parameters from the perspective of three technological pillars: (i) learnability indicates the presence of rules underlying antibody–antigen interactions as well as antibody developability, (ii) modularity signifies that antibody design parameters could be impacted by multiple regions on the antibody and the extent to which they can be recombined interdependently, and (iii) unconstrained generation signifies the capacity of high-throughput *in silico* synthesis of fit-for-purpose mAb candidates.

affinity, and developability.<sup>27</sup> Such efforts have begun to increase the number of datasets to a level where the benchmarking of data-intensive methods, such as deep learning to study antibody-antigen binding at the paratope-epitope level as well as deep learning-based antibody sequence generation, started to become feasible.<sup>27,54</sup> More generally, large-scale 3D-atomistic resolution data generation may represent the next major step where abundantly available antibody sequence data will be leveraged to obtain large quantities of antibody-antigen complexes via recent advances in computational structural biology methods such as antibody modeling,<sup>59–63</sup> molecular docking,<sup>64–67</sup> and molecular dynamics.<sup>68,69</sup>

## 2. Learnability of antibody–antigen binding

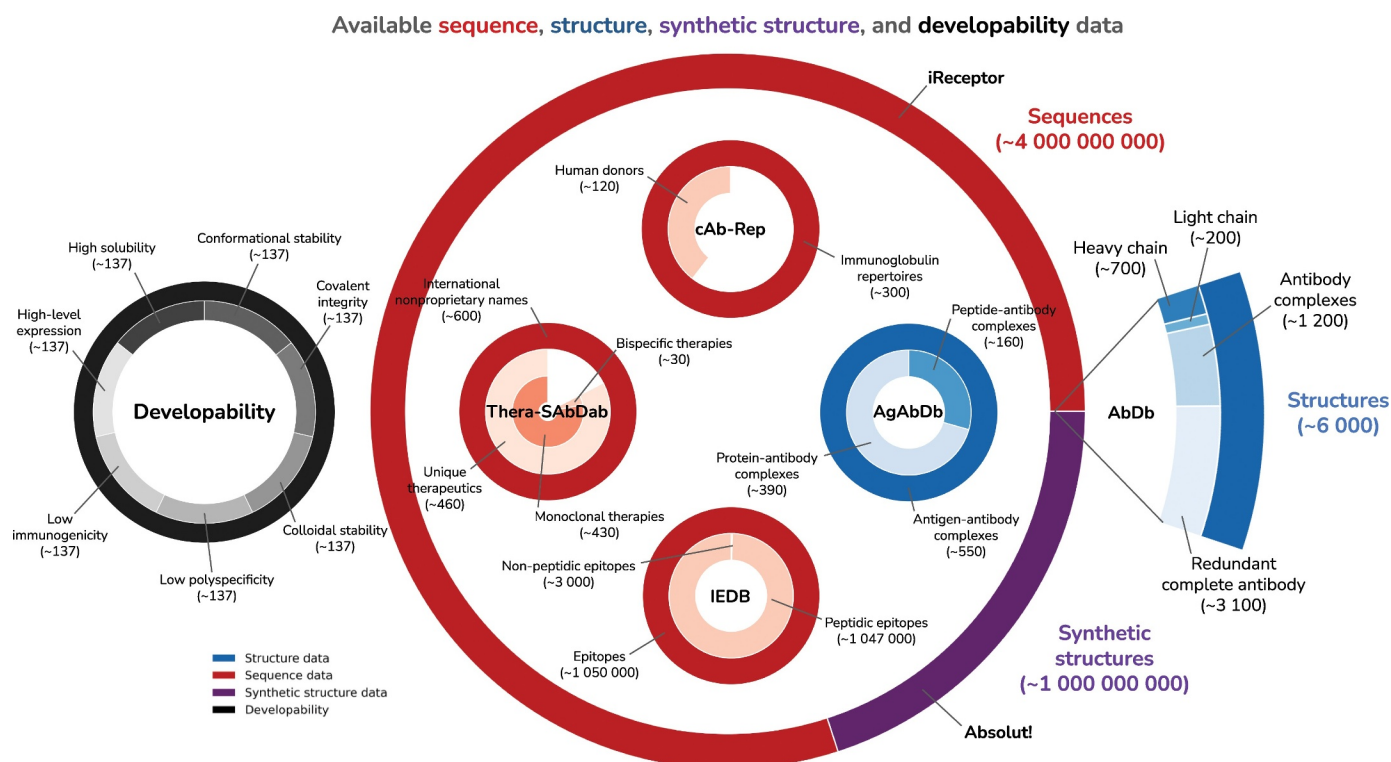
The hurdles of antibody–antigen binding prediction may be subdivided into five ML challenges. Figure 3 illustrates how these challenges are intertwined with each other in a typical ML workflow. We group these challenges as the ‘learnability’ problem, i.e., the capacity of an ML method for a certain type

of dataset and biological question to achieve generalization and provide surrogate rules responsible for its predictions from only a limited set of examples (the training dataset). We discuss herein aspects of learnability pertaining to antibody-antigen binding (affinity), while the following sections review aspects of learnability from the perspective of modularity, developability, and unconstrained sequence generation.

**ML challenge 1: Predictability.** The capacity to predict properties of antibody-antigen binding with high accuracy is the *sine qua non* prerequisite for computationally aided mAb discovery. The predictability of antibody-antigen binding is often obscured by the biological complexity and the limited information content of the considered datasets.

**ML challenge 2: Generalization.** Specifically, ML-based mAb discovery relies on the generalizability of the models, i.e., information learned from “dataset A” will be valid for predicting binding in “dataset B”, provided that the two datasets are “similar enough” (Figure 3). In general, antibody sequence similarity is not necessarily associated with phenotypic similarity since sequence-similar antibodies may bind





**Figure 2.** Overview of public datasets on antibody developability, experimental, or synthetic sequence and structural antibody(antigen) data. The available sequence and structural datasets were queried from Europe pubmed central (europepmc.org) using keywords “antibody” and “database” and filtered for publications that contain these keywords in the title in addition to manual literature curation (codes and data are available as mentioned in the *Code availability* section of this manuscript). The datasets are visualized with respect to the sequence or structure, and the availability of binding affinity, antigen annotation, developability parameters, or paratope and epitope information. Sequence (red), structure (blue), synthetic structural data (purple) and developability (grey) are color-coded. Each circle corresponds to a specific type of data. The outer circles correspond to the global data (sequences, structures, synthetic structures, and developability), and the inner ones – to the subdata (antibody-antigen complexes, Ig repertoire, mAbs, and paratope and epitope). A separate outer circle for developability is used as its data types differ from the others. Since there is not a single database containing quantitative information about the available developability parameters, we used the data from<sup>52</sup> as an example for visualizing the scarcity of available experimental developability information. The outer red ring represents the number of antibody sequences in the iReceptor database (the largest publicly available sequence data,<sup>53</sup> the outer purple ring the number of synthetic antibody–antigen binding structures from Absolut! (the largest publicly available synthetic antibody–antigen structural dataset),<sup>54</sup> the outer blue ring displays the number of structures from AbDb (curated antibody–antigen structural data<sup>55</sup> obtained from the protein data bank),<sup>56</sup> and the outer grey ring represents developability information.<sup>52</sup> Inner rings illustrate information about antibody-antigen complexes, Ig repertoire, therapeutic antibodies, and paratope and epitope data. For a curated overview of available databases, see Focus Box 1.

different antigens.<sup>86</sup> Therefore, the similarity of antibodies should be considered both in terms of sequence similarity and binding behavior (function). Of note, while transfer learning aims at performing a new task from subsets of a pre-trained model that is further trained for a certain task, generalization refers to performing the same task with the same model (without additional training) on different datasets.

**ML challenge 3: Interpretability.** When it comes to prospective antibody engineering as well as clinical practice, the most beneficial setting would be an interpretable ML model that proposes rules to explain the reasons underlying its generalization.<sup>4,59,87,88</sup> This would both decrease the risk of predicting dataset-dependent properties, and provide guidelines to generate new possible antibody sequences based on those rules. So far, rule inference via, for instance, attribution methods, remains a challenge and is poorly standardized.<sup>54,89</sup>

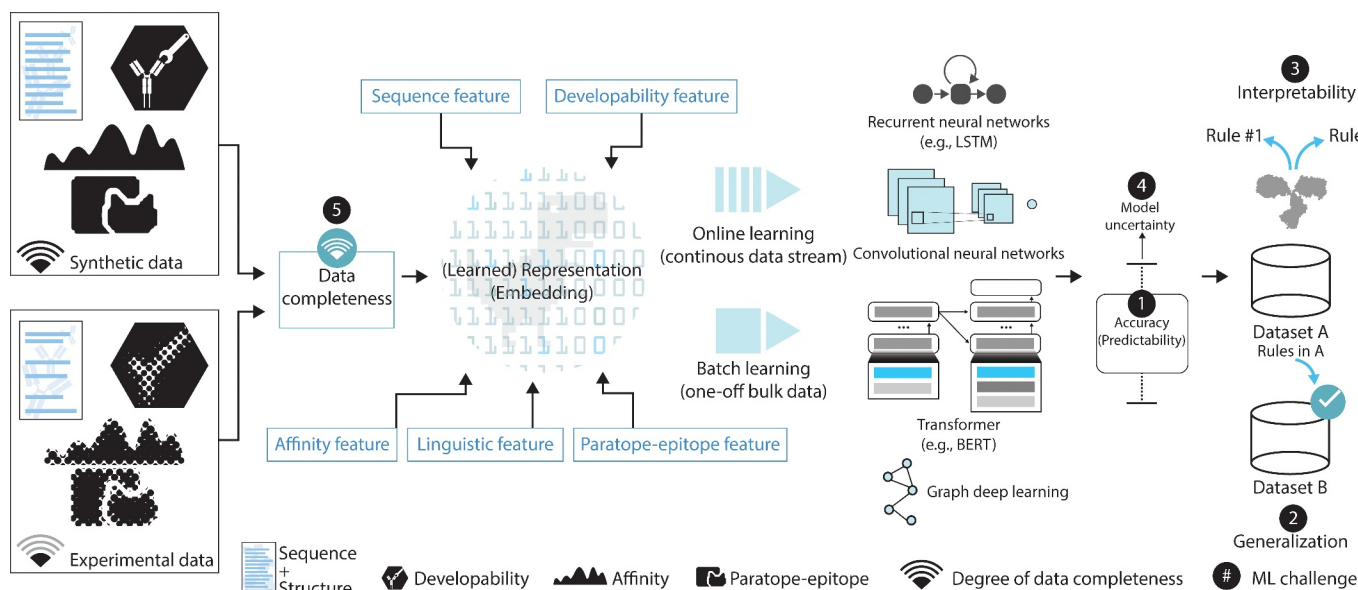
**ML challenge 4. Model (also called epistemic) uncertainty.<sup>90</sup>** This describes the situation where multiple models predict a dataset with equally high accuracy while relying on different sets of rules that might or might not be equivalent. For ML, as the training data is often noisy and sparse, exhaustive learning

of the “rules” is likely intractable. Instead, we argue that a successful learning model for antibody-antigen binding could converge to an approximate (surrogate) set of rules, such that its predictions are sufficiently accurate across multiple datasets, indicating that these rules have only retained minimal dataset bias.

**ML challenge 5: Dataset completeness.** Intuitively, the presence of instances in the dataset illustrating a certain rule is required to infer this rule. We refer to the “completeness” of a dataset as the amount of information it contains, in comparison to the information needed to infer the rules that we believe are underlying the properties of the dataset. Currently, it remains unclear how to determine if a dataset is complete to infer (surrogate) rules (see ML challenge 3). If the rules are explicit (for instance by learning a scoring function or using interpretable ML architectures), it can be easier to test the completeness of a dataset.<sup>91</sup> When the rules are not directly interpretable, it can become difficult to assess dataset completeness, except by practically testing the extent of the data coverage of the rules.<sup>92</sup> Therefore, interpretable ML methods are preferable for assessing dataset completeness.

## Focus Box 1 | Databases that curate antibody sequences or structures (see Figure 2)

- AB-Bind<sup>70</sup> (<https://github.com/sarahsirin/AB-Bind-Database>) is a dataset containing experimental results for wild-type and mutant antibodies and antigens, including the change in Gibbs free energy of binding ( $\Delta\Delta G$ ), linked to crystal structures of the parent complexes. Year of publication: 2016.
- ABCD<sup>71</sup> (<https://web.expasy.org/abcd/>) database is a manually curated depository of sequenced antibodies. Year of publication: 2019.
- AbDb<sup>55</sup> (<http://www.abbybank.org/abdb/>) is a compilation of antibodies (including nanobodies) extracted from the PDB<sup>56</sup> with standard numbering schemes applied and redundancy information. Year of publication: 2018.
- abYsis<sup>72</sup> (<http://www.abysis.org/abysis/>) is a web-based antibody research system that includes an integrated database of antibody sequence and structure data. Year of publication: 2017.
- AgAbDb<sup>73</sup> (<http://196.1.114.46:8080/agabdb2/home.jsp>) is a derived knowledge base archive of molecular interactions of protein and peptide antigens characterized by co-crystal structures. Year of publication: 2014.
- bNAb<sup>74</sup> (<http://bnaber.org/>) is a database of HIV broadly neutralizing antibodies providing neutralization profiles, sequences and three-dimensional structures. Year of publication: 2013.
- cAb-Rep<sup>75</sup> (<https://cab-rep.c2b2.columbia.edu/>) is a database of curated human B cell immunoglobulin sequence repertoires. Year of publication: 2019.
- CoV-AbDab<sup>76</sup> (<http://opig.stats.ox.ac.uk/webapps/covabdb/>) is a database of published or patented binding antibodies and nanobodies to coronaviruses, including SARS-CoV2, SARS-CoV1, and MERS-CoV. Year of publication: 2021.
- IEDB<sup>77</sup> (<https://www.iedb.org/>) is a resource of experimental data on humans, non-human primates, and other animal species antibody and T cell epitopes. Year of publication: 2018.
- IMGT<sup>78</sup> (<http://www.imgt.org/>) is a sequence, genome and structure knowledge resource specialized in the immunoglobulins, T cell receptors, MHC, and in the immunoglobulin and MH superfamilies, and related proteins of the immune system of vertebrates and invertebrates. Year of publication: 2018.
- OAS<sup>57</sup> (<http://opig.stats.ox.ac.uk/webapps/oas/>) is a database of annotated immune repertoires. Year of publication: 2018.
- PROXIMATE<sup>79</sup> (<https://www.iitm.ac.in/bioinfo/PROXIMATE/>) is a database of interaction kinetics and thermodynamics data (including wild-type vs mutant  $K_D$  and  $\Delta\Delta G$ ) for mutations in protein-protein complexes including antibody-antigen complexes, collected from literature and previously published databases. Year of publication: 2017.
- SABDab<sup>80</sup> (<http://opig.stats.ox.ac.uk/webapps/sabdab/>) is a database containing annotated antibody and nanobody structures available in the PDB.<sup>56</sup> SABDab also contains affinity data for antibody-antigen complexes, taken from the PDBbind database.<sup>81</sup> Year of publication: 2013.
- sdAb-DB<sup>82</sup> (<http://www.sdab-db.ca/>) is a dedicated single-domain antibody repository and database. Year of publication: 2018.
- SKEMPI 2.0<sup>83</sup> (<https://life.bsc.es/pid/skempi2/>) is a database contains kinetics and energetics data upon mutation, for protein-protein interactions including antibody-antigen complexes of which structure are available in the PDB.<sup>84</sup> Year of publication: 2019.
- Thera-SABDab<sup>85</sup> (<http://opig.stats.ox.ac.uk/webapps/newsabdab/therasabdab/search/>) is a database curating WHO recognized antibody-related therapeutics. Year of publication: 2020.



**Figure 3.** Major ML components that could enable the identification of the rules that govern antibody design parameters (binding, paratope-epitope, and developability). These components relate to the five ML challenges namely (1) predictability, (2) generalization, (3) interpretability, (4) model uncertainty, and (5) data completeness. Multiplexing (integration and augmentation) of data with varying degrees of information may improve the completeness of the training data which would consequently produce an informed representation (learned or otherwise) and allows for data-driven mAb design. As synthetic data tend to be superior (crisp icons) in comparison to experimental data (fuzzy icons) with respect to quantity and the extent of completeness (the parameters and rules underlying the data are known), the augmentation of sparse experimental data with synthetic data may yield a dataset that contains a fuller degree of completeness than either subset thereof. The training of advanced deep learning architectures on informed representation (containing sequence, developability, affinity, linguistic [Focus Box 2], and paratope-epitope feature) either via online (continuous) or batch (one-off bulk data) learning would result in high accuracy models that may well be capable of generalization. Importantly, the mapping of features that are critical for the predictive performance of the model (interpretability) must be undertaken to allow for rule inference, and consequently, to allow rule-driven design.

## Focus Box 2 | A formal language perspective of learnability applied to antibody discovery problems

Multiple articles relate linguistics to the study of proteins by applying neural network (NN) language models to protein sequences.<sup>58,93–100</sup> Another fruitful way to relate linguistics and biological research is to translate formal perspectives from linguistic research into biological research questions, such as computational learning theory. It provides a precise way to define learnability,<sup>101</sup> and it has been used for computationally defining natural language learning.<sup>102</sup> Below, we adapt learning theory to antibody discovery problems: we formalize antibody discovery questions as formal language learning questions and discuss aspects of learnability as they pertain to antibody discovery.

A language is a formal system that consists of a potentially infinite set of structures, built from a finite set of elements (the alphabet) with a finite set of rules (a grammar).<sup>103</sup> In the context of antibody discovery, the language to be learned depends on the research question. If the goal is to predict if input antibodies bind to a given antigen (a binary classification problem),<sup>54</sup> then the language is the set of encoded representations of antibody structures that bind to the antigen, and the learner's task is to discriminate between the structures that are part of the language and ones that are not. If the goal is to predict the set of antigens that bind to input antibodies (a multiclass classification problem),<sup>54</sup> the language consists of antigen–antibody pairs that exhibit high affinity. A learner in this case has to be able to recognize these pairs. For both types of research questions, the target grammar to be learned are the physicochemical rules that govern antibody structures and antibody–antigen interactions.

When learning a language, the learner maps from an observable subset of all possible data (examples) to a grammar that describes the language.<sup>102</sup> The learner can be either a black box learner that can answer whether an input belongs in a language (or give a probability for it) without showing the grammar it operates on, or an interpretable one that returns the full grammar it learned. It is possible, though often difficult, to extract the grammar from black-box learners. We argue that for successful antibody discovery, it is crucial to have access to the rules, and have an interpretable model. A fully interpretable model enables more informed antibody discovery because it clarifies which properties might be entirely dataset dependent versus which properties might be generalizable across datasets.

Another question raised by learning theory is the definition of successful learning. The criteria for successful learning can range from exact convergence to some defined value of approximate convergence. Exact convergence requires the inferred grammar to be identical to the target grammar of antibody discovery problems, while approximate convergence means that the inferred grammar is not completely identical, but “close enough” to the target grammar.<sup>102</sup> Approximate convergence is easier to achieve and is thus a more practical criterion for successful learning. This is especially appropriate for antibody discovery problems, where the target grammar is a set of highly complex and largely unknown physicochemical rules, and currently, available data is too limited and noisy for exact convergence to be feasible. Moreover, it is difficult to assess how approximate any inferred ruleset is to the target. It can therefore be useful to use synthetic data to study the performance of a given ML algorithm first, as synthetic data are generated with explicit rules.<sup>54,104,105</sup>

Lastly, there is a possibility that the data presented to a learner is not complete. A complete dataset contains every kind of structure from the target language that would be sufficient for the learner to converge successfully to the target grammar, while incomplete datasets might lead to alternative grammars that only account for a subset of the examples but not all.<sup>102</sup> If the dataset is not complete, the learner might reach high prediction accuracy for dataset-specific properties rather than converging to the more fundamental grammar that describes general binding specificity. The completeness of the dataset is only loosely related to its size: a very large dataset can still be incomplete if it lacks crucial data points for inferring the target grammar, and a complete dataset can be relatively small as long as it has everything necessary for successful learning. It is therefore important to aim for completeness rather than merely size in the dataset in order to achieve successful learning.

In conclusion, formalizing antibody–antigen binding questions as formal language learning questions helps clarify various aspects of learnability. It particularly draws attention to the nature of the learner, defining the standard for successful learning, and the completeness of the dataset.

These ML challenges stem from the theoretical foundations of computational learning theory, which has been applied to natural language (linguistics). Focus Box 2 provides further discussion of the theoretical background and the parallels with linguistics.

Altogether, learnability and availability of suitable data ensure high prediction accuracy on new tasks.

## 2.1. Formalization of antibody–antigen binding problems

Three main types of prediction problems have been investigated using ML in antibody–antigen binding: 1) prediction of the antibody–antigen binding interface (paratope, epitope or paratope–epitope prediction), 2) prediction of binding affinity (in particular following AA substitution), and 3) prediction of binding partners (binary and/or many-to-many).<sup>54</sup> In view of the above ML challenges, we delineate to which extent these studies have achieved the first proof of principle steps of antibody–antigen learnability. We focus on the type and size of datasets they use and how antibody–antigen sequence or structural data are embedded into data representations.

## 2.2. Epitope prediction

Epitope prediction may be divided into two different application areas. Antibody-agnostic epitope prediction seeks to identify the most probable epitopes without prior knowledge of the corresponding antibody(ies), and antibody-aware epitope prediction seeks to identify the epitope to which a known antibody will bind.

### 2.2.1. Antibody-agnostic epitope prediction

Early epitope prediction methods infer contiguous epitope residues based on a few hundred linear epitopes via propensity scales (e.g., PREDITOP,<sup>106</sup> BEPITOPE,<sup>107</sup> BcePred,<sup>108</sup> see,<sup>109,110</sup> for more details). ABCPred used a Jordan network (a version of RNN) to perform binary classification on segments of the antigen via sliding windows.<sup>111</sup> Another ensemble method, iBCE-EL, used physicochemical properties, AA composition, and combined extremely randomized tree (ERT) and gradient boosting (GB) to predict linear epitope with higher accuracies.<sup>112</sup> However, the vast majority of described epitopes are conformational,<sup>113</sup> hence, linear epitopes may not account for non-flanking residues as they may only represent contiguous subsequences of the full epitopes.

Other prediction tools used support-vector machines (SVM) to classify each antigen residue as epitope or non-epitope residue (Söllner and Mayer<sup>114</sup> BCPred,<sup>115</sup> BEST,<sup>116</sup> EPSVR,<sup>117</sup> Chen et al.<sup>118</sup>). These tools combined physicochemical properties with sequence conservation, similarity to other known epitopes, predicted 2D structural features, or even structural properties of similar known sequences. SePre<sup>119</sup> first predicts individual immunogenic residues then clusters them as an epitope in a second step. These methods reported high prediction accuracy, indicating that sequence information only allowed the prediction of non-contiguous epitopes. The inclusion of sequence conservation makes it challenging to understand which information in the (explicit) training dataset versus (implicit) alignment was important for high prediction accuracy.

In parallel, structure-based discontinuous epitope prediction methods have been trained on antibody-antigen structures and then tested on the antigen structures alone (i.e., antibody agnostic) to predict the epitopes, using AA propensity scales as above but adding geometric predictors such as the number of neighbors according to different distance thresholds, triangle-based propensity measures, or ellipsoids (SEPPA,<sup>120</sup> Discotope,<sup>121</sup> PEPITO/BEpro,<sup>122</sup> ElliPro<sup>123</sup>) and reported ~0.75 AUC on 75 antibody-antigen structures. Moreover, Lu et al.<sup>124</sup> combined a graph convolution network to leverage local spatial neighborhood information with an attention-based long short-term memory-recurrent neural network (LSTM-RNN). They examined whether spatially distant information on the antigen sequence can improve prediction accuracy and reported an AUC of ~0.8.

Nevertheless, we argue that antibody-agnostic epitope prediction is an ill-defined problem<sup>125,126</sup> because only in the context of an antibody (a paratope) does an epitope become functional and vice versa. Indeed, it is now a general consensus that nearly any surface accessible region of an antigen may be recognized by an antibody.<sup>127</sup> In addition, epitopic and other surface residues were found to be mostly indistinguishable in their amino-acid composition.<sup>128</sup>

### 2.2.2. Antibody-aware epitope prediction

Bepar<sup>129</sup> utilizes correlations of AAs usage on sliding windows between the antigen and the CDR loops of the antibody in antibody-antigen complexes to predict epitope residues from the antibody and antigen sequences only.

Several structure-based studies attempted to improve the quality of antibody-antigen docking by including geometrical features on both antibody and antigen to re-rank the list of predicted possible poses. For instance, EpiPred<sup>130</sup> measures the conformational matching of an input pair of antibody and antigen structures. DLAB-Re<sup>131</sup> models the antibody structure from its sequence,<sup>132</sup> generates docking to the antigen structure and uses a convolutional neural network (CNN) to predict the paratope-epitope complementarity of a pose as a re-ranking score, therefore predicting both epitope and paratope.

PEASE<sup>133,134</sup> takes the antibody and antigen structures, calculates a solvent accessibility score per residue, predicts the pairs of interacting epitope-paratope residues using random forest, followed by patch reconstruction in order to reconstruct the epitope. Another study<sup>20</sup> has defined antibody and antigen surface patches using a Monte Carlo method that includes or excludes neighboring residues with a probability defined from features initially learned from antibody-antigen complexes. From the observation that matching paratope and epitope patches share correlated features in shape or AA composition, a deep feed-forward network was built to predict whether a paratope patch would bind an epitope patch. PECAN<sup>135</sup> used CNNs with an attention layer directly from the antibody and antigen structures to predict the binding interfaces of antibody and antigen structures. We discuss DLAB<sup>131</sup> and PECAN<sup>135</sup> in detail in the paratope prediction section below.

Altogether, these studies have shown that, at present, *in silico* epitope prediction tools yield moderately accurate predictions and that structural information of the antibody or the paratope is critical to improving epitope prediction performance.

## 2.3. Paratope prediction

Although paratope prediction may look like the symmetric reverse problem of epitope prediction, paratope residues are both sequentially and spatially close to each other as they are most often contained within the CDR loops,<sup>45</sup> in contrast to epitope residues that can be spatially close but sequentially distant over the span of the antigen length.<sup>45</sup> Further, the AA usage of paratopes is distinct to those of epitopes<sup>45</sup> as each CDR has its own preferential AA usage, and the subset of epitope residues bound by a CDR also have a preferential AA usage specific to which CDR it was bound to.<sup>128</sup>

### 2.3.1. Sequence-based antigen-agnostic paratope prediction

Parapred<sup>136</sup> uses either an LSTM-RNN-based or a deep NN-based architecture on top of a CNN to predict the 1D paratope, starting from the antibody sequence alone. In this process, only the antibody CDRs are considered and one-hot encoding is combined with biochemical encoding for each residue. proABC<sup>137</sup> outperformed Parapred using a random forest model with additional features on the full antibody sequence to predict 1D epitope. Briefly, along with the one-hot encoding of the full variable heavy (VH) and variable light (VL) chains, proABC includes information on the species of origin, the inferred germline VH and VL families, the predicted canonical structure associated with each CDR sequence, and predicts the binding status of each of the residues. In a refined version proABC-2,<sup>138</sup> a CNN architecture has been implemented as a replacement to the random forest, following the same data processing and problem formulation as pro-ABC. The authors showed that the output of proABC-2 (for instance, including the predicted types of interactions) can be used as additional constraints when later performing docking of the antibody to the antigen.

Paratope prediction tools have also been leveraged to identify novel binders that originate from different clonotypes. In immune repertoire mining, for example, known binders are typically used to identify new binders via clonotyping<sup>34,139</sup> (i.e., finding sequences with close genetic history). By design, this approach limits the diversity of the identified binders. In contrast, an approach called paratyping aimed at identifying convergent binders from different clonotypes by using the predicted paratope to cluster antigen-specific antibodies that originate from diverse clonotypes.<sup>140</sup> Re-epitoping, on the other hand, used ML to predict AA substitutions that would improve the complementarity of the resulting paratope to the epitope of interest.<sup>141</sup> Another application is the mapping of sequence features, or combinations of subsets thereof, to discern phenotypic traits such as inhibitors or non-inhibitors.<sup>142</sup>



### 2.3.2. Structure-based antigen-agnostic paratope prediction

Paratome web server<sup>143</sup> uses structural alignment to identify consensus antigen-binding regions on a given antibody sequence or structure. The server uses the structural consensus regions from multiple structure alignment of a reference set of antibody-antigen complexes to identify binding regions of antibodies.

AntibodyInterfacePrediction combined 3D Zernike Descriptors (3DZDs) and SVM to predict antibody-antigen interface.<sup>144</sup> It firstly obtains geometrical representation, physico-chemical and biological characteristics of the residues on the antibody surface starting from an input of the antibody 3D structure. A rotationally invariant local descriptor is calculated for each uniform spherical patch sampled from the antibody surface. On the 3DZDs, randomized logistic regression was used to decrease the overall number of features. SVMs were employed as a classifier to distinguish the paratope interface LSPs from the non-interface ones. As a result, AntibodyInterfacePrediction outperformed Parapred,<sup>136</sup> Paratome,<sup>143</sup> and Antibody i-Patch.<sup>145</sup> However, Parapred remains competitive against AntibodyInterfacePrediction as it does not require structural data.

As discussed in antibody-agnostic epitope prediction earlier, we reaffirm our assessment that paratope prediction without the context from the epitope may not be very insightful.

### 2.3.3. Sequence-based antigen-aware paratope prediction

The subsequent update of Parapred, called AG-Fast-Parapred<sup>21</sup> makes use of the six CDR sequences and the sequence of the cognate bound antigen, with each AA encoded separately with their AA and seven chemical features as descriptors, and returns a binary vector of the binding status of each position in the CDR3 (linear paratope prediction) to train an architecture combining an “à trous” CNN with an attention layer. They compared antibody-only prediction (i.e., antigen-agnostic) against prediction including antigen information using cross-modal attention. The new architecture moderately improved the accuracy (AUC = 0.90) compared to Parapred (AUC = 0.88).<sup>21</sup>

Lu et al.<sup>124</sup> proposed a sequence-based paratope prediction tool from the antigen sequence by separately predicting the probability of each antibody residue to be a paratope residue (binary classifications). The antigen and antibody sequences were transformed into 80 predicted structural features, including evolutionary information, secondary structure prediction,<sup>146</sup> solvent accessibility, and backbone dihedral angles with NetSurfP2.0.<sup>147</sup> Antibody and antigen information is then processed by two parallel attention-LSTM-RNN architecture, while a CNN leverages local information on the antibody side, and fully connected layers transform the CNN and LSTM-RNN outputs into binary prediction per antibody residue. Their method showed moderate improvement in accuracy by including the partner antigen sequence, as observed in AG-Fast-Parapred.

### 2.3.4. Structure-based antigen-aware paratope prediction

Antibody i-Patch, relies on the structures of antibody and antigen as input to predict the paratope.<sup>145</sup> Antibody i-Patch, annotates each residue with a binding likelihood score rather than providing an entire binding region as Paratome, and

outperformed Paratome in precision. In addition, the usage of Antibody i-Patch prediction with the fast docking algorithm, ZDOCK,<sup>148</sup> increased the number of near-native poses.

Furthermore, Paratope and Epitope prediction with graph Convolution Attention Network (PECAN) is a deep learning framework that predicts the binding interfaces of antibody-antigen-antibody complexes.<sup>135</sup> The local spatial connections of the interfaces were captured using graph convolutions while an attention layer connects distant information, and transfer learning was performed using a base network trained on generic protein-protein interactions. PECAN outperformed EpiPred<sup>130</sup> and DiscoTope<sup>121</sup> in epitope prediction and AntibodyInterfacePrediction<sup>144</sup> in paratope prediction. The attention layer showed only a little improvement in paratope prediction performance over convolution, probably because paratopes are mostly located around CDRs, while it improved epitope prediction significantly. From the observation that PECAN sometimes predicts spatially too distant epitope residues, a new strategy termed Contiguous Epitope – Sub-sampled Convolution Attention Network (CE-SCAN<sup>149</sup>) was proposed. CE-SCAN succeeded in predicting localized epitopes, while leveraging long-distance information from multiple patches and sequentially distant residues, and provided a small increase in prediction accuracy compared to PECAN.

Schneider et al.<sup>131</sup> modeled 3D antibody structures from their sequence using ABodyBuilder<sup>60</sup> and performed docking using ZDOCK<sup>150</sup> on their known cognate antigen structure. Interestingly, docking the modeled structure was a harder task in comparison to using the known bound antibody structure, and the authors developed a CNN-based strategy (DLAB-Re) to re-rank the docking poses proposed from ZDOCK to prioritize those with the correct epitope. DLAB-Re takes as input a proposed antibody-antigen docking pose, transforms the binding interface in voxels, and learns a ‘compatibility score’ based on the 3D distribution of the AAs along the voxels.

Vecchio et al.<sup>151</sup> used epitope-paratope message passing (EPMP) for paratope-epitope prediction. Considering that epitope residues are distant and antigen-dependent, the architecture combines a paratope model (Para-EPMP), sequentially processing antibody input features and followed by a graph structure, and an epitope model (Epi-EPMP), where only structural features are used with GNN layers and substantially merged with contextual cues from the cognate antibody.

More recently, geometric deep learning (GDL) has emerged as one of the most promising advances to generate a molecular representation for the prediction of interacting interfaces (e.g., antibody-antigen interface).<sup>152,153</sup> The method extends neural networks to allow for the incorporation of geometric priors (structure and symmetry) of the input in order to improve the quality of the signal captured by the model. GDL has been used for instance in developing molecular surface interaction fingerprints (MaSIF).<sup>154</sup> MaSIF was mostly trained on non-immune protein-protein interaction including antibody-antigen data. The authors note that geometric models, such as MaSIF, are able to capture geometric matching across protein-protein interfaces that may extrapolate to paratope-epitope interfaces pending further validation. Hence, it would be of interest to benchmark MaSIF against antibody-antigen binding prediction tools as the model is increasingly being

used to study antibody–antigen interface.<sup>155</sup> Briefly, MaSIF starts with a mesh representation of a protein surface where each point on the surface is annotated with both geometric and chemical features that capture degrees of curvature, concavity, electrostatic potential, hydrophobicity, and hydrogen potential. Subsequently, a set of geodesic filters generate a one-dimensional embedding of the protein surface. MaSIF was used to classify interacting versus non-interacting residues with satisfactory performance. A GDL model with a simpler surface representation for large-scale learning has also recently been made available.<sup>156</sup> However, GDL, or any other deep learning-based tool, has yet to be configured to account for the dynamics of the interaction at the interfaces. In particular, antibodies sample multiple conformations even at the unbound stage,<sup>157</sup> and bound antibody structures differs from their corresponding unbound structures.<sup>49,158</sup> Incorporating the dynamics and conformational changes upon binding at the interfaces between two molecules remains one of the major challenges in protein design in general, as well as in the design of antigen-specific antibodies.<sup>159</sup>

#### 2.4. From single paratope-epitope pair to many-to-many binding partner prediction

In addition to paratope or epitope prediction of already known binding pairs, learning the rules for paratope-epitope matching, and generating all possible binding partners of an antibody or antigen represents a difficult challenge. Leveraging antibody-antigen complexes in the database AbDb, graph theory, and deep learning, we<sup>45</sup> discovered a set of antibody-antigen structural interaction motifs that demonstrates the potential predictability of antibody–antigen interaction in general, and the prediction of paratope-epitope pairs more specifically. Indeed, these interaction motifs were shared across unrelated antibody-antigen complexes (but were largely distinct from non-immune protein–protein interaction motifs), suggesting the existence of a general interaction vocabulary of antibody–antigen interfaces that may help, in the future, learn antibody–antigen interaction rules. However, the lack of large structure and affinity datasets for antibody-antigen hinders the exhaustive benchmarking of deep learning-based many-to-many binding and affinity prediction.

By generating large-scale synthetic antibody-antigen structural datasets,<sup>54</sup> we investigated the relative influence of structural and sequence-based features on the accuracy of paratope-epitope prediction (i.e., predicting a compatible epitope of an epitope). Both an encoder-decoder with attention, and the transformer architectures yielded accuracies of  $\approx 90\%$  at generating the cognate epitopes using at least 2000 to 10,000 unique encoded paratope-epitope training pairs. In contrast, sequence information alone led to unsatisfactory accuracy even with 200,000 distinct paratope-epitope pairs in the training dataset. Interestingly, the binding degree of paratope and epitope residues (number of binding residues on the other protein) was the structural feature that contributed most to increase prediction accuracy.

Ab-Ligity<sup>158</sup> uses the ABodyBuilder tool<sup>160</sup> to reconstruct the paratope structure of the full antigen-binding fragment (Fab) region (based on CDR sequences and homology modeling) and to cluster the antibody sequences that would bind the same

epitope. This is done by hashed encoding of the physicochemical property of the binding (paratope-epitope) pairs of residues and their distance binned per groups of 1.0 Å. A binding similarity site is then calculated from the encoded paratope-epitope interaction code. As such, it was possible to identify dissimilar antibody sequences that would bind the same epitope, a task that is usually very challenging. With a conceptually similar goal, Ripoll et al.<sup>160</sup> computationally constructed 3D-models of epitope-specific antibody sequences to train image-based deep neural networks for antibody-epitope classification showing a potential route towards applying image recognition techniques to sequence-based datasets for antigen specificity discovery.

DLAB-VS (Virtual Screening) transforms paratope or epitope prediction into binding prediction<sup>131</sup> by virtual screening of a docked antibody-antigen pair and using a CNN to predict their compatibility. The CNN was trained on the best poses of known cognate antibody-antigen pairs as the positive class, while two types of negative pairs were selected: docking of non-cognate pairs, and the lowest range (FNAT < 0.1) of docked poses for a binding pair.

Xu et al.<sup>161</sup> used a structure-based clustering of CDRH3 sequences to cluster supposedly phenotypically similar sequences and based on this created a group of sequences that bind the same epitope on human immunodeficiency virus (HIV) or influenza virus. They predicted whether sequences bind the same epitope with SVM.

Altogether, the different strategies for paratope and epitope prediction have shown that antibody-antigen binding is predictable and ML may be able to learn complex rules that govern antibody–antigen interaction. In light of the main learnability challenges, we would argue that prediction accuracy is not the only goal of concern. A major open question is the robustness of the prediction accuracies against information that was either absent from the data (for instance cross-reactive antibodies or antigens), or that has leaked between test and training datasets (i.e., the separation of sequence-similar or homologous sequences between both datasets).<sup>54,162</sup>

#### 2.5. Learnability of sequence-induced affinity change

The prediction of the binding affinity of antibody sequences toward antigens (binding prediction) is among the major applications of deep learning in antibody research. Affinity is the strength of the interactions between an antibody and an antigen. It is typically governed by proximity, contact surface area, and the distribution of charged, polar, and hydrophobic groups. When an associated antibody-antigen complex is favored, the antibody is categorized as high affinity.<sup>163</sup> Thus, in the sequence to affinity setting, a deep learning model maps the sequence space to the affinity space.

Experimentally, the affinity of an antibody toward a target antigen is measured as the change in free energy of binding ( $\Delta G$ ) and can be determined by techniques such as surface plasmon resonance (SPR), amplified luminescence homogeneous assay (AlphaScreen), enzyme-linked immunosorbent assay (ELISA), phage display ELISA (phage ELISA), yeast surface display flow cytometry, isothermal titration calorimetry (ITC), biolayer interferometry (BLI) and enzymatic

assays.<sup>70,86,164</sup> Alternatively, when the structure of an antibody in complex with an antigen is resolved, the free energy of binding can be inferred with knowledge-based scoring functions (statistical potential) or molecular mechanics force fields,<sup>165,166</sup> which are frequently used in molecular docking and molecular dynamics studies.<sup>167</sup>

Guest et al.<sup>49</sup> built a docking benchmark dataset comprising antibody-antigen complex structures (single domain or multiple domain antibodies) for which the unbound antibody and antigen structures were also known ( $N = 67$  antibody-antigen pairs). The dataset allows the testing of the performance of docking strategies to predict the docking pose or binding affinity to the target antigen knowing only their unbound conformation. They showed a high discrepancy in docking methods' capacity to predict the correct docking pose and a wide variety of correlations between 20 affinity prediction tools and the experimental  $\Delta G$  of antibody-antigen binding. These observations underline the challenge in the prediction of the affinity, the binding pose, and consequently the interacting interface (paratope-epitope) of an antibody binding to its cognate antigen.

Lippow et al.<sup>168</sup> proposed a computational design alternative to directed evolution for affinity maturation by studying the effect of CDR single AA substitutions on electrostatic-binding contributions. Briefly, using a classical physics-based energy function combined with a hierarchical search indexing, single AA substitutions were performed to replace each of the CDR positions with the 20 common side chains, excluding proline and cysteine. Combining multiple AA substitutions led to a 10-fold affinity improvement to an anti-epidermal growth factor receptor IgG1 antibody (cetuximab), and similarly, a 140-fold improvement in affinity was observed for an anti-lysozyme IgG1 antibody.<sup>168</sup>

If antibody-antigen interaction is predictable, it must follow that affinity could also be predicted by leveraging the combination of sequence and structural data. Indeed, Kurumida et al.<sup>164</sup> used single AA substitutions from SiPMAB dataset<sup>169</sup> to train an ensemble of ML-based predictors for affinity prediction and reported notable improvements over molecular mechanics-based affinity scoring function. Pires and Ascher<sup>170</sup> built the mCSM-AB webserver to predict the effect of AA substitutions, trained on structural signature and pharmacophore count differences between wild-type and mutant residue, together with experimental affinity difference from the AB-Bind dataset.<sup>70</sup> mCSM-AB2<sup>171</sup> was trained on an expanded dataset including mutant variants with binding affinities obtained from the AB-Bind, PROXiMATE,<sup>79</sup> and SKEMPI 2.0<sup>83</sup> databases. mCSM-AB2 uses graph-based signatures (pharmacophore and distance pattern) for the wild-type residue, structural-based signatures (distance changes, interatomic interactions, solvent-accessible area), evolutionary score and potential energy difference calculated using FoldX.<sup>172</sup> mCSM-AB2 achieved a higher Pearson's correlation coefficient than the previous version, between predicted and experimental  $\Delta\Delta G$ . mmCSM-AB<sup>173</sup> analyzes the effect of multi-point mutations on antigen-binding affinity, using graph-, sequence- and structure-based signatures. Topology-based network tree (TopNetTree) was developed to predict changes in protein-protein interaction

(PPI) affinity upon engineering,<sup>174</sup> and was built by combining the CNN with gradient-boosting trees (GBT). The TopNetTree model outperformed TopGBT (topology-based GBT), TopCNN (topology-based CNN) models, and previously published methods on the AB-Bind dataset and SKEMPI database. A similar method, GeoPPI<sup>175</sup> consists of two components, a graph neural network trained on topology features from protein structure via self-supervised learning and a gradient-boosting tree (GBT) trained on learned features of both wild-type residue and its mutant to predict  $\Delta\Delta G$  upon AA replacement.

## 2.6. High-throughput experimental methods to generate data for the prediction of antibody-antigen binding using ML

Sequence data, as opposed to 3D structures, can be produced at larger scales, higher efficiencies, and at markedly reduced costs making it the leading choice to study antibody-antigen binding. Typically, the utility of sequence data for studying antibody-antigen binding is restricted to the prediction of binders and non-binders, as it does not afford a sufficient resolution to recover paratope-epitope information. Deep mutational scanning, for instance, can be paired with screening tools, such as ELISA or SPR-based platforms, to obtain large collections of binding and non-binding sequences for an antigen of interest. For example, Mason et al.<sup>86</sup> combined deep mutational scanning, ELISA, and CNN to discover new antibody candidates. Specifically, they used CRISPR-Cas9-mediated homology-directed repair mutagenesis to create  $10^4$  antibody variants, which were subsequently screened for binding against human epidermal growth factor receptor 2 (HER-2). The resulting binders and non-binders were used to train a deep learning model, which was subsequently used to screen a much larger ( $10^8$ ) *in silico* library, inaccessible to experimental exploration, of antibody variants for HER-2 binders.

Sequencing technologies that study, at high-throughput, many antibodies against many antigens (a logical step forward to the many antibodies against a single antigen as described in Mason et al.<sup>86</sup>) have begun to emerge as well. Setliff et al.<sup>176</sup> developed *Linking B-cell receptor to antigen specificity through sequencing* (LIBRA-seq) and demonstrated the utility of LIBRA-seq in high throughput screening of antibodies ( $10^3$ ) against nine antigens (five HIV envelope proteins and four influenza hemagglutinins) and its efficacy to discover broadly neutralizing antibodies. Briefly, the methods use DNA-barcoded antigens to tag B cells which are then subsequently single-cell sequenced to recover the B-cell receptor (BCR) transcripts and the antigen barcodes, and thus providing a direct readout of BCR-antigen binding. Importantly, the LIBRA-seq score was shown to correlate well with the observations from ELISA making it a useful metric to partition the resulting data as binder and non-binders for subsequent ML training and exploration. LIBRA-seq has also been used to delineate cross-reactive antibodies against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) with distinct epitopes and Fc effector functions<sup>177</sup> as well as rapid profiling of SARS-CoV-2 specific memory B cells.<sup>178</sup>



The selection of many antibodies (or variants thereof) against many antigens (or variants thereof) in parallel has been coupled to a display-based library on library (L-o-L) screening platforms. While L-o-L screening represents a key technology for the large-scale symmetric antibody-antigen binding generation, progress in that direction has been slow. Briefly, Hu et al.<sup>179</sup> screened a phage-based human antibody library against an active mutant library of Mac-1 inserted domain displayed on the yeast surface. The library enrichment process was bridged with a yeast two-hybrid system for the final quantitative selection of antibody-antigen pairs. A similar L-o-L screening approach has been used to screen an antigen library of the HIV-1 gp160 protein against an antibody library generated from an HIV-1 infected individual.<sup>180</sup> Further, Younger et al.<sup>181</sup> developed a yeast synthetic agglutination-based improved single pot L-o-L screening platform, which enables high throughput methods for screening protein-protein interactions by reprogramming yeast mating where they quantitatively characterized 7000 distinct protein-protein interactions. Recently, a high-throughput yeast-based synthetic agglutination assay (AlphaSeq) was used to characterize the binding profiles of tens of antibodies against thousands of SARS-CoV-2 receptor-binding domain (RBD) variants. Specifically, 178,760 protein-protein interactions were measured between 33 antibodies and single AA substitutions corresponding to 165 binding sites within the panel of RBD variants.<sup>182</sup>

In summary, emerging high-throughput experimental assays that are capable of generating large (developability-adjusted) antibody-antigen binding data in the order of  $10^4$ – $10^5$  have begun to unlock the potential of ML for the prediction of antibody-antigen binding.<sup>3,176,183,184</sup> However, for the prediction or generation of paratope-epitope pairs on the sequence level without any structure-aided encoding, much larger data at a higher resolution may still be necessary, as previously suggested by us.<sup>54</sup>

## 2.7. Leveraging ground-truth synthetic data to establish lower bounds on learnability

The generation of synthetic data via simulations is a crucial, but yet under-explored tool in computational antibody design.<sup>185</sup> Estimating (ML prediction) error requires us to know the ground truth about the training data. We define ground truth as a system in which any parameter (and the value thereof) that contributed to training data generation is known and controlled – this is the case for synthetic data but usually not the case for experimental data. Only if we know how the training data has been generated, can we benchmark ML methods not only with respect to accuracy but also with respect to feature discovery and interpretability. To objectively benchmark ML approaches, special care should be put on the distribution of elements and property of elements in the datasets as to faithfully represent experimental datasets because method benchmarking on simulated data is only useful if conclusions gained on simulated data are transferable to experimental data. By distributions we mean, in the case of simulation of antibody-antigen binding data, for example, parameters such as positional amino acid frequency, antibody and antigen topology, sequence dependencies.<sup>185</sup> Specifically,

simulations that allow to precisely define different antibody-antigen binding problems, which requires explicit datasets with all required levels of annotation allowing any kind of encoding, are not yet available in experimental data (Figure 1, challenges in Learnability). Commonly used data encodings can be divided into sequence-based and structure-based ones, while hybrid formalizations leverage both types of datasets.<sup>54</sup> To summarize, define, and compare ML approaches on the same basis, it is critical that simulated data represent 3D features of antibody-antigen binding (especially for defining paratopes and epitopes), allow the generation of large-scale datasets, and the integration with other data types, such as sequence-based datasets. Integration of structure and sequence-based datasets is especially important given the large imbalance in the availability of sequence and structural experimental data (Figure 1, challenges in learnability).

We define synthetic datasets as computer-generated datasets that mimic a set of observed properties of experimental datasets that are the most important in determining the biological outcome to predict. Synthetic datasets can be generated by data augmentation, for instance, by starting from experimental antibody-antigen structures, and generating other possible docking poses that are added to the dataset,<sup>131</sup> or structures that are calculated based on physical-based simplified models.<sup>54,186</sup> Alternatively, structure-independently, antibody sequences may be simulated according to the principles of V(D)J recombination and, partially, somatic hypermutation.<sup>105,187–191</sup>

Sequence-based Ig simulation tools, such as IGoR<sup>187,192</sup> and immuneSIM,<sup>105</sup> enable the generation of large numbers of Ig sequences with moderate computational needs. They have the advantage of generating sequence data that is native-like, which means that data generation is performed, to a large extent, in agreement with the rules of V(D)J recombination, resulting in the generation of data that are largely indistinguishable from experimental data. Importantly, immuneSIM also allows the insertion of sequence motifs (“immune signals”) into the generated sequences, which may be used to model motifs implicated in antigen binding. Therefore, such simulated data can be used for exploring antibody-specificity prediction tasks where in a binary or multi-class/label fashion, sequences are to be classified for their antigen-binding behavior (see Use Cases 1 and 2 in ref.<sup>54</sup>). Of note, simulations with implanted motifs have also been used for repertoire-based ML with applications to immunodiagnostics.<sup>104,193</sup> Independently of established simulation frameworks, experimental-based simulations for training sequence classifiers may also be performed to augment Ig sequence data by reflecting experimentally determined AA position bias.<sup>86</sup>

A current drawback in these simulation frameworks is the lack of nuance pertaining to VH-VL pairing. Since the rules of VH-VL pairing remain underexplored, chain pairing is either not simulated at all or implemented by simple random pairing of VH and VL chains.<sup>105,187,189</sup> Although it has been shown that the CDRH3 is the most important site for antigen binding,<sup>44,45</sup> considering chain pairing is crucial to fully reflect the biological complexity of antigen binding.<sup>69,194</sup> Pioneering work on jointly modeling TCRalpha/beta chain pairing may potentially be ported to VH-VL modeling.<sup>195,196</sup>



To summarize the advantages of synthetic data for the development of computational and machine learning applications for antibody engineering: we agree that the discovery of novel biology can only be performed using experimental data (unless synthetic data perfectly reflects biology complexity). Rather, the advantage of synthetic data over experimental data, if carefully designed, is that due to its arbitrary size and specification, it enables the exploration of the capacity and limits of computational methods as well as the ranking of methods for a given task.<sup>185</sup> In other words, synthetic data allows the development and refinement of computational methods in the absence of suitably large and complete experimental data.<sup>197</sup>

Large-scale synthetic structural antibody-antigen datasets mimicking key aspects of natural antibody-antigen (i.e., paratope-epitope interaction) are needed to develop and benchmark antibody-adapted ML approaches. Therefore, we have recently established the computational framework “Absolut!” for simulating *in silico* antibody-epitope interaction datasets.<sup>54</sup> This framework enables automatic conversion of antibody-antigen structure into a (3D)-lattice representation followed by modeling of 2D/3D antibody-antigen binding of each antibody sequence around the discretized antigens using structural lattice affinity computational method based on experimentally derived coarse-grained amino-acid interaction potentials.<sup>186,198</sup> The Absolut! framework was mainly developed to address the issue of antibody-antigen binding data availability for ML method development, formalization, and benchmarking. The simulated binding structures incorporate a range of physiological properties of antibody-antigen binding (a large number of possible binding structures, AA composition and surface topologies, complex positional AA dependencies in binding antibody sequences, existence of immunogenic binding hotspots, and complexity of the paratope-epitope binding network) and allow for the exploration of various types of negative control datasets that are largely infeasible to create experimentally. Using Absolut!, we have generated close to one billion antibody-antigen structures. To further close in on the physiological reflection of Absolut!-generated structures (or any other framework that aims to simulate antibody-antigen binding), further work is needed to establish 1) full VH-VL chain binding (so far, we can only model CDRH3-antigen binding), 2) smaller angle grid in the lattice as our framework was limited to integer positions in a 3D grid and 3) adding constraints at the CDR3 ends in order to reproduce the anchoring of the CDR chains to the framework region (FR) of the antibody. In the even more long-term future, atomistic and molecular dynamics resolution are needed to add further biological complexity to the Absolut! antibody-antigen binding simulation framework.<sup>51,54,131</sup> Of note, given that Absolut! simulations are based on physics-based (“equation-based”) principles, Absolut!-generated datasets can also be used to develop novel deep learning approaches such as end-to-end differentiable ML architectures that combine mathematical equations specific to a particular domain (in this case, for example, antibody-antigen affinity) with general-purpose, machine-learnable components.<sup>197</sup>

Although much progress has been made in the learnability of antibody-antigen binding and developability (see next section), key challenges such as interpretability as well as data completeness have only begun to be addressed.

On interpretability. Interpretability encompasses the effort to infer the rules underlying the data. However, there is not yet a way to mechanistically and comprehensively map the rules that govern antibody-antigen interaction due to the combination of large search space and scarcity of data (see the Section entitled “Learning from nature: considering biological complexity in computational antibody design”). As the immunology field begins to accumulate more data (experimental as well as synthetic), we will become increasingly reliant on large ML models to infer these rules. Drawing parallels from the natural language processing (NLP) field where large transformer-based models (Figure 3) continue to advance the state-of-the-art results in many different problems and benchmark studies at the expense of building larger and larger models.<sup>199</sup> It begs the question of whether continuing along the lines of building large and more sophisticated architecture will perpetuate the improvements we have seen thus far at the cost of interpretability. For instance, the Bidirectional Encoder Representations from Transformers (BERT),<sup>200</sup> a prominent language representation model, has grown from 110 million parameters to 17 billion parameters in Turing-NLG and 175 billion parameters in GPT-3.<sup>201</sup> The massive complexity of these models gave birth to a subspecialty that focuses exclusively to study BERT models – BERTology.<sup>202</sup> Emphasis has been particularly given on the overparameterization of these large models as they do not seem to use the parameters to their fullest potential. Accumulating evidence reveals that many BERT models can be pruned without impacting their predictive prowess, i.e., most heads in the same layers converge to a similar attention pattern, and thus many layers can be consolidated into a single head.<sup>203,204</sup> In biology, attention layers of transformer-based models, including BERT, have been shown to capture long-range interaction in protein and antibody folding by folding AAs that are distant in 1D sequence but spatially adjacent in the 3D structure, to identify active sites and to capture the hierarchy of complex biophysical properties with increasing layer depths<sup>100,205</sup> – properties that are also critical for antibody-antigen binding. Nevertheless, as in NLP, these models remain susceptible to overparameterization and lack of interpretability. Future deep learning methods would benefit greatly from architectures that accommodate the mapping of rules underlying the data instead of merely focusing on prediction accuracy.

On data completeness. Our immune system is, at least partially, a reactive system where germline gene base diversity can be expanded via stochastic recombinations, insertion, deletion, and mutation. By that definition, our collective antibody repertoires expand or converge to the prevailing landscape of pathogens. Consequently, generating experimental datasets that contain exhaustive multiparameter information (a complete dataset) for the purpose of training and benchmarking ML models remains challenging (Figure 3). In addition to having access to key design parameters (Figure 4) on the

same dataset (something that has not been achieved thus far), even more “exotic” data on biological parameters would be crucial, such as structural information on bound and unbound state,<sup>49</sup> chain flexibility,<sup>206</sup> molecular dynamics simulations.<sup>69</sup> Indeed, only large and exhaustive data will allow us to perform subsampling studies<sup>27,54</sup> for determining the minimal dataset size necessary to achieve satisfactory prediction accuracy on a given prediction task. In order to reach data completeness faster, it may be interesting to explore experimentally to what degree some parameters may be set constant, such as for example only working on the CDRH3<sup>86</sup> or with single-chain antibodies<sup>207</sup> or only with linear epitopes (or antigen immunizations with simple peptides).<sup>208,209</sup>

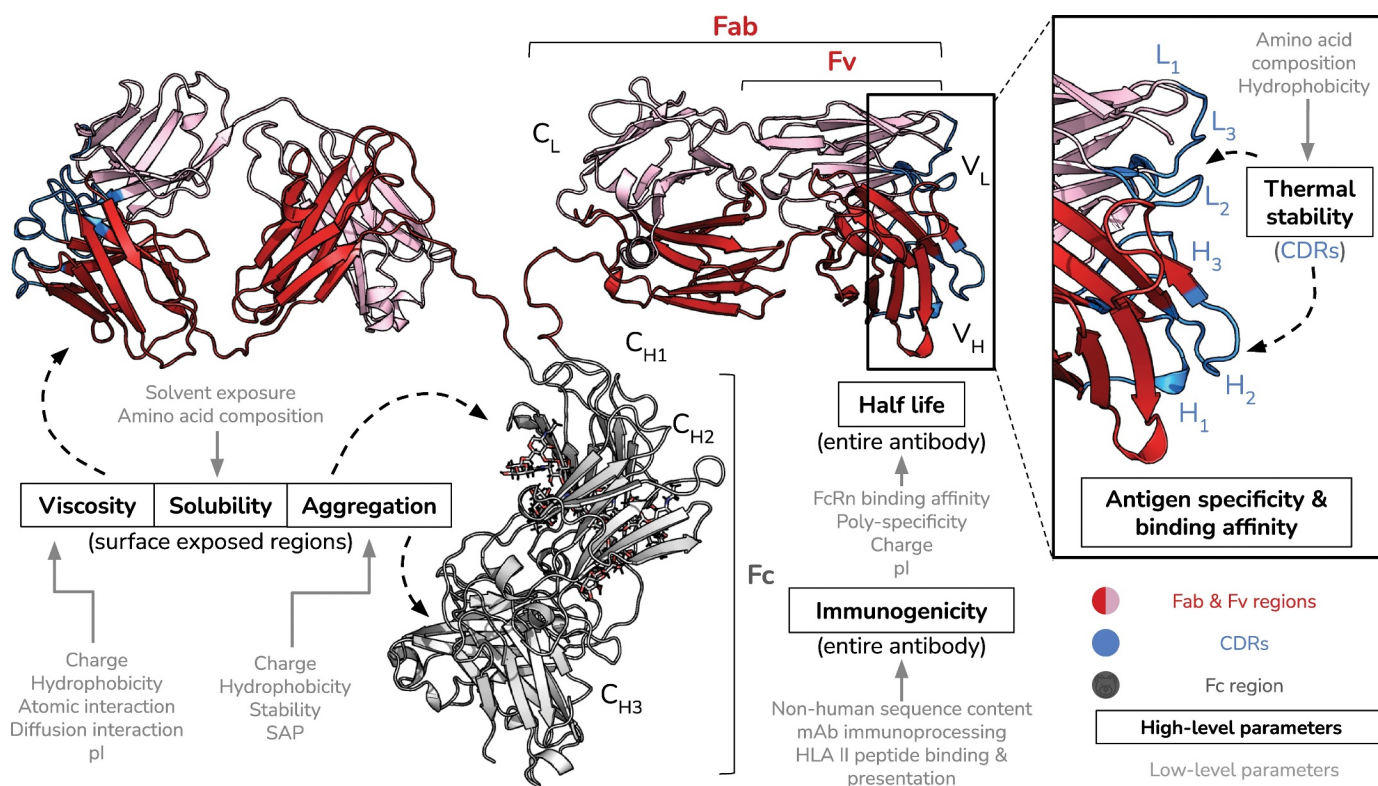
Furthermore, we and others have shown that learned representation from one problem (e.g., one antigen) can be leveraged to improve the predictive capability of a deep learning model that was built for a different problem (a different antigen) by way of transfer learning.<sup>27,97,210,211</sup> Large complete knowledge datasets have been conceived by simulating large antibody-antigen pairs,<sup>54</sup> although possible at reduced resolution, the computational bottleneck to efficiently simulate these pairs at full atomistic resolution presents yet another challenge.

Future ML models may benefit from integrating continuous streams of data (either experimental or simulated) in an online fashion where the data comes in a sequential manner, and the model is updated constantly to allow it to evolve along with the prevailing scenario, in contrast to the typical batch learning where the model is trained once (often with incomplete data) and is expected to generalize well (Figure 3).<sup>212</sup>

### 3. Capacity to modularly learn antibody design parameters

#### 3.1. Modularity of antibodies and developability parameters

mAb therapeutic candidates need to pass several developability hurdles for feasible commercial-scale manufacturing and clinical application.<sup>213,214</sup> The developability of an antibody encompasses the likelihood of the antibody to successfully progress to the clinical phase, which is assessed based on several biophysical properties including a tendency to aggregate, stability, immunogenicity, and plasma half-life (Figure 4).<sup>215</sup> The conventional approach for antibody design



**Figure 4.** Mapping of developability parameters to the antibody regions. The high-level developability parameters are shown in bold font and placed within black boxes with respective mapped antibody regions listed in brackets below each box and referred to with dashed black arrows. The widely used low-level physicochemical developability parameters are also shown in grey text and connected to respective high-level developability parameters with solid grey arrows (detailed further in Table 1). Antibody regions are color-coded as follows; Fc: grey, V<sub>H</sub>: red, V<sub>L</sub>: purple, CDRs: blue. **High-level developability parameters.** Viscosity, solubility, and aggregation propensity of mAbs are mainly linked to the surface-exposed regions of mAb molecules. Antigen specificity and binding affinity, on the other hand, are mainly associated with the CDRs as well as thermal stability. All regions of the antibody can impact half-life and immunogenicity. **Low-level developability parameters.** Viscosity has been reported to be influenced by charge, hydrophobicity, atomic/diffusion interaction, and the isoelectric point (pI) of the mAb molecule. Solvent exposure area and AA composition are frequently reported to impact the solubility of the antibody. Charge and hydrophobicity were also found to affect antibody preparation aggregation likelihood together with stability and spatial aggregation propensity (SAP) measures. The binding affinity of the Fc region to FcRn significantly impacts mAb PK, in addition to the reported role of poly-specificity, charge, and pI on mAbs half-life. The likelihood of a mAb to elicit an immune response (immunogenicity) is linked to the non-human AA sequence content of the mAb, in addition to the way it is processed (digested) into smaller peptides by APCs, bound to the human leukocyte antigen II (HLA II) and presented to T-helper cells. The hydrophobicity and AA composition of mAb CDRs were often reported to affect its thermal stability.

is focused on segregating different biophysical properties to different components of antibody.<sup>8,43</sup> However, in our view, a modular approach for antibody design would need to consider the interdependence and non-linear optimization of the antibody design parameters (both developability and antigen-binding related), which will lead to the desired function and functionality (Figure 4). In the following section of this review, we extensively review critical knowledge of the developability and pharmacokinetics of mAbs. An experienced reader in antibody developability and mAbs therapeutics might find it more convenient to directly resume reading from the section entitled “Designing antibodies with desirable efficacy and developability remains challenging”.

### 3.2. Background: therapeutic mAbs

Among the five isotypes of human Igs – IgA, IgD, IgE, IgG, and IgM, the gamma class (IgGs) comprises all clinically approved mAb therapeutics.<sup>2,216–218</sup> This is due to the combined features of distinct effector functions with advantageous pharmacokinetic properties of the IgG subclasses. In addition, the high abundance of endogenous IgGs in humans (10–12 mg/ml in blood, accounting for up to 80% of the native antibody repertoire<sup>219</sup> and 60% of serum Igs<sup>217</sup> intravenous or subcutaneous injection and robust manufacturing processes well established at an industrial scale<sup>220–222</sup> makes them suitable for therapeutic applications.

Four subclasses of IgG exist in humans, named in decreasing serum abundance, IgG1, IgG2, IgG3, and IgG4.<sup>223</sup> Although they share high similarity in their structural architecture and AA composition, they have distinct differences that dictate unique effector molecule binding and pharmacokinetic properties.<sup>219,224</sup> Specifically, while IgG1 and IgG3 trigger potent immune responses upon engagement of antigen, IgG2 and IgG4 induce more subtle responses.<sup>216,225</sup> Thus, for the development of an antigen-specific therapeutic mAb candidate, it is a prerequisite to select the most preferable subclass.<sup>224–227</sup>

Early developability screening for fit-to-manufacture properties is crucial to minimize the cost and time used for the selection of lead mAb candidates.<sup>215,228</sup> For this purpose, major efforts have been invested to develop *in silico* tools and ML algorithms that could ultimately improve antibody design parameters by implementing modular learning strategies (Table 1).<sup>4,215,228</sup> Here, we discuss each of the developability parameters with the main focus on computational developability prediction tools.

### 3.3. Tailoring the plasma half-life of therapeutic mAbs

Although the IgG plasma half-life is three weeks on average in humans, the half-life of therapeutic IgG mAbs is actually in the range of 6–32 days.<sup>254,257</sup> Importantly, large differences are not necessarily a direct effect of target-mediated clearance as half-life variation is also measured for IgG1 mAbs against pathogens.<sup>258</sup> An illustrating example is briakinumab and ustekinumab, both IgG1s targeting the same antigen (interleukin-12/23), which in humans have half-lives of 9 and 23 days, respectively.<sup>259,260</sup> Understanding the molecular basis for these striking differences is the key to predict *in vivo* pharmacokinetic properties. However, the parameters that determine the pharmacokinetics of mAbs are multifactorial, including

target-mediated clearance, nonspecific off-target binding as well as specific off-target binding via liver receptors and charge characteristics.<sup>24,261</sup> While IgG mAbs have a size above the renal clearance threshold, which excludes renal filtration, FcRn operates as a global half-life regulator as discussed above. Thus, Fc-engineering for improved pH-dependent FcRn binding has resulted in the generation of Fc technologies that can extend the half-life beyond that of natural IgG.<sup>224</sup>

While the Fc technologies can extend the half-life of IgG, each mAb will have a unique pharmacokinetic profile, as a result of its variable domain sequence composition, which is determined by the targeting-binding properties, but also cellular handling (in an FcRn-independent but also likely in an FcRn-dependent manner). As such, the distinct sequences generally have a unique pharmacokinetics profile. In this regard, physicochemical properties of the variable region, such as hydrophobicity, isoelectric point (pI), and charge patches may have a major influence on mAb pharmacokinetics (Figure 4).<sup>24,216,261</sup> For instance, positively charged antibodies more readily interact with the negatively charged plasma membranes, and therefore, be more susceptible to cellular uptake.<sup>262,263</sup> In accordance with this, generating mAb with increased charge in the variable domains has been shown to result in increased nonspecific binding and consequently faster clearance.<sup>261,263</sup> On the contrary, reducing the pI or balancing the charge distribution of the CDRs has been shown to extend the plasma half-life by reducing non-specific binding.<sup>22,264</sup>

While the principal binding site for FcRn is at the Fc elbow region, recent findings support that charge features of the variable domains may modulate engagement of the receptor, and as such affect cellular transport and half-life.<sup>24,42,265,266</sup> This layer of complexity is far from understood, and thus is under intense investigation.

Although non-human primates generally offer reliable pharmacokinetic parameters that can be translated to a human setting, they are not suitable surrogates for screening of panels of mAbs due to impractical handling and ethical considerations. As such, mice are easier to use, but differences exist in how mouse FcRn binds human IgG compared with the human receptor, which must carefully be taken into consideration.<sup>267,268</sup> Thus, mouse strains expressing human FcRn have become the state-of-the-art preclinical standard for investigating the pharmacokinetic properties of IgG mAbs.<sup>269,270</sup> Furthermore, Grevys et al.<sup>271</sup> have developed a human endothelial cell-based recycling assay (HERA) that can be used to screen IgG mAbs for their ability to be taken up and sorted in an FcRn-dependent manner, which has been demonstrated to correlate with half-life values obtained in human-FcRn transgenic mice.

*In silico* screening of antibody candidates for favorable PK properties prior to pre-clinical investigations can increase the convenience and cost-effectiveness of mAbs development. However, identifying the most impactful parameters that affect mAbs PK is challenging due to its multifactorial nature (Figure 4). In this context, Goulet et al.<sup>254</sup> used a LASSO (least-absolute shrinkage and selection operator) ML strategy to identify the combination of parameters that best correlate with mAbs clinical clearance data. They reported that FcRn affinity together with mAb thermal stability is the most



powerful parameters for mAb half-life prediction. Most recently, Grinshpun et al.<sup>255</sup> investigated the effects of 40 physicochemical parameters (12 measured *in vitro*, 28 calculated *in silico*) on 48 IgG1 mAbs clearance profiles. They implemented a random forest ML algorithm and identified *in silico* computed sequence-based features “pI” and *in vitro* measured feature “binding poly-specificity reagent (PSR)” as the top two ranked parameters based on 10,000 repeated runs of the random forest model.<sup>255</sup> These findings align with the previously reported impact of pI and PSR measures on mAbs PK.<sup>22,264,272</sup>

In summary, the half-life of IgG mAbs can be tailored via the optimization of numerous physicochemical parameters, including FcRn affinity, thermal stability, pI, and PSR. ML and the increasing availability of mAb PK data have been aiding the identification of the parameters and their threshold values to facilitate *in silico* estimation of mAb PK.

### 3.4. Improving the stability of mAbs

The stability term of antibodies comprises thermodynamic or conformational stability (thermal stability) and colloidal stability (solubility, viscosity, and aggregation), which are physically related and sometimes used interchangeably. These parameters are in particular important to consider during development and manufacturing processes as part of risk assessment, to reduce the need for cold-chain storage, extend shelf life, and expand the range of applications for practical use. The applicability of experimental assays is limited for antibody development due to the high mAb concentration requirement for some of these steps (i.e., >50 mg/mL) and the lack of high throughput methods.<sup>273,274</sup> These drawbacks may limit the complete screening of all parameters during early-stage development. However, there has been significant progress in the development of high-throughput computational methods to compensate for the time-consuming lab-based biophysical experiments (Table 1).

The generally recommended temperature for storing biopharmaceuticals is in the range of 2°C – 8°C. However, protein denaturation can occur during freezing and freeze-thawing cycles, affecting both conformational and colloidal stability of proteins.<sup>275,276</sup> A study on eight human IgG mAbs (6 IgG1 and 2 IgG4) suggests that focusing on strategies that increase the thermal unfolding temperature of the Fab arms is an attractive approach to improve storage stability.<sup>277</sup> The development of generic antibody fragments to improve the stability of antibodies against a range of denaturing conditions (e.g., temperature, denaturants, polar and non-polar solvents, surfactants, and proteases) while maintaining antibody-specificity, is widely studied experimentally.<sup>278–280</sup>

Among the computational approaches, molecular dynamics (MD) approaches are widely used to assess the stability of antibodies in the context of different solvent conditions,<sup>281</sup> spatial aggregation propensity (SAP),<sup>229</sup> fraction of native contacts (Q-value).<sup>230</sup> In comparison to simulation studies, ML-based models are still at a nascent state to predict the stability parameters of antibodies. However, an ANN-based model has been developed using the AA composition as a feature for studying melting

temperature (Tm), aggregation onset temperature (Tagg), and diffusion interaction parameters (kD) as a function of pH and salt concentration.<sup>231</sup> Jia et al.<sup>282</sup> used a sequence-consensus approach combined with structural residue pair covariance methods to predict the thermostability of antibodies. In another study, authors used the Rosetta platform for protein design to achieve thermal stabilization of anti-HA33 (*Clostridium botulinum* hemagglutinin protein) antibody, through clusters of mutation in the FR region, and verified the results through experiments.<sup>283</sup> In summary, antibody-specific MD simulations are widely accepted as a more robust way to study thermal stability, in comparison to generalized ML/mathematical model development (Table 1).

Aggregation describes the accumulation of denatured antibodies into large clusters due to high concentration or environmental factors (such as temperature, pH, salt concentration, additives, etc.). In general, aggregation-prone region (APR) prediction methods are widely used to predict the aggregation capability of proteins, including antibodies. Several studies on antibodies have identified potential aggregation-prone regions in the relatively exposed CDR of the VH domains.<sup>234,284–286</sup> However, a recent study observed that almost all the latest APR prediction algorithms perform poorly on identifying aggregation.<sup>287</sup> This can be attributed to (1) limited overall variations in the antibody sequence (except for CDRs) leading to higher sequence conservation and (2) low sensitivity of these algorithms toward similar protein sequences. Importantly, these algorithms do not account for aggregation-related environmental factors and protein concentration. While aggregation kinetics prediction methods account for these external factors, the lack of significant dataset size for training limits their robustness.<sup>233,288,289</sup>

In antibody-specific studies, the developability index (DI) allows the prediction of aggregation propensity and long-term stability based on the antibody structure and AA sequence charge information.<sup>232</sup> In an attempt to define success limits for developability parameters, Jain et al.<sup>52</sup> assessed 12 assay-based biophysical properties of 137 mAbs that had reached at least phase II clinical trials and observed that decreased protein stability, an increased disposition for protein aggregation, and polyreactivity are linked to poor developability. This study established thresholds for desirable drug-like developability measures, suggesting practical rules for mAb candidates. Subsequently, in an effort to recreate a ‘Lipinski’s rule of five’ for antibodies, Raybould et al.<sup>213</sup> examined five developability properties of 242 post-phase-I clinical-stage IgG1 antibodies and implemented them into Therapeutic Antibody Profiler (TAP) online tool. Specifically, TAP scores take into account developability factors, such as the length of the CDRs, hydrophobicity, and the presence of charge patches, which are linked to poly-specificity, aggregation, and viscosity of mAb preparations. Rawat et al.<sup>234</sup> developed an ML-based light chain aggregation prediction method and highlighted that lambda light chains are inherently more aggregation-prone. Notably, most approved IgG mAbs harbor the kappa light chain, and the pool of human IgG in serum has about 2-fold more of kappa light chain than the lambda. Van der Kant et al.<sup>290</sup> combined the aggregation propensity and thermodynamic stability prediction



methods to rationally improve the developability parameters of mAbs, which was implemented as the Solubis server.<sup>235</sup> Another example is the aggresscan3D (A3D) 2.0 web server, primarily developed to predict aggregation propensity of proteins, which recently was implemented for simultaneous prediction of change in solubility and stability for improved antibody developability.<sup>256</sup> In conclusion, *in silico* studies on antibody-specific aggregation have emerged in the past few years, whereas generalized protein aggregation predictions have matured for over decades (Table 1).

Solubility is another aspect of colloidal stability, which is inversely proportional to aggregation. SOLpro is one of the early solubility prediction methods that used 23 groups of features computed from the primary sequence to design a two-stage support vector machine (SVM) architecture.<sup>236</sup> Another method, Protein-Sol, combines 35 sequence-based properties including AA composition and other conventional solubility/aggregation related properties (i.e., hydrophathy, charge, disorder,  $\beta$ -strand propensity, etc.) in a linear model to predict the solubility of proteins.<sup>237</sup> Further, CamSol is a structure-based method to generate the intrinsic solubility profile of proteins. Similar to aggregation prediction algorithms, CamSol also identifies low solubility patches in protein structures that may elicit the self-assembly process.<sup>238,291</sup> A recent paper discusses 'Solubility-Weighted Index' (SWI), which is derived from a simple sequence composition scoring method, to predict the solubility of proteins.<sup>239</sup> The availability of a large dataset(s) for solubility led to the implementation of advanced deep learning models as well. For example, Khurana et al.<sup>240</sup> used a convolutional neural network that exploits k-mer structure and additional sequence and structural features extracted from the protein sequence to develop the DeepSol model. Solubility prediction methods in general are relatively more robust compared to other developability parameters due to the availability of large-scale datasets. However, antibody-specific solubility data is still scarce.

Concentration-dependent viscosity is the part of colloidal stability that may depend on pairwise and higher-order intermolecular interactions, non-native aggregation, and concentration-dependent fluctuations of distinct structural regions of antibodies.<sup>292</sup> An increase in viscosity has been a challenge for concentrated antibody formulation, which can reduce the volume of antibody dose, increase dose interval by improved pharmacokinetic profile, reduce the healthcare cost, and improve the bioprocessing of drugs during downstream ultrafiltration and diafiltration steps.<sup>293</sup> Most of the *in silico* studies on limited datasets correlated viscosity with sequence-structural properties, such as net charge, spatial charge map (SCM), pI, zeta-potential, hydrophobic parameters, AA composition/aggregation propensity of the fragment variable (Fv) region.<sup>241–246</sup> Although MD simulation-based parameters, such as short-range interactions, van der Waals attractions and electrostatic repulsions are also used to develop models to predict viscosity of antibodies under a wide range of

concentration and ionic strength.<sup>247,294</sup> A mutagenesis study using MD simulations and experiments showed that replacing surface-exposed aromatic AA residues reduces the viscosity of antibodies.<sup>248</sup> Schwenger et al.<sup>249</sup> measured the viscosity as a function of concentration using Ross-Minton model and temperature using the Arrhenius equation and tested it on four mAbs in the range of potential clinical formulation. An interesting study on a relatively large dataset of 59 mAbs showed that diffusion interaction parameter (kD), a dilute-solution measure of colloidal self-interaction, can predict solution viscosity with high accuracy.<sup>295</sup> Viscosity of antibodies is dependent on intermolecular interaction, and therefore, MD simulation-based studies are heavily exploited. The low-level computational parameters related to viscosity are still at a preliminary stage of development and should be explored further on large datasets.

### 3.5. Reducing the immunogenicity of therapeutic antibodies

All protein-based therapeutics, including mAbs, may potentially be immunogenic and elicit immune responses when administered to humans, resulting in the generation of anti-drug antibodies (ADAs). ADAs may affect the therapeutic efficacy of mAbs by neutralizing their activity and accelerating their circulatory clearance.<sup>2,253,296</sup> For instance, ADA formation occurs in up to 35% of inflammatory bowel disease patients treated with the anti-tumor necrosis factor- $\alpha$  (anti-TNF- $\alpha$ ) adalimumab (Humira), subsequently resulting in a loss of clinical response within 12 months of treatment initiation.<sup>297,298</sup> ADAs could also result in adverse effects ranging from topical rashes to systematic fatal inflammatory reactions.<sup>253,299</sup> Thus, immunogenicity is a key concern for mAb development.<sup>300,301</sup>

Similarly to exogenous proteins, mAbs may be internalized by antigen-presenting cells (APCs), processed (digested) into shorter peptides, and subsequently bound to the major histocompatibility molecule II (MHC II) and presented for T-helper cells on the surface of APCs.<sup>302</sup> Anti-drug immunogenic responses only occur when these complexes (termed as T-cell epitopes) are recognized by T-helper cell receptors, thereafter activating the adaptive immune cascade and leading to the production of ADAs against the mAbs.<sup>303,304</sup>

While the first approved therapeutic mAb was a mouse IgG2 antibody,<sup>305</sup> mAbs have evolved to include an increasing proportion of human sequences to avoid the generation of ADAs.<sup>299,300</sup> Thus, murine mAbs were followed by the engineering of (1) chimeric versions where the constant regions of the mAb are of human origin, (2) humanized antibodies where only the CDRs are of murine origin, and finally (3) fully human mAbs where murine sequences are completely absent from the mAb sequence as it is obtained from human cell libraries.<sup>299,306</sup> mAb humanization has been widely implemented due its advantageous *in vivo* tolerability.<sup>307</sup> In fact, almost 50% of approved or investigational therapeutic mAbs in the EU or US were humanized antibodies as of 10th July 2021 making them the leading class of mAbs in development.<sup>308</sup>

Humanization of a mAb refers to the partial replacement of murine sequences in an antibody sequence precursor that has been initially identified using animal (often, mouse) models with human sequences, to improve their tolerability while maintaining their specificity, affinity, and stability (Figure 4).<sup>306</sup> Antibody humanization is usually achieved by selecting and grafting the murine CDRs from the antibody precursor into human FR regions.<sup>309</sup> In this process, human FRs are selected from the human germline Ig genes that produce the most homologous FRs to the original murine. While humanization seems straightforward in principle, further AA substitutions are often required to retrieve the desirable properties of the antibody that were lost in the grafting process.<sup>306,309</sup> AA substitutions are usually performed on a trial-and-error basis until an antibody sequence with desirable immunogenicity and binding properties is identified, which can be both time- and resource-intensive.<sup>309</sup> A recent study envisaged that human antibody repertoires can be a useful predictive tool for mAb development.<sup>310</sup> They analyzed the AA substitutions in mAbs using position-specific scoring matrices (PSSMs) and observed that positions with high frequency of AA alteration may potentially reduce immunogenicity and improve other developability parameters.

To measure the extent of “humanness”, Gao et al.<sup>253</sup> introduced the “humanness score” as a quantitative measure to reflect the distance between the mAb sequence and the human consensus sequence. Also, several *in silico* tools have been developed that could potentially accelerate mAb humanization (Table 1).<sup>251</sup> For example, Hu-mAb is a computational tool built on an extensively trained ML model on native human and mouse repertoires to compare an input sequence to the closest human germline Ig gene, and suggests as few AA substitutions as possible on the FRs in order to achieve maximal sequence humanness score while reducing the likelihood of impacting the efficacy of the mAb.<sup>251</sup> Hu-mAb humanness predictions have shown to be interpretable relative to clinical immunogenicity data when tested on a set of 217 mAbs. In their study, Marks and colleagues illustrated that high Hu-mAb humanness scores were linked with a low proportion of patients with observed ADAs titers.<sup>251</sup> Most recently, Prihoda et al.<sup>57,252</sup> devised an *in silico* platform BioPhi that offers three complementary tools: 1) OASis, short for Observed Antibody Space (OAS) identity search, is an interpretable humanness scoring system based on an exact 9-mer peptide search within the OAS database, capable of accurately distinguishing human and non-human sequences with clinical immunogenicity correlation; 2) Sapiens, is an ML-based humanization method trained on the OAS human database using language modeling to recognize and substitute non-human sequences with human native equivalents in FR regions to improve sequence humanness (the OASis score); and 3) an interactive interface, to incorporate AA substitutions in the sequence and visualization.<sup>57,252</sup> In their study, Prihoda et al.<sup>57,252</sup> compared the humanization performance of Sapiens on 152 precursor sequences of humanized mAbs against Hu-mAb (computational) and mutation-based humanization (experimental). They reported that Sapiens achieved higher humanness improvement than Hu-mAb and comparable results to experimental methods, suggesting AA substitutions that were experimentally validated to be advantageous for sequence humanization, while maintaining mAb specificity and binding affinity. In summary, BioPhi is an open platform based on deep learning from the

human native antibody repertoire providing *in silico* tools for antibody design, humanization, and humanness evaluation with a graphical interface aiming for user-friendliness.

In contrast to expectations, mAbs completely derived from human sequences (human mAbs) can still be immunogenic which invites further immunogenicity investigations.<sup>300,311,312</sup> Another approach to estimate mAb immunogenicity is inspired by the adaptive immune system activation mechanism. It has been suggested that analyzing the peptidic pool presented by the MHC II molecules to T-helper cells, termed as immunopeptidome, could provide valuable insights for immunogenicity estimation.<sup>313</sup> However, the complexity of the human MHC II immunopeptidome is amplified by the large genetic pool coding for structurally distinct MHC II molecules, termed as human leukocyte antigen (HLA) molecules.<sup>314</sup> Over 8000 human allelic forms HLA class II have been identified (EBI IMGT/HLA: accessed 20th July 2021<sup>315</sup>), and each person typically expresses up to eight different HLA II allelic forms.<sup>316</sup>

Experimental data from EL assays have been empowering the construction of immunopeptidome public databases (IEDB, accessed 20th July 2021, last updated 11 July 2021<sup>317</sup> and others reviewed by Doneva et al.<sup>301</sup>). These databases have been implemented for the development of *in silico* tools that can predict protein immunogenicity based on the content of immunogenic peptides. These tools, as reviewed by Doneva et al.<sup>301</sup> could use protein sequence or structural data to predict its potency to stimulate a T-cell response. Due to the limited availability and high cost of generating structural data, *in silico* immunogenicity prediction methods that rely on sequence input for motif search and ML-based approaches are heavily investigated.<sup>301</sup> Among alternative methods reviewed by Doneva et al.,<sup>301</sup> netMHCIIpan provides an ANN-mediated holistic approach to predict peptide processing, presentation, and binding to any human MHC II molecule (Table 1).<sup>250</sup> Importantly, netMHCIIpan benefits from the advanced abilities of the NNAlign\_MA ML algorithm to handle peptide ligands with multiple potential HLA allele annotation to produce pan-specific T-cell epitope predictions.<sup>250,318</sup> The most recent version of netMHCIIpan (4.0) has been trained with extensive multi-allele EL datasets and showed a significant improvement when benchmarked against state-of-the-art T-cell epitope prediction methods.<sup>250</sup> This tool allows the prediction of binding affinity of AIRR-seq and stretches of mAb-derived AA sequences to selected HLA II alleles.<sup>27,86</sup> netMHCIIpan can be implemented for the prediction of global immunogenicity by specifying the HLA II supertypes found in the majority of the human population in the command arguments.<sup>86</sup> Of note, HLA II supertypes refer to just over 25 HLA II alleles that were found to be responsible for T-cell epitope presentation in over 98% of the universal human population.<sup>319</sup>

### 3.6. Designing antibodies with desirable efficacy and developability remains challenging

*In silico* prediction of mAb developability parameters have been evolving in efficiency and accuracy, however, several challenges remain. Specifically, computational immunogenicity predictions cannot yet fully replace the *in vitro* animal testing due to the safety element associated with this particular parameter, as discussed above.<sup>301</sup> Also, considering the fact that even fully human

antibodies may be immunogenic, it might be difficult to solely rely on *in silico* tools for immunogenicity assessment until the biological rules for immunogenicity are better understood.<sup>320</sup> Indeed, we believe it will be of interest to explore whether mimicking antibody design parameter combinations found in natural antibody repertoires would improve *in silico* antibody

development.<sup>213,321</sup> Furthermore, some tools do not allow including essential variables that might change the developability prediction outcome. For example, most of the solubility and aggregation prediction tools that have been developed for proteins, in general, do not take the concentration of the molecule into consideration which is a critical factor for mAbs (Table 1).<sup>288,322</sup>

**Table 1.** | Overview of *in silico* methods for antibody developability parameter computation. We summarize the most prominent computational tools to predict the value of high-level developability parameters (thermal stability, solubility, aggregation, viscosity, immunogenicity and half-life shown in Figure 4). We detail the methodology used in each tool, the corresponding lower-level developability parameters, and method availability.

Method name	Methodology/approach	Main low-level parameter(s)	Availability
<b>Thermal stability</b>			
Spatial aggregation propensity (SAP) <sup>229</sup>	Custom code, MD simulation	Surface hydrophobicity	Mathematical equation
Bekker et al. <sup>230</sup>	MD simulation	Fraction of native contacts (Q-value)	NA
ANN model <sup>231</sup>	ML model	AA composition	NA
<b>Aggregation</b>			
Developability Index (DI) <sup>232</sup>	Custom code	Charge, spatial aggregation propensity (SAP)	Mathematical equation
AbsoluRATE <sup>233</sup>	ML model for aggregation kinetics prediction	Environmental conditions, disorderness, aggregation related properties etc.	<a href="https://web.iitm.ac.in/bioinfo2/absoluterate-pred/">https://web.iitm.ac.in/bioinfo2/absoluterate-pred/</a>
Therapeutic Antibody Profiler (TAP) <sup>213</sup>	Developability rules as per authors	CDR length, surface hydrophobicity, charge	<a href="http://opig.stats.ox.ac.uk/webapps/newsabdab/sabpred/tap">http://opig.stats.ox.ac.uk/webapps/newsabdab/sabpred/tap</a>
V <sub>L</sub> AmY-Pred <sup>234</sup>	ML model	Charge, hydrophobicity, Disorderness, $\beta$ -propensity	<a href="https://web.iitm.ac.in/bioinfo2/vlamy-pred/">https://web.iitm.ac.in/bioinfo2/vlamy-pred/</a>
Solubis <sup>235</sup>	Custom code	Aggregation propensity, Stability	<a href="https://solubis.switchlab.org/">https://solubis.switchlab.org/</a>
<b>Solubility</b>			
SOLpro <sup>236</sup>	ML model	23 sequence-based features	<a href="http://scratch.proteomics.ics.uci.edu/">http://scratch.proteomics.ics.uci.edu/</a>
Protein-Sol <sup>237</sup>	Regression model	35 sequence-based features	<a href="https://protein-sol.manchester.ac.uk/">https://protein-sol.manchester.ac.uk/</a>
CamSol <sup>238</sup>	Custom code	solvent exposure, intrinsic solubility profile	<a href="http://www.vendruscolo.ch.cam.ac.uk/camsolmethod.html">http://www.vendruscolo.ch.cam.ac.uk/camsolmethod.html</a>
SoDoPE <sup>239</sup>	Custom code Solubility-Weighted Index (SWI)	AA composition	<a href="https://tisigner.com/sodope">https://tisigner.com/sodope</a>
DeepSol <sup>240</sup>	Convolutional neural network, Deep learning	57 sequence-structure features	<a href="https://zenodo.org/record/1162886#.YQvaxJNKhaQ">https://zenodo.org/record/1162886#.YQvaxJNKhaQ</a>
<b>Viscosity</b>			
Fv region-based qualitative screening profile <sup>241</sup>	Developability rules, MD simulation	Charge, $\xi$ -potential, isoelectric point (pI)	Mathematical equation
Sharma et al. <sup>242</sup>	Developability rules, MD simulation, principal component regression	Hydrophobicity, dipole distribution, charge	Mathematical equation
Tomar et al. <sup>243</sup>	Regression model	Surface hydrophobicity, charge, hinge regions	Mathematical equation
Nicholas et al. <sup>244</sup>	Mutational analysis	Negatively charged surface patches	NA
High viscosity index (HVI) <sup>245</sup>	ML model	Charge, AA composition	Mathematical equation
spatial charge map (SCM) <sup>246</sup>	Custom code	Partial charge of the atom	Mathematical equation
Lai et al. <sup>247</sup>	MD simulation, ML model, concentration dependent	Charge, Hamaker constant (short-range interaction parameter)	Mathematical equation
Tilegenova et al. <sup>248</sup>	MD simulation, Mutational study	Aromatic interaction (cation- $\pi$ and/or $\pi$ - $\pi$ )	NA
Schwenger et al. <sup>249</sup>	Ross-Minton model	Temperature and concentration dependent	Mathematical equation
<b>Immunogenicity &amp; tolerability</b>			
netMHCIIpan(T-cell epitope prediction method) <sup>250</sup>	ML model	Antigen (mAb) processing, HLA II peptide binding and presentation	<a href="https://services.healthtech.dtu.dk/service.php?NetMHCIIpan-4.0">https://services.healthtech.dtu.dk/service.php?NetMHCIIpan-4.0</a>
Hu-mAb(mAb humanization method) <sup>251</sup>	ML model	Non-human sequence content	<a href="http://opig.stats.ox.ac.uk/webapps/newsabdab/sabpred/humab">http://opig.stats.ox.ac.uk/webapps/newsabdab/sabpred/humab</a>
BioPhi(mAb humanness evaluation, humanisation and design) <sup>252</sup>	ML model	Non-human sequence content	<a href="https://biophi.dichlab.org/">https://biophi.dichlab.org/</a>
Humanness (T20) score <sup>253</sup>	Quantitative distance measure	Non-human sequence content	<a href="https://dm.lakepharma.com/bioinformatics/">https://dm.lakepharma.com/bioinformatics/</a>
<b>Half-life</b>			
Combinatorial LASSO approach <sup>254</sup>	ML model	FcRn affinity at pH 7, thermal stability	Multiple regression & mathematical equation (methods)
Random forest approach <sup>255</sup>	ML model	pI ( <i>in silico</i> ) and poly-specificity ( <i>in vitro</i> )	Clearance (PK) classification thresholds
<b>Multiple high-level parameter prediction/calculation methods</b>			
Aggrescan3D (A3D) For aggregation and solubility <sup>256</sup>	Custom code	Residue wise aggregation propensity scale, relative surface accessibility	<a href="http://biocomp.chem.uw.edu.pl/A3D2/">http://biocomp.chem.uw.edu.pl/A3D2/</a>

Additionally, the current state-of-the-art *in silico* tools (discussed in this review) are mostly mono-parameter tools, implying the need for setting up a multi-parameter pipeline to compute all the necessary parameters. Moreover, some computational tools developed by pharmaceutical businesses are not made publicly available, which can hinder their implementation and further assessment.<sup>243,323</sup> More generally, the lack of a comprehensive atlas mapping different developability parameters to different regions hinders computational antibody design (Figure 4). Finally, finding an equilibrium for all developability parameters in one antibody, and thus achieving the longstanding goal of modular antibody design, has proven to be a challenging task as working on improving one developability measure might result in compromising another (Figure 4). For example, Kuroda and Tsumoto argued that improved antibody stability may be accompanied by increased aggregation.<sup>320</sup> One experimental solution that may contribute to improving the overall percentage of candidates with a fitting developability profile prior to computation and optimization is the development of developability-optimized screening libraries.<sup>183</sup> An intriguing computational solution to optimizing the number of mAb candidates with respect to multiple design parameters is the combination of ML models trained on data from different experimental campaigns.<sup>324</sup>

## 4. Unconstrained parameter-driven *in silico* antibody sequence synthesis

### 4.1. Antibody (sequence) generation with deep generative models

The term “deep generative model” describes a set of deep learning-based methods that enable the learning of data distributions and subsequent sampling of new unseen points (Figure 5). Currently, there exist, to our knowledge, eight reports that take advantage of deep generative models for antibody sequence generation with diverse objectives: optimizing binding affinity toward a specific antigen, generating new antibodies that replicate developability parameters of the original distribution, realistic backbone structure sampling, unsupervised identification of antibodies in latent space.<sup>25–27,94,325–328</sup> These studies each used one of the three most popular architectures namely Variational Autoencoders (VAE),<sup>329</sup> Generative Adversarial Networks (GAN),<sup>330</sup> and Autoregressive models (AR) namely long short-term memory recurrent neural network (LSTM-RNN) and transformer (Table 2).

### 4.2. GAN-based approaches for antibody design

GANs aim to learn the potential distribution of the actual data by setting up a generator and a discriminator in a zero-sum game. Equilibrium is achieved when the discriminator can no longer discriminate the generator’s outputs from the actual distribution.<sup>331</sup> For biological sequences, GANs are usually used to generate sequences with a particular phenotype of interest. GANs have also been used to generate novel samples (out-of-distribution sampling) from existing distributions (Table 2 and Figure 5).<sup>332</sup>

#### 4.2.1. Demonstrating the capability of GANs to generate feature-controlled antibody sequences

Amimeur et al.<sup>25</sup> demonstrated that GANs are a viable option for novel antibody design. They trained a GAN on the sequences of the light and heavy chain variable regions from the Observed Antibody Space (OAS) database.<sup>57</sup> Subsequently, they sampled new sequences from the model and showed that the model can generate large and diverse libraries of novel antibodies that mimic the features (CDRH3 length, isoelectric point, representative maximum patch size, and predicted affinity to MHCII) of the antibodies from the OAS. They also demonstrated that they can bias the model to generate feature-controlled antibody sequences with a lower binding affinity toward MHCII or a higher isoelectric point by conditioning the training dataset on the respective variable. The authors experimentally validated their method by expressing newly generated antibody sequences *in vivo*.

#### 4.2.2. GAN-based approaches for general protein design

Repecka et al.<sup>333</sup> trained a GAN architecture with temporal convolutional networks and a self-attention layer, named ProteinGAN, to generate novel malate dehydrogenase (MDH) sequences. Their 20,000 generated sequences had a median sequence identity of 64.6% when compared to the best matching training sample, which was similar to the median of the training data against the validation set (64.9%), indicating that GANs can generate realistic sequences. The resulting sequences were also four times more diverse than the training subset at 75% sequence identity. A sequence with 106 substituted AAs was identified among the functional subset – an example of the exhaustive exploration of the functional sequence space that GANs are capable of.

Additionally, GANs can also be conditioned on a secondary input, which is often a set of categorical labels.<sup>334</sup> Combining conditioned models with multiple computational oracles (classifiers for key design parameters) may enable fast multi-parameter/multi-objective optimization (Figure 5). Integrating conditional labels remains a challenging undertaking.<sup>335,336</sup> Despite their realistic sequence or image generation, GANs can often suffer from mode collapse, where the generator is stuck in a local minimum of a few valid samples. There are, however, methods to circumvent mode collapse such as implementing a different loss function.<sup>337</sup>

### 4.3. VAE-based approaches for antibody design

VAEs provide a unique avenue to interpretable protein design via their latent representation where functionally similar sequences group together due to their conserved residues, and novel proteins can be obtained by decoding points nearby these clusters.<sup>338</sup> Thus, VAEs can be used for lowering the dimensionality of a dataset, obtaining biologically meaningful representations and clusters, sampling to generate *de novo* sequences, and interpolating in the latent space to obtain proteins with the desired function (navigating from one sequence to another in the latent space), all in the same model (Table 2 and Figure 5).



#### 4.3.1. Generative modeling of antibody backbone structure

Eguchi et al.<sup>326</sup> used VAEs to generate new backbone structures of antibodies that are filtered for desirable properties by evaluating them with simulators. This resulted in new randomly sampled structures that were different from the training data and constrained optimization with Rosetta<sup>339</sup> does not lead to large changes to the overall structure. They also verified generated structures by linearly interpolating the latent representation of existing antibody structures. The authors sampled 5000 antibody structures from the IG-VAE and identified candidates with binding affinity for the SARS-CoV-2 RBD with PatchDock.<sup>340</sup>

#### 4.3.2. Clustering antibody sequences by applying Gaussian Mixture Models to the latent space of VAEs

Friedensohn et al.<sup>26</sup> used a VAE that incorporated Gaussian mixture models in the latent space to identify clusters of potentially antigen-specific antibody sequences, which were obtained from antigen-immunized mice. Then, they sampled from the VAE new antibodies from those putatively antigen-associated clusters. Twelve antibodies from one cluster were recombinantly expressed and all 12 were confirmed to be antigen specific.

#### 4.4. VAE-based approaches for general protein design

An initial study in VAE-generated protein sequences was conducted by Costello and Martin.<sup>341</sup> Their architecture (BioSeqVAE) employed residual networks, dilated convolutions, and an autoregressive layer on top of the decoder, resulting in a latent space that captures residue interactions along the entire sequence. Furthermore, they used the latent space to generate proteins with the desired phenotype by training a classifier on the latent representation of a protein dataset with a desirable function, then sampling points from the latent space until they were validated by the classifier. They also showed that multiple phenotypes could be integrated by training other classifiers, further extending the idea of multi-parameter optimization as a key step in highly specific protein generation. Additionally, Gane et al.<sup>342</sup> provide a benchmark for protein design on synthetic data that investigates VAEs among other models.

#### 4.5. AR-based approaches for antibody design

Autoregressive models are inherently sequential, thus, they are ideally suited for modeling biological sequences as they decompose into a fixed ordering (one AA after the other). Although they can be powerful estimators for the distribution of interest, the training and generation can be exceedingly slow as they are done in a sequential manner (Table 2).<sup>343</sup> A comprehensive benchmark over three different AR-based approaches to mAb generation, conditioned on protein structure can be found in the work of Melnyk et al. where “causal convolutions”, GNNs, and transformer-based generation methods are compared. The authors also provide guidelines as to which of the three AR-based approaches are best suited to specific antibody design tasks (e.g., CDR3 grafting, broad or narrow sequence diversity generation).<sup>328</sup>

#### 4.5.1. Optimizing the binding affinity of antibody sequences with LSTM-RNNs

Saka et al.<sup>325</sup> used LSTM-RNNs to examine the capacity of deep generative models to improve the affinity of kynurenine-binding antibodies. The authors generated a dataset of kynurenine-binding antibodies through two rounds of phage-display panning. An LSTM-RNN was trained on the sequence data of the Fv region of the heavy chain. They found that the predicted likelihood values of the generated sequences correlate well with binding affinity ( $R^2 = 0.52$ ) and the best LSTM-RNN generated sequence yielded over 1800-fold lower dissociation constant over the original kynurenine-binding antibody.

#### 4.5.2. Demonstrating the capability of LSTM-RNNs to learn distributions of CDRH3 sequences with a wide variety of antibody design parameters

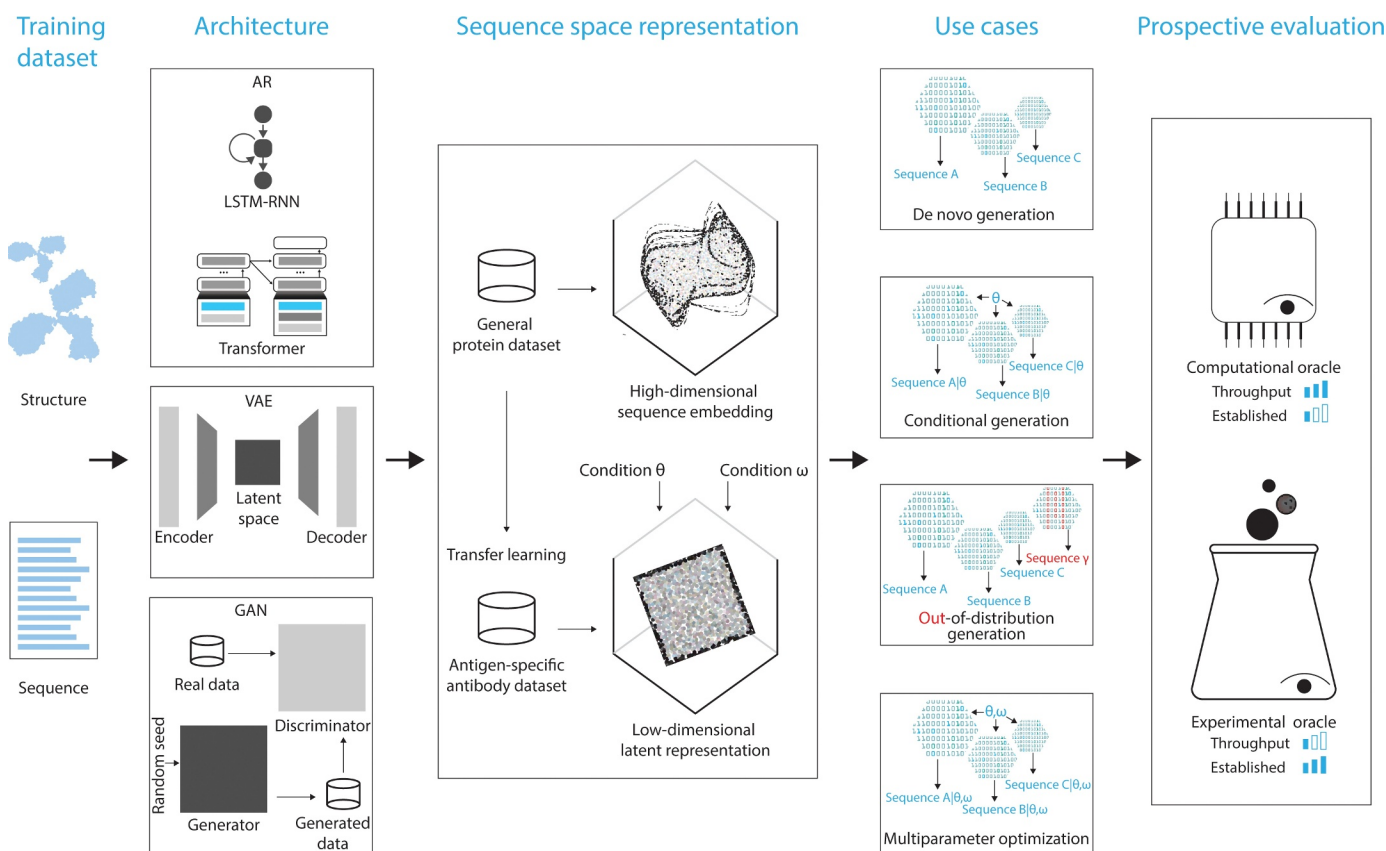
We have recently demonstrated the feasibility of *in silico* antibody design with deep generative methods.<sup>27</sup> Briefly, we trained LSTM-RNNs on ground truth synthetic data antibody (CDRH3) sequences where for each CDRH3 sequence, the design parameters (affinity, epitope, developability) were known<sup>54</sup> and showed that LSTM-RNN can generate new CDRH3 sequences that match and/or exceed and extend the antibody design parameters of the training dataset, but greatly differ sequence-wise from those sequences contained in the training dataset. Additionally, we showed that pre-training models for transfer learning can improve prediction results. Finally, we validated the antibody-design conclusions reached from ML training on simulated antibody-antigen binding data by training on experimental antibody sequence data and evaluating the generated sequences using an experimentally validated computational oracle published by Mason et al.<sup>27,86</sup>

#### 4.5.3. AR models for nanobody design

Shin et al.<sup>94</sup> demonstrated the utility of causal CNN models to generate new nanobody sequences. This was done by training a causal CNN model to learn a conditional distribution over CDRH3 sequences, given the CDRH1 and CDRH2 sequences, to avoid CDRH3 sequences that are chemically incompatible with the other CDRHs. They also showed that the generated CDRH3s have a similar distribution to the developability parameters hydrophobicity and isoelectric point of the reference CDRH3s. In addition, they evaluated the method by training on a llama dataset<sup>344</sup> which contains 1.2 million nanobody sequences from seven different immune repertoires, and evaluated the hydrophobicity and isoelectric point by computational methods.<sup>345,346</sup>

#### 4.5.4. Improved AR-based models through simultaneous estimation of structure

Jin et al. developed an AR-based model that generates new AAs in a sequence while iteratively refining the sequence's predicted global structure. Simultaneously, the inferred structure guides subsequent residue choices. The structure is modeled with a graph representation that models the position of the AAs and the angles that define the backbone structure. Edges within the graph are defined through proximity.<sup>327</sup>



**Figure 5.** Generative models can be trained on generic or custom-designed datasets to obtain sequence space representation and to generate new sequences for a variety of use cases in antibody design. AR models enable the generation of highly diverse proteins and can be used to obtain meaningful sequence embeddings, circumventing the need for hand-crafted features. VAEs and GANs have been employed in protein generation in a similar manner to generate functionally relevant leads, obtain biologically meaningful latent representations, and condition them on additional features (e.g., solubility). As such, these models can be employed in de novo generation of sequences, conditional, or out-of-distribution generation, as well as optimization of multiple parameters. Evaluating the specificity (or any other design parameter of interest) of the *in silico* designed antibody sequences requires either computational or experimental oracles. As deep generative models output a large number of sequences, experimental prospective evaluation methods may not possess the time- and cost-efficiency to evaluate these sequences at scale, thus creating considerable demand for *in silico* oracles (Figure 5). Transfer learning may be leveraged to infer higher-order, functionally specific interactions from a small number of available sequences (low N). Integrating computational and experimental oracles or directly conditioning the generative models on additional features would enable high-yield multiparameter optimization of machine-learning engineered antibody sequences.

**Table 2.** | (Dis)Advantages of the three most common generative methods (GAN, VAE, AR) with respect to five properties. Polyspecific training objective indicates if the training objective assumes only one possible target. Supervision indicates whether the model can be trained in a completely unsupervised manner or if the definition of an identity error function is required. Categorical indicates whether the model can deal with categorical data (most common datatype in protein sequence generation problems). The difficulty of training indicates the tendency of the model to experience numerical instabilities during training.

	pecific training objective	Approximate training objective	Supervision	Categorical	Difficulty of training
GAN	Yes	Direct	Unsupervised	Not out-of-the-box	3/3
VAE	No	Lower Bound	Unsupervised (supervised Identity function)	Yes	2/3
AR	No	Direct	Unsupervised (supervised Identity function)	Yes	1/3

## 4.6. AR based approaches for general protein design

### 4.6.1. On the impracticality of simple AR-based models

The capacity of Ar-based models to generate highly diverse sequences was illustrated in an antimicrobial peptide design task via an LSTM-RNN model: out of 2000 generated peptides, 1747 were unique.<sup>347</sup> These were further assessed for their antimicrobial activity via a random forest classifier (computational oracle) against both the training dataset and against randomly sampled sequences using the original AA

distribution: de novo peptides had a higher probability of being antimicrobial compared to the randomly sampled group and as high as the training ones.

However, AR models are often impractical on multidimensional (vast sequence space), multi-feature data: incorporating other physicochemical, affinity, or structural properties to direct the sequence generation would require pre-trained vector embeddings of protein sequences,<sup>210,211</sup> or carefully engineered features (by hand). These embeddings often require a much larger sequence database for training. For example,

Alley et al.<sup>97</sup> used 24 million UniRef50 sequences to construct their embeddings, which was later used in an *in silico* optimization framework to improve the fluorescence of a GFP.<sup>348</sup>

#### 4.6.2. Advanced AR-based approaches for general protein design – sequence embeddings (self-supervised learning)

The above-mentioned problems (lack of a functionally meaningful latent space, which could represent structural/physico-chemical information and high-dimensionality of the sequence space) could be addressed with LSTM-RNNs<sup>97</sup> or Transformer models.<sup>58</sup> These models were trained on large unlabeled sequence databases and can capture the secondary and tertiary structures, AA biochemical properties, homology, and function of a protein in a learned, sequence embedding (self-supervised learning). Moreover, Villegas-Morcillo et al.<sup>210</sup> discovered that such embeddings solely obtained from sequence data outperform even well-engineered features on classification tasks, as well as other structure-based protein embeddings via distance maps (as designed by ref. <sup>349</sup>). Surprisingly, when combining their sequence embedding with contact maps, their classifier performed similarly (AUC-ROC = 0.76) to when such information was omitted (AUC-ROC = 0.77), indicating that the sequence embedding encompassed enough of the structural information. Sequence embeddings provide, therefore, a biologically interpretable reduction of the vast protein sequence space.

It is of interest to investigate how such sequence embeddings can be used in protein generation. A first insight was recently gained by ref. <sup>348</sup> into how this might be possible for *in silico* directed protein evolution: first, an LSTM-RNN network was trained on 20 million general protein sequences to obtain a general embedding, which was later fine-tuned on sequences evolutionarily related to the protein to optimize, followed by the sampling of a small number of mutants (low-N engineering), quantifying their specific functional property (e.g., the fluorescence of a GFP) and building a linear regression model (inputs = embedding representation, outputs = quantified property of protein). The starting sequence was mutated, embedded, then fed into the linear regression model – sequences with large enough values can be functionally assessed *in vitro*.

#### 4.6.3. Transformer networks for general protein design

To tackle the problem of low receptive fields (i.e., the size of the regions in the input that informs the output<sup>350</sup>) in RNNs, Transformer or general attention models have been increasingly used for various NLP tasks and for protein sequence modeling as well, achieving state-of-the-art results.<sup>351</sup> For example, Wu et al.<sup>352</sup> trained a 5-layer Transformer network to generate signal peptide sequences, a task where (self)-attention is advantageous to scrutinize the entire sequence of an instance. In total, 25,000 paired proteins without signal peptides were fed into the model along with their respective signal peptides, in an attempt to translate protein sequences to specific peptides. The generated signal peptides had a 73% sequence similarity to their corresponding BLAST result from SwissProt, therefore showing some diversity, yet had

poor AUC-ROC values on a signal peptide deep learning classifier (AUC-ROC = 0.59, almost equal to baseline classification).

Recently, the ProGen model<sup>353</sup> was able to generate label-conditioned sequences: by training a Transformer network on sequences with a conditioning tag prefix (e.g., organism, function, location, etc.), their model learned conditional probabilities on both the previous residue and the label of interest. Integrating such conditioning tags allowed for protein generation without any starting residue: using the tags Flavoprotein and FMN, they were able to sample a 400 AA protein which matched numerous other similar proteins (oxidoreductases). The work above showed that conditional transformers for text generation can be applied to protein engineering problems. The extent to which sequences generated from conditional labels differ from similar ones in the training data may be used to gauge the potential for out-of-distribution generation in these models. Another example on conditioning transformers for protein design is the work from Ingraham et al, who condition a transformer on folding information by utilizing a graph neural network as representation.<sup>354</sup>

#### 4.7. Remaining challenges in generative antibody design

Limited application of generative ML approaches to antibody design: The current literature on generative modeling of antibodies already incorporates many approaches currently used in generative protein design, such as sampling of 3D backbone structure of antibodies for finding new antibodies with relevant properties,<sup>326</sup> sampling of antibody sequences for optimization,<sup>325</sup> interpolation of a latent space for antibody property design,<sup>326</sup> and generation of novel and highly diverse antibodies that faithfully reproduce developability parameter distributions. However, there are still several approaches that have not been explored in the antibody generation domain, such as using learned amino-acid vector representations,<sup>210,211</sup> combining adversarial training with modern autoregressive models (e.g., transformers), and conditioning models directly on developability parameters.<sup>353</sup>

High-throughput prospective evaluation: In a typical ML study, a dataset is split into training, validation, and test sets to allow for the model to be retrospectively evaluated with the validation and test sets upon the completion of the training. In such a setup the data comes in the format of input-output pair, thus during evaluation, the correct label for a sample either in the validation or the test set is known *a priori*. In generative learning, however, the label (i.e., binding affinity, developability, and plasma half-life or a subset thereof) is not known *a priori* as the model generates new sequences that may or may not overlap with the training data. Thus, generative learning necessitates external (computational or experimental) validators (oracles) to evaluate its output as the evaluation process is performed post-generation (prospective evaluation; Figure 5).

An experimental prospective evaluation workflow usually involves the expression and testing of 10<sup>1</sup>–10<sup>2</sup> binders.<sup>26</sup> A computational validation workflow might involve, for example, the sequence-based modeling of the antibody structure with tools such as



ABodyBuilder,<sup>132</sup> followed by molecular docking,<sup>66,355,356</sup> or MD simulation (all-atom simulation; computationally expensive<sup>357</sup>) to validate whether the generated sequence overlaps with the desired antibody-antigen binding pose. However, given that *de novo* docking approaches remain at low accuracy, such computational validation workflows require further refinement. Furthermore, so far, there exist only a few ML-based experimentally validated computational oracles published.<sup>86</sup> Recent studies<sup>27,54</sup> led by us were among the first efforts to tackle the high-throughput prospective evaluation problem in antibody generative learning by leveraging a high-throughput oracle in the form of virtual (coarse-grained) docking albeit at a reduced lattice resolution.

**Out-of-distribution generation (functional novelty):** A common challenge in deep generative learning is that the model tends to reproduce the training data extremely faithfully, a phenomenon known as the copy problem.<sup>358</sup> Such a model remains useful when the objective of the study is to generate new samples that are very similar to the training data. In antibody design, however, sequence similarity may not reflect binding behavior faithfully. It has been shown, for example in HER2 binding antibodies, that two very similar sequences (Levenshtein distance < 2) had opposing binding behavior.<sup>86</sup> Secondly, it is often desirable to discover new modes of binding (novel target epitopes) when designing antibodies for a target of interest, these functionally novel antibodies represent out-of-distribution samples as the novel epitopes were never learned from the training data. A naïve strategy to obtain out-of-distribution samples is to couple a simple architecture with unconstrained generation, i.e., the simple architecture reduces the risk of overfitting the training data (reduces the risk of copy problem) and unconstrained generation allows the model to explore a larger sampling space. Indeed, we employed such a strategy to obtain novel epitopes and a diverse set of developability parameter combinations rather successfully.<sup>27</sup> A more sophisticated strategy may include conditioning the model in such a way that the output is biased toward out-of-distribution samples.<sup>359</sup>

**All-round optimization – conditioning simultaneously on multiple developability parameters in a single model:** In the two pioneering studies from Amimeur et al.<sup>25,86</sup> and Mason et al.,<sup>25,86</sup> the developability optimization step is a separate entity. Next-generation antibody design tools must be developed with all-round optimization in mind where multiple developability parameters and binding affinity are simultaneously optimized. For instance, models such as conditional VAEs have been deployed to generate drug-like molecules where five target properties were simultaneously optimized during training.<sup>360</sup> Another challenge is that different developability parameters localize in different regions of the antibody (Figure 4) whereas many studies such as ours and Mason et al.<sup>25,86</sup> conveniently focus on the most important segment for antigen engagement, the CDRH3. In summary, a holistic all-round antibody generator represents a crucial component for the on-demand generation of fit-for-purpose mAbs.

## 5. Concluding remarks

In this review, we outlined strategies toward ML-based mAb design and the associated necessary computational and experimental steps required. We argue that a resolution to the *in silico* antibody design problem lies in the development of novel experimental and computational technologies for large-scale generation combined with a screening of antibody, antigen, and antibody-antigen parameters. Furthermore, self-supervised learning may provide a means to leverage large amounts of unlabeled data to boost *in silico* protein design efficiency.<sup>197</sup> As a bridge between experimental and simulated data, more investment is needed in the development of data augmentation algorithms that can expand training dataset sizes. Correspondingly, powerful simulation frameworks to generate ground-truth synthetic data are mission critical for testing the accuracy and performance of novel *in silico* antibody specificity prediction and generation approaches. Furthermore, for maximum generalizability, it will be paramount to learn from and combine *in vitro* and *in vivo* data since these datasets underlie different generative distributions (e.g., *in vitro* antibody libraries may display broader diversity that have not undergone biology self-reactivity-driven selection).<sup>3,184</sup> Finally, we believe the antibody design field requires closer collaboration with ML experts. As was witnessed in the case of protein structure prediction, the infusion of domain-specific ML knowledge can propel an entire field substantially forward.<sup>361,362</sup>

## Abbreviations

3DZD: 3D Zernike Descriptor; AA: Amino Acid; AB-Bind: Antibody-Bind dataset; ABCD: AntiBodies Chemically Defined Database; ADA: Anti-Drug Antibody; ADCC: Antibody-Dependent Cell-mediated Cytotoxicity; ADCP: Antibody-Dependent Cellular Phagocytosis; AgAbDb: Antigen-Antibody Interaction Database; AlphaScreen: Amplified luminescence homogeneous assay; ANN: Artificial Neural Network; anti-TNF- $\alpha$ : anti-Tumor Necrosis Factor- $\alpha$ ; APC: Antigen Presenting Cell; APR: Aggregation Prone Region; AR: AutoRegressive model; AUC: Area Under the Curve; AUC-ROC: Area Under the Receiver Operating Curve; BCR: B-cell Receptor; BERT: Bidirectional Encoder Representations from Transformers; BLI: BioLayer Interferometry; bNAber: broadly Neutralizing Antibodies electronic resource; cAb-Rep: Curated human B cell immunoglobulin sequence repertoires; CDC: Complement-Dependent Cytotoxicity; CDR: Complementarity-Determining Region; CDR3H: Complementarity-Determining Region 3 on the heavy chain; CNN: Convolutional Neural Network; CoV-AbDab: Coronavirus Antibody Database; DI: Developability Index; EL: Eluted Ligand; ELISA: Enzyme-Linked Immunosorbent assay; EPMP: Epitope-Paratope Message Passing; ERT: Extremely Randomized Tree; Fab: Fragment antigen-binding; Fc: Fragment crystallized; FcRn: Neonatal Fc receptor; FR: Framework Region; GAN: Generative Adversarial Network; GB: Gradient Boosting; GBT: Gradient-Boosting Trees; GDL: Geometric Deep Learning; HER-2: Human Epidermal growth factor Receptor 2; HERA: Human Endothelial cell-based Recycling Assay; HLA: Human Leukocyte Antigen; HVI: High Viscosity Index; IEDB: Immune Epitope Database; Ig: Immunoglobulin; IMGT: International ImMunoGeneTics information system; ITC: Isothermal Titration Calorimetry; kD: diffusion interaction parameter; L-o-L: library-on-Library; LASSO: Least-



Absolute Shrinkage and Selection Operator; LIBRA-seq: Linking B-cell Receptor to Antigen specificity through sequencing; LSP: Local Surface Patches; LSTM-RNN: Long Short-Term Memory-Recurrent Neural Network; mAb: monoclonal Antibody; MaSIF: Molecular Surface Interaction Fingerprints; MD: Molecular Dynamics; MERS-CoV: Middle East Respiratory Syndrome Coronavirus; MDH: Malate Dehydrogenase; MHC II: Major Histocompatibility Molecule II; ML: Machine Learning; MS: Mass Spectrometry; NLP: Natural Language Processing; NN: Neural Network; OAS: Observed Antibody Space; PECAN: Paratope and Epitope prediction with graph Convolution Attention Network; pH: Potential hydrogen; pI: Isoelectric point; PK: Pharmacokinetics; PPI: Protein-Protein Interaction; PROxIMATE: PROtein-protein complex Mutation Thermodynamics Database; PSR: Poly-Specificity Reagent; PSSM: Position-Specific Scoring Matrix; Q-value: Fraction of native contacts; RBD: Receptor-Binding Domain; RNN: Recurrent Neural Network; SABDab: Structural Antibody Database; SAP: Spatial Aggregation Propensity; SARS-CoV-1: Severe Acute Respiratory Syndrome CoronaVirus 1; SARS-CoV-2: Severe Acute Respiratory Syndrome CoronaVirus 2; SCM: Spatial Charge Map; sdAb-DB: Single-Domain Antibody Database; SiPMAB: Single-Point Mutant Antibody Binding; SKEMPI: Structural Kinetic and Energetic database of Mutant Protein Interactions; SPR: Surface Plasmon Resonance; SVM: Support-Vector Machines; SWI: Solubility-Weighted Index; Tagg: Aggregation onset temperature; TAP: Therapeutic Antibody Profiler; Thera-SABDab: Therapeutic Structural Antibody Database; Tm: Melting temperature; TopCNN: Topology-based Convolutional Neural Network; TopGBT: Topology-based Gradient-Boosting Trees; TopNetTree: Topology-based Network Tree; VAE: Variational Autoencoder; VH: Variable Heavy; VL: Variable Light; WHO: World Health Organization;  $\Delta G$ : Gibbs free energy of binding;  $\Delta\Delta G$ : The change in Gibbs free energy of binding
















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## Data and code availability

Datasets, codes, and figures are available at [https://github.com/csi-greifflab/manuscript\\_progress\\_challenges\\_on-demand\\_antibody](https://github.com/csi-greifflab/manuscript_progress_challenges_on-demand_antibody). Plots were generated in Matplotlib (version 3.3.4)<sup>363</sup> and R (version 3.6.1).<sup>364</sup>

## Author contributions

Conceptualization: V.G. and R.A.; Writing - Original Draft: R.A., P.A.R., E.S., H.B., P.R., M.H.V., J.T.A., K.F.K., B.B.M., T.Z., J.G.M., R.F., T.S.C., V. G.; Writing - Review & Editing: R.A., P.A.R., E.S., H.B., P.R., M.H.V., K.F. K., B.B.M., T.Z., J.G.M., R.F., T.S.C., F.L.J., J.T.A., V.G.; Visualization: V. G., E.S., R.A., H.B., T.S.C.; Supervision: V.G., P.A.R., and R.A. The authorship order was determined alphabetically within each tier of contribution (H and L). Tier H: R.A., H.B., P.R., P.A.R., and E.S. Tier L: T.S.C., K.F.K., R.F., B.B.M., M.H.V., and T.Z. Within each tier authors are free to list their names first in their C.V. All authors contributed and approved the submitted version of the article.

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