Separating selection from mutation in antibody language models

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Abstract

Antibodies are encoded by nucleotide sequences that are generated by V(D)J recombination and evolve according to mutation and selection processes. Existing antibody language models, however, focus exclusively on antibodies as strings of amino acids and are fitted using standard language modeling objectives such as masked or autoregressive prediction. In this paper, we first show that fitting models using this objective implicitly incorporates nucleotide-level mutation processes as part of the protein language model, which degrades performance when predicting effects of mutations on functional properties of antibodies. To address this limitation, we devise a new framework: a Deep Amino acid Selection Model (DASM) that learns the selection effects of amino-acid mutations while explicitly factoring out the nucleotide-level mutation process. By fitting selection as a separate term from the mutation process, the DASM exclusively quantifies functional effects: effects that change some aspect of the function of the antibody. This factorization leads to substantially improved performance on standard functional benchmarks. Moreover, our model is an order of magnitude smaller and multiple orders of magnitude faster to evaluate than existing approaches, as well as being readily interpretable.

Introduction

Antibodies are remarkable molecules that can bind essentially any target with high affinity and specificity. Natural antibodies are generated through V(D)J recombination, and refined by somatic hypermutation and affinity-based selection in germinal centers. Antibodies are also important drugs, and improving binding and other important properties is thus an area of active research. A major goal in the field is to predict the effect of changing one amino acid for another at a given site of an antibody, both for antibody engineering and for understanding naturally occurring antibodies.

Antibody "foundation" language models are trained on large datasets of naturally occurring antibody sequences to assist with this and related problems [1, 2]. These models are trained using the masked objective, in which a site is masked from an antibody amino-acid sequence, and the model is trained to predict the masked amino acid given the remaining sequence. Recent models of this type have hundreds of millions or billions of parameters, and are trained on around a billion sequences [3].

While the masked objective has been very useful for modeling human language [4], this approach may not be ideal for learning functional effects of mutations to antibody sequences. To understand why, it is useful to consider: what could a language model learn in order to succeed under the masked modeling objective? It could memorize the germline genes [5,6] and learn about the probabilities of V(D)J recombination. It could learn the codon table, as according to this table some amino-acid mutations are much more likely than others. It could learn rates of somatic hypermutation, because codons containing mutable nucleotide sites are more likely to deviate from germline than those in sites that are less mutable [7]. It could also learn about the impact of amino acid mutations on antibody function through natural selection in the course of affinity maturation, which is the desired signal [8]. However, this desired signal is confounded by the preceding factors.

In this paper, we first demonstrate that masked language models learn all these factors shaping antibody sequences, despite most being irrelevant for functional prediction. Indeed, we show that conflating mutation and selection processes degrades performance on functional prediction tasks. We then develop a model that explicitly accounts for phylogenetic relationships, the codon table, and somatic hypermutation patterns, allowing it to focus exclusively on functional effects.

Our approach separates mutation and selection processes by encoding functional effects in a Deep Amino acid Selection Model (DASM) while explicitly modeling mutation using a separate fixed model trained on neutrally evolving data [9]. This fixed model uses convolutions on 3-mer embeddings to deliver wide context sensitivity without needing a large number of parameters: the variant we use has around the same number of parameters as the classic S5F [10] 5-mer model. The DASM, trained on substantially less data, outperforms AbLang2 [5] and general protein language models including ESM2 [11,12] and ProGen2-small [13]. This outperformance holds on the largest benchmark

datasets of the FLAb collection [8] and on recent high-throughput binding assays [14, 15]. Unlike existing models, DASMs process complete sequences in a single pass and directly output selection factors for all possible mutations. DASMs are thus orders of magnitude faster than existing models, enabling intensive use on a laptop without a GPU. We provide a paired (heavy and light chain) model with open weights and associated code as part of our `netam` package `https://github.com/matsengrp/netam`.

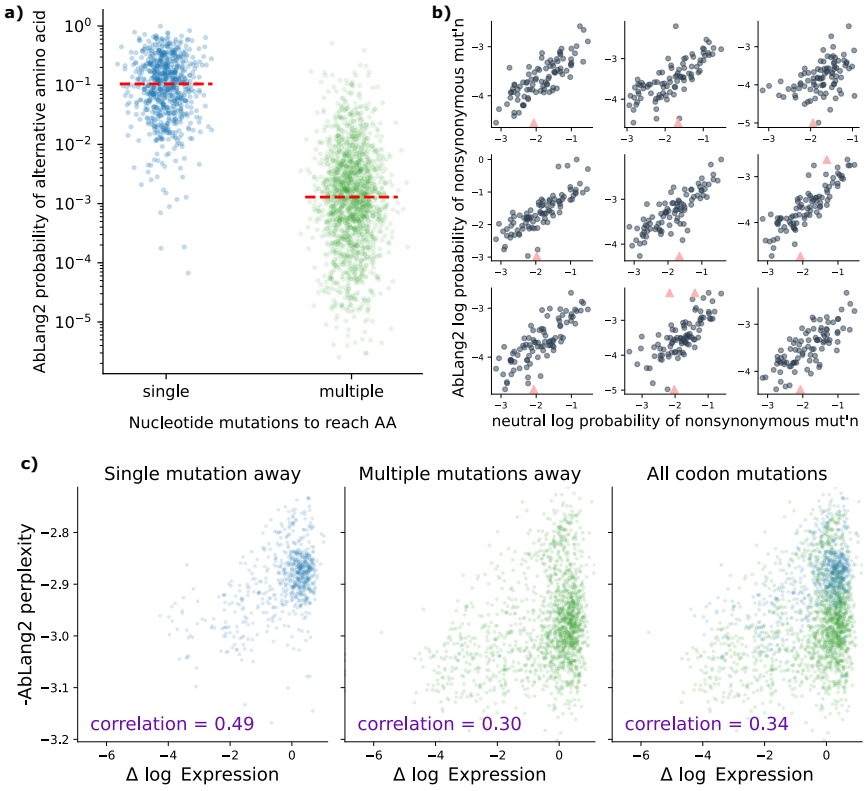

Figure 1: Nucleotide-level mutation processes distort protein language model predictions. **a**: AbLang2 assigns almost 100× lower probabilities to amino acids requiring multiple nucleotide mutations compared to single-mutation variants. Each point represents a possible amino acid substitution at a single site in the amino acid sequence. **b**: AbLang2 probabilities correlate with neutral somatic hypermutation probabilities across the V-encoded portion of nine naive sequences, demonstrating how the model is strongly impacted by mutation bias. Each point represents a site in the sequence. Triangles are outliers that have been brought into the y range. **c**: AbLang2 functional prediction accuracy drops substantially for amino acids that are multiple (2 or 3) nucleotide mutations away from the wildtype codon. Data from [16].

fig:ntProcessInLLMs

Results

Antibody language models are biased by nucleotide-level mutation processes

We first sought to understand the extent to which processes such as neutral mutation rate and the codon table influence antibody language model prediction at masked sites. To do so, we used AbLang2 [5] as a case study. It has been implemented with more consideration of biology than other models, as it distinguishes between germline-encoded and non-germline-encoded sites in its training. To start, we examined a single naive BCR sequence obtained from a recent study that performed deep sequencing of human antibody repertoires [17]. We iterated over each site in this antibody's protein sequence, masked the site's amino acid, and used AbLang2 to compute the likelihood of each of the 19 alternative amino acids at that site, then normalized to get a probability. Next, using the antibody's nucleotide sequence, we split the alternative amino acids at a given site into two groups: those that can be encoded by a codon a single nucleotide change away from the original codon, and those that require multiple mutations.

We found a striking difference in the AbLang2 amino-acid probabilities (Figure 1a). The median probability for amino acids requiring multiple mutations to a codon was almost two orders of magnitude lower compared to those that only required one. This bias is consistent with the hypothesis that the AbLang2 predictions are influenced by mutation processes unrelated to selection.

The bias can be explained by the masked training procedure. It has already been established that language models trained with the masked objective memorize germline sequences [5, 6]. During somatic hypermutation (SHM), single-nucleotide-per-codon mutations to the germline sequence are much more likely than multi-nucleotide codon mutations. As a result, when predicting relative probabilities of alternative amino acids, language models would be expected to assign much higher probabilities to alternative amino acids that only require a single-nucleotide codon mutation (Figure 1a).

Given this observation, we also hypothesized that AbLang2 probabilities are influenced by differences in the rate of SHM between sites. SHM is a purpose-built enzymatic process that introduces mutations into BCR-coding DNA [18], which occurs independently of the process of natural selection in the germinal center. The rate of SHM varies by an order of magnitude or more between sites, and these biases are well characterized using probabilistic models [9, 10]. To test our hypothesis, we examined nine arbitrarily selected sequences from the Rodriguez *et al.* dataset [17]. For each sequence, we used a recent model of SHM [9] to compute per-nucleotide-site rates, and then used the strategy from our previous paper [19] to convert these rates into per-codon-site probabilities of nonsynonymous mutations.

We found a clear correlation between these neutral SHM probabilities and probabilities of mutations estimated using AbLang2 (Figure 1b). The Wald test for a nonzero slope reported a p-value below machine precision in each case.

We next sought to understand if these biases distorted predictions on a functional prediction task. To do so, we used the largest dataset [16] of the FLAb [8] collection of benchmarks. Following the protocol in FLAb, we investigated the Pearson correlation between a mutation's effect on an experimentally measured phenotype, here expression in a phage display library, and the mutation's plausibility (quantified as pseudo-perplexity) according to a model. Perplexity (as defined in the Methods) is the standard way of evaluating the plausibility of a sequence according to a model: it is the across-site geometric mean of the inverse probability of the observed amino acid. Pseudo-perplexity is a variant of perplexity (Methods) which is the standard means of evaluating perplexity for masked language models [8]. In both definitions, lower perplexity corresponds to a more plausible sequence, and we use negative perplexity here so that correlations between model predictions (negative perplexity) and observable (expression) should be positive. We split these predictions by number of nucleotide mutations per codon mutation, as before.

We found a significant drop (from a correlation of 0.49 to 0.30) in predictive performance when going from amino acids that required one mutation to those that required multiple mutations (Figure 1c). Furthermore, when we considered all amino acids together, the correlation remained at 0.34. When we colored these data points by their probability of mutation under an SHM process (Figure S1), we can clearly see that the data points are spread out by the AbLang2 model according to their SHM rate, hindering functional prediction.

In summary, we found that nucleotide-level effects hamper the ability of AbLang2 to predict functional effects of mutations. We then developed an alternative modeling framework that directly factors out nucleotide-level effects.

Fitting a deep amino acid selection model (DASM)

We implemented a model to learn amino-acid preferences of antibodies without being influenced by germline genes, the codon table, or SHM biases (Figure 2). To do so, we extended our previous work estimating a single selection value for every site [19] to estimating a value for every alternative amino acid at every site. This extension is analogous to going from a dN/dS type estimate [20,21] to a sitewise mutation-selection model [22]. Our previous model only operated on antibody heavy chains. This new model operates on heavy chains, light chains, or heavy-light pairs.

As in this previous work, we performed clonal-family clustering, phylogenetic inference, and ancestral sequence reconstruction to generate collections of nucleotide "parent-child pairs" or PCPs (Figure 2a). This resulted in around 2 million PCPs that were used for training (Table S1). Instead of predicting the likelihood of nonsynonymous mutations, we predicted the likelihood of codon mutations using a deep-learning analog of a mutation-selection model. The neutral-probability model was inferred separately using out-of-frame data [9]. We also added a "multihit correction" (see Methods) to this neutral model which accounts for the spatial clustering of SHM [23], resulting in an elevated probability of multiple mutations in a given codon.

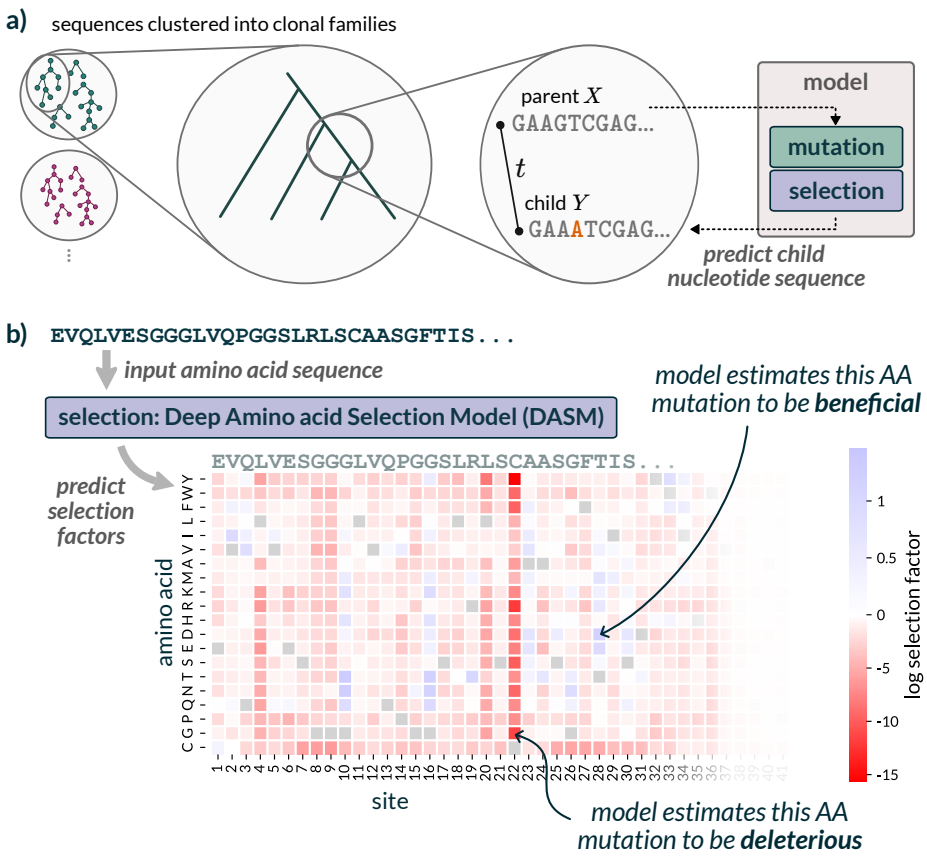

Figure 2: Our model separates mutation from selection to predict functional effects without nucleotide-level biases. **a**: Our model combines a fixed mutation component (trained on non-functional data) with a learned selection component (DASM transformer). Training uses inferred parent-child sequence pairs from reconstructed B cell phylogenies to predict natural affinity maturation after a jointly-inferred time t. **b**: The DASM directly predicts selection factors for all amino acid substitutions at every position in a single forward pass. Positive factors indicate beneficial changes, and negative factors indicate deleterious changes.

fig:methods

The selection component of the model estimates per-site per-amino-acid selection factors given an input amino-acid sequence via a transformer-encoder (Figure 2b). We trained DASMs of several sizes (∼1M, ∼4M, ∼7M) using joint optimization of branch length t and parameters of the DASM (see Methods for details). We found that the ∼4M parameter model performed the best according to our objective function. This DASM has 8 attention heads, 32 dimensions per head, a feedforward dimension of 1024, 5 transformer layers, and a dropout

probability of 0.1; we will use this version for the rest of the paper.

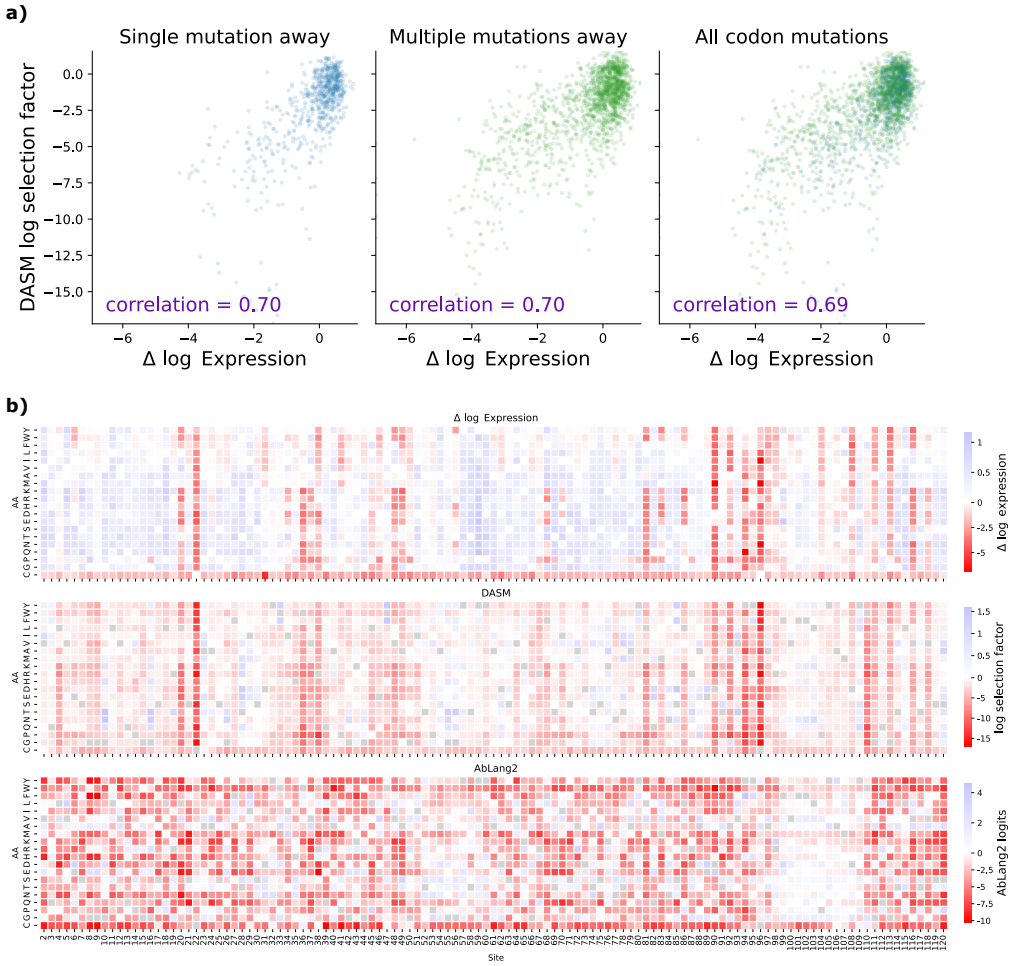

Figure 3: Comparing model predictions with experimentally measured effects of mutations on antibody expression from [16]. **a**: The DASM maintains high predictive accuracy on functional effects of mutations regardless of codon accessibility. The correlation is equally high for amino-acid mutations that only require a single-nucleotide mutation (left plot) vs. amino-acid mutations that require multi-nucleotide mutations (center plot), demonstrating successful separation of mutation bias from functional effects. Compare Figure 1c. **b**: DASM predictions mimic patterns in the expression data. For additional heatmap comparisons see Figure S4.

fig:koenigDASMExpression

As an initial comparison between DASM and AbLang2, we used DASM to predict selection factors for the unmutated antibody sequence used in the Koenig benchmark [16]; we found that the selection factors were predictive of functional

measurements irrespective of the number of mutations per codon (Figures 3a and S2). We were surprised by the strength of the correlation for amino-acid mutations that require multi-nucleotide codon mutations, given that training signal should be weaker for those rarer mutations. We also found that the selection factors showed very similar distributions for amino-acid mutations requiring single- vs. multi-nucleotide codon mutations (Figure S3). Furthermore, the DASM selection factors captured the alternating pattern of selective constraint on beta sheets evident in the expression data (red columns in Figures 3b and S4).

Thrifty+DASM accurately predicts affinity maturation

Next, we evaluated the ability of the DASM to predict the course of natural affinity maturation. To do so, we used PCPs from the `Rodriguez` data (Table S1), which were not used for training the DASM, nor for training AbLang2. For each PCP, we quantified each model's ability to predict both the location of nonsynonymous mutations in the child sequence and the identity of the mutant amino acid. For the DASM, we computed a mutation's probability by multiplying the mutation's selection factor, predicted by the DASM, with its neutral mutation probability, predicted using the same fixed neutral mutation model used to train the DASM [9].

We found that the DASM-based approach was better than AbLang2 at predicting the location of nonsynonymous mutations observed in the PCPs (Figure S5ab). In fact, the overlap between observed and expected is substantially better than what we were able to obtain in a highly controlled mouse experiment [24] with a customized mutation model and a deep mutational scan that quantified how mutations affect binding to the relevant antigen [25].

We also found that the DASM-based approach was better than AbLang2 at predicting the identities of mutant amino acids. To compare the models at this task, we used a notion of "conditional perplexity". Specifically, for each PCP where the parent and child sequences differ on the amino-acid level, we calculated the perplexity of the residues in the child that are different from the parent, conditioning probabilities on there being a substitution (see cond-ppl definition in Methods). We do this to give AbLang2 the best chance of succeeding: although it might have difficulty predicting the occurrence of mutations (Figure S5/conseb) it might still be able to predict the identity of mutations.

Indeed, the DASM had lower conditional perplexity than AbLang2 on 1,000 sequences from the `Rodriguez` [17] dataset (Figure S5c). The median value for DASM was 4.88, compared to 7.39 for AbLang2. In addition to having a lower median, the DASM also has fewer very large values.

The DASM outperforms masked and autoregressive models at predicting functional effects of mutation

We next performed a more comprehensive characterization of the ability of models to predict mutational effects. Because the DASM is trained exclusively

on evolutionary trajectories rather than functional measurements, evaluation on expression and binding benchmarks is strictly zero-shot with no risk of data leakage. We expanded our suite of comparator models to include ESM2 [11, 12], a general protein language model trained with a masked objective, and ProGen2 [13], an autoregressive language model. We used the small general variant of ProGen2, which the FLAb benchmarking paper found to be the best overall model [8], and the 650M variant of ESM2. To predict the plausibility of mutant sequences under these models, we followed current practice [8] and calculated each sequence's pseudo-perplexity for AbLang2 [5] and ESM2 [26], each sequence's perplexity for ProGen2, and then compared the model outputs to experimentally measured mutational effects using Pearson correlation. To predict mutational effects using the DASM, we simply fed the DASM with the unmutated sequence from the DMS experiment and used the output selection factors as predicted effects. We cannot use perplexity because selection factors alone do not give likelihoods.

We based our evaluations on the April 2024 version of the FLAb benchmarking project [8], which preceded our work and thus was not subject to selection bias by us. We also benchmarked high-throughput binding data (more recent than FLAb) from the Whitehead lab [14,15] that provided affinity measurements across many variants and antigens.

To start, we evaluated these models on the two largest datasets from the FLAb collection. The first data set, from Koenig et al. [16], is a deep mutational scanning experiment performed on the Fab of the anti-VEGF antibody G6.31. The authors generated single-site saturated mutagenesis libraries incorporating all possible amino-acid mutations to both the variable heavy and variable light domains. Using phage display, they then performed two independent selection steps: one in which they selected for Fab variants that were stably expressed, and another in which they selected for Fab variants that could bind VEGF. They quantified mutational effects on these properties by computing enrichment ratios of each mutation in selected versus unselected pools, as quantified using deep sequencing.

	Binding		Expression	
Model	Heavy	Light	Heavy	Light
AbLang2	−0.032	0.049	0.344	0.084
DASM	**0.335**	**0.316**	**0.688**	**0.674**
ESM2	−0.001	0.308	0.418	0.524
ProGen2	0.156	0.276	0.559	0.568

Table 1: Correlation of models with predicting effects of single mutations on antibody expression and antigen binding, as measured in [16]. tab:koenig

We found that the DASM outperformed the other models on both binding and expression (Table 1, Figure S4). Scaling ESM2 from 650M to 3B parameters did not improve performance: indeed, the larger model showed slightly

degraded correlations, particularly for light chain predictions (Table S2). This is consistent with recent observations that medium-sized protein language models can outperform larger ones on transfer learning tasks [27]. Thus we only used the 650M model in the rest of our analyses.

We next turned to the second-biggest dataset of the FLAb benchmark, from Shanehsazzadeh et al. [28]. In this study, the authors took an anti-HER2 antibody, trastuzumab, and used deep generative models to redesign the heavy chain complementarity determining regions (HCDRs). They generated libraries of HCDR variants, including both HCDR3-only designs and HCDR123 designs. Unlike the first dataset described above, many variants had multiple mutations relative to the unmutated antibody sequence. The experiments expressed antibody variants in E. coli, and sorted by FACS based on binding signal. We restricted our attention to sequences with the two most common heavy chain amino acid lengths (119 and 120) as the other lengths did not have enough data to make a full comparison.

We assessed the ability of models to predict these binding measurements. For the language models, we computed the perplexity of each variant, as before. For the DASM, we calculated a consensus sequence for each sequence length, and then used the DASM to compute selection factors for that sequence. Then, we computed a score for each variant by summing the log selection factors for each amino-acid mutation in the variant relative to the consensus sequence. As above, the resulting correlation is substantially higher for the DASM compared to the other models (Table 2).

Seq. length	AbLang2	DASM	ESM2	ProGen2
119	0.263	**0.458**	0.248	0.074
120	0.166	**0.518**	0.337	0.052

Table 2: Correlation of models with binding measurements on the data of [28], which typically involves multi-mutant variants. See Figure S6 for scatterplots. tab:shane

For our third validation, we sought to see how our model could predict affinity in the context of large-scale yeast display experiments using MAGMA-seq [14]. We were especially interested in this assay because the measurement is affinity-only rather than a conflation of affinity and expression as in the previous data sets. Because none of these models are trained in an epitope-specific way this will be a challenge for the models. Specifically, MAGMA-seq determines quantitative monovalent binding affinities through deep sequencing of barcoded Fab libraries sorted at multiple antigen concentrations in a manner analogous to Tite-Seq [29]. These data are not present in the FLAb benchmarks. We used the largest datasets in the original MAGMA-seq paper [14] which test variants of influenza antibodies. We also used MAGMA-seq data from [15] which combinatorially applied mutations from development trajectories of mature human antibodies against SARS-CoV-2 spike protein.

We found that the DASM performed substantially better than other models

Source	Antibody	AbLang2	DASM	ESM2	ProGen2
Petersen [14]	222-1C06	0.041	**0.248**	−0.039	−0.030
	319-345	0.079	**0.279**	0.199	0.222
Kirby [15]	002-S21F2	−0.246	**−0.165**	−0.283	−0.353
	Ab_2-15	−0.325	**0.094**	−0.265	−0.069
	C118	−0.624	**0.276**	−0.293	−0.159

Table 3: Correlations between model predictions and binding affinity. The "Petersen" data is from an experiment probing the rules of recognition for influenza neutralizing antibodies [14] and "Kirby" data is from combinatorial libraries applying combinations of mutations on the path from naive to mature SARS-CoV-2 antibodies [15]. See Figure S7 for corresponding scatter plots. tab:magmaCorrelations

for this task (Table 3, Figure S7). Nearly all correlation coefficients were small, pointing to the difficulty in predicting effects of mutations on antigen-specific binding affinities. Nevertheless, the DASM was the only model to have a positive correlation for most datasets. The UCA_002-S21F2 lineage proved challenging for all models, with all models having a negative correlation. This may not be surprising given that 002-S21F2 uses a rare VH5-51/VK1-33 gene combination found in only 3 out of 5252 SARS-CoV-2 antibodies in the CoV-AbDab database [30].

DASM models are orders of magnitude faster than competing models, and much smaller

We next compared the computational requirements for doing these evaluations. We imagined two settings: one where a scientist wishes to evaluate a small collection of sequences on their laptop without a GPU, and the other where they wish to evaluate a larger collection of sequences on a GPU server. Our timing script ran the DASM model, as well as AbLang2 and ESM2 using stepwise masking to obtain amino acid likelihoods. The local machine was a MacBook Pro with a M2 Max chip and 96 GB of memory. The GPU server had an AMD EPYC 75F3 32-core processor with 995 GB of memory and an NVIDIA A100 80GB GPU.

Model	CPU (s/seq)	GPU (s/seq)
DASM	0.0097	0.0053
AbLang2	11.0529	0.5196
ESM2	112.5989	7.6090

Table 4: Computational efficiency comparison on sequences from the MAGMA-seq experiments. 10 sequences were run on CPU, and 100 on the GPU server. tab:timing

The DASM achieved dramatic computational efficiency gains compared to

masked language models (Table 4). On a CPU, the DASM evaluates sequences over 1,000 times faster than AbLang2 and more than 10,000 times faster than ESM2. On a GPU, the DASM is 100 times faster than AbLang2 and over 1,000 times faster than ESM2. This speed advantage comes from the DASM providing predictions for all variants in a single pass, eliminating the need for iterative masking procedures required by masked language models. (We note that it is possible to make predictions from masked language models without masking, although this is not considered best practice because of the influence of the unmasked residue.)

This evaluation was actually generous to the masked language models, as it assumes that we are evaluating likelihoods of masked sites and combining them to evaluate multi-mutant variants. That is in contrast to what was actually done in the performance evaluation, which is direct evaluation of the sequence perplexity for each sequence individually (which should be more accurate). ProGen2 was not included in this comparison because it is categorically slower for this use case: autoregressive models for a panel of variants require running each variant individually through the model.

The DASM benchmarked here is also significantly smaller than alternate models. It has 4M parameters, compared to 45M for AbLang2, 650M for ESM2, and 151M for ProGen2. We suspect that this efficiency is enabled by DASM learning selection effects only, rather than selection and mutation-level effects as for existing models.

In summary, we imagine end-users will find it convenient to download a small (23 MB) weights file and run the DASM on their laptop, as compared to existing models requiring more powerful hardware.

Discussion

We have motivated and developed a new direction for protein language modeling. To motivate this approach, we showed how masked language modeling implicitly learned the codon table and somatic hypermutation rates, properties that are orthogonal to antibody function. This incorporation degrades model performance for predicting effects of mutations on antibody expression and binding.

To address this limitation, we introduced a new framework: a Deep Amino Acid Selection Model (DASM), which models selection effects separately from mutation effects. By modeling these components independently, the DASM more accurately predicts the functional consequences of amino-acid mutations while having dramatically reduced computational requirements. The success of our approach highlights the importance of incorporating biological realities into machine-learning models for protein engineering. This aligns with recent calls for deeper dialogue between machine learning and evolutionary biology to address phylogenetic biases in biological foundation models [31].

Thrifty+DASM can be viewed as a neural-network extension of the models rooted in the work of Halpern and Bruno [22]. There, the probability of

a codon mutation is expressed as the product of that mutation under a neutral nucleotide process, times a term representing the selection for or against the corresponding amino-acid substitution at that site. Although the original model expressed selection coefficients in a parameter-sparse way using equilibrium frequencies, further model elaborations allowed for per-site-per-amino acid selection factors, as described here, either in a fixed-effects [32, 33] or random-effects [34] framework. Other related work includes developing evolutionary models using deep mutational scanning (DMS) experiments [35,36], and models of sequence-structure compatibility [37]. Thrifty+DASM also extends our previous work that estimates a single value of natural selection at every site [19]; such a model is not comparable to an antibody foundation model because it does not estimate per-amino-acid probabilities.

By separating out selection from mutation and the effect of evolutionary contingency, DASMs provide direct interpretability: the selection factors indicate which amino-acid mutations are beneficial or deleterious at each position. This interpretability could prove valuable for antibody engineering, where understanding which specific mutations would drive improved expression or binding is crucial for rational design. We have dedicated a companion paper to leveraging this interpretability to provide new perspectives on the operating rules of affinity maturation [19]: that work provides a nuanced sitewise perspective on natural selection in antibodies that challenges classical oversimplified views of selection patterns. For users wishing to explore the relationship between DASM selection factors and structure for human antibodies in the SAbDAb database [38], we have made interactive 3D visualizations of DASM selection factors using `dms-viz` [39] available at `https://matsen.group/dasm-viz/v1/`.

The current generation of DASM model does not use any antigen-labeled training data. The signal that it leverages to infer some limited ability to predict binding comes from natural affinity maturation. This affinity maturation comes through natural repertoires and so represents a mix of all of the antigens to which the sampled individuals have been exposed.

In future work we will explore fine-tuning of these models with antigen-specific data. While DASM provides better-than-state-of-the-art zero-shot performance on binding benchmarks, recent work for binding focuses on using protein embeddings as inputs to subsequent classifiers [40], or fine-tuning for binding prediction [3, 41]. Because the DASM framework separates mutation from functional properties, a fine-tuned DASM may improve on these previous efforts. We also have plans to extend the DASM framework to estimate the effect of natural selection on insertion and deletion events.

We are beginning the process of extending DASMs to other settings. Although antibodies form an interesting first application of DASMs, and have many properties that make DASMs a useful tool, DASMs are not restricted to the antibody case. Viral sequences also exist in abundance and may be amenable to the DASM approach. Rather than many clonal families for antibodies, we will fit a DASM with many separate alignments for related but distinct evolutionary histories.

Taking this idea to its logical extent, we would like to train a DASM model

analogous to ESM [26] for all proteins. However, this will be a major computational undertaking. Even setting training such a model aside, doing phylogeny and ancestral sequence reconstruction on all protein alignments will require careful planning. If we followed the steps used here for phylogeny and ancestral sequence reconstruction on the 2.6 million sequence alignments used for the MSA Transformer [42] it would take around 3,000 CPU-years.

DASMs represent a new paradigm for deep models of protein function that leverage evolutionary information directly. Even in this initial implementation, DASMs outperform existing foundation models while requiring orders of magnitude less computation, parameters, and training data. This efficiency suggests that evolutionary structure provides a powerful approach for understanding protein function.

Methods

Data

BCR sequence data was processed with `partis` [43] to cluster into clonal families and infer germlines. Inferred insertions or deletions were reversed, so that all sequences align to the naive sequence without gaps. We selected clonal families with at least two productive sequences; a sequence is considered productive if the canonical cysteine and tryptophan codons that flank the CDR3 are in the same frame as the start of the V segment (although they can be mutated), and there are no stop codons. We excluded sequences with stop codons. Following the training of other LLMs (e.g. [5]) we also excluded sequences with mutated conserved "signature" cysteines, in contrast to our previous work [19].

As in our previous work, tree inference and ancestral sequence reconstruction were performed per clonal family with the K80 substitution model using the naive sequence as outgroup, allowing mutation rate heterogeneity across sites using a 4-category FreeRate model using IQ-Tree [44]. However, for paired data we used the *edge-linked-proportional* partition model in IQ-Tree that allowed the heavy and light chains to evolve at overall different rates [45]. Because these clonal families are independent these phylogenetic inferences were run in parallel.

Once this was done, we had a set of parent-child pairs (PCPs) that correspond to the pairs of parent and child sequences on the edges of the phylogenetic tree (Figure 2a). We used these PCPs to train the model.

We denote pairs of parent and child sequences as (X, Y), where X is the parent sequence and Y is the child sequence. We use $\bar{X}$ to denote the amino acid sequence corresponding to X.

Model

Formulation and loss

Assume we are given a parent codon sequence X and a child sequence Y. We will use $\bar{c}$ to denote the amino acid sequence of codon c, and use $\bar{Z}$ to denote the amino acid sequence of codon sequence Z. We will use j to denote codon sites. As before [19], we model the neutral probability of a mutation to codon c as the product of per-nucleotide-site mutation probabilities: specifically, the probability of mutating from the parent codon to codon c is the product of the probabilities of each constituent nucleotide mutation (or non-mutation) under the neutral model. This results in the probability $p_{j,c}(t, X)$ of a mutation to codon c at site j after time t.

The selection term $f_{j,\bar{c}}(\bar{X})$ is a "selection factor" that quantifies the natural selection happening at site j if it was to be changed to $\bar{c}$. If this value is greater than 1, it predicts that the mutation would be beneficial in the course of affinity maturation, while if it is less than 1, it predicts that the mutation would be deleterious.

We parameterize the DASM f using the standard transformer-encoder architecture [46]: an amino-acid embedding, sinusoidal positional encodings, and PyTorch's `TransformerEncoder` module. The only non-standard component to this architecture is a custom "wiggle" activation function to the output layer that prevents extreme selection factors as previously described [19]. This function asymptotes to zero for highly deleterious mutations and grows sub-linearly for beneficial ones.

We will now define the likelihood $\ell_{j,c}(t, X)$ of codon c at site j given time t and parent sequence X. When c is a non-wildtype codon it is

$$\ell_{j,c}(t, X) := \begin{cases} p_{j,c}(t, X) f_{j,\bar{c}}(\bar{X}) & \text{if } c \text{ codes for an amino acid} \\ 0 & \text{if } c \text{ codes for stop.} \end{cases} \tag{1}$$

eq:mutsel

where $f_{j,a}(\bar{X}) := 1$ when a is the amino acid for the wildtype codon. We then take the likelihood of the wildtype codon to be 1 minus the sum of these non-WT codons.

The overall likelihood for a parent-child pair is then

$$\prod_j \ell_{j,y_j}(t, X)$$

where y_j is the jth codon of Y. We optimize this likelihood jointly over the branch lengths t and parameters of the selection model f. This joint optimization is performed cyclically, in which a complete cycle consists of neural network optimization followed by branch length optimization for every parent-child pair. The parent sequence and the child sequence are pre-estimated, fixed, and used as training data. The branch lengths are independent and so are optimized in parallel.

Because $\ell_{j,c}(t, X) = p_{j,c}(t, X)$ when c codes for the wildtype amino acid, this approach effectively fixes the selection factors for neutral substitutions to

be 1 for the purposes of branch length optimization. This is useful because it gives us a "gauge" that eliminates a potential unidentifiability in the model.

Especially early in training it can happen that $p_{j,c}(t, X) f_{j,\bar{c}}(\bar{X})$ is greater than one, or that the sum of such terms is greater than one. In these cases, the sum is clamped to be a little less than 1.

Perplexity

Perplexity is a common metric for evaluating autoregressive language models such as ProGen2 [13]: it is the geometric mean of the inverse probabilities of the model generating each observed token given its context. These inverse probabilities can be interpreted as the effective number of tokens that the model considers plausible at each position. This is equivalent to the exponential of the average negative log probability of each token given its preceding context:

$$\text{ppl}(x) = \exp\left(-\frac{1}{n}\sum_{i=1}^{n} \log p(x_i \mid x_{<i})\right),$$

where $x = (x_1, x_2, \ldots, x_n)$ is a sequence of n tokens, and $x_{<i}$ represents all tokens preceding position i.

For encoder-only models like ESM2 and AbLang2, which mask tokens rather than using autoregressive prediction, we follow the authors of these models and instead calculate a "pseudo-perplexity" using the probability of each token given all other tokens in the sequence:

$$\text{pseudo-ppl}(x) = \exp\left(-\frac{1}{n}\sum_{i=1}^{n} \log p\big(x_i \mid x_{\setminus i}\big)\right),$$

where $x_{\setminus i}$ denotes the sequence with token i masked out.

We also use a notion of "conditional" perplexity: for each parent-child pair (x, y) of sequences that differ on the amino acid level, calculate the perplexity of the residues that are different from the parent, conditioning probabilities on there being an amino acid substitution. That is, if we let $S_{x,y}$ be the sites that differ between x and y, then

$$\text{cond-ppl}(x, y) = \exp\left(-\frac{1}{|S_{x,y}|}\sum_{i \in S_{x,y}} \log p(\bar{y}_i \mid x;\ \bar{y}_i \neq \bar{x}_i)\right)$$

where bar represents amino acid sequence as before.

Multihit correction

In the SHM process, having a mutation at a site increases the probability of mutations at nearby sites [23]. Although a general solution to this problem can easily lead down the path of intractability, we wanted to incorporate this phenomenon into our work.

Inspired by the work of [47], we added several simple "multihit" rate multipliers to our neutral model. These multipliers account for the varying probabilities of mutations based on the number of nucleotide changes required.

We found that, on neutrally-evolving out-of-frame data, such a correction substantially improved model fit (Figure S9). Before correction, the model systematically underestimates multi-hit mutations. After training the multihit model with correction factors for 1, 2, and 3 mutations per codon, the observed-expected agreement improved substantially for these classes.

This multihit correction was trained on the same separate out of frame data as used in training our neutral model [9] and was incorporated into the neutral mutation probabilities for DASM training.

Heavy and light rates

Light chains mutate at a lower rate than heavy chains during affinity maturation. To quantify this relative rate, we used IQ-Tree's rate partition feature during phylogenetic inference on paired heavy-light chain data (see Data section). This allowed us to estimate separate substitution rates for heavy and light chains within each clonal family. We found the median relative rate of light to heavy chains across all clonal families to be 0.63, which we used as our fixed light chain rate adjustment parameter. This estimate is broadly concordant with previous observations that light chains evolve at roughly half the rate of heavy chains [48].

This relative rate is incorporated into the likelihood calculation by scaling the neutral mutation rates for light chain sequences by the light chain rate adjustment factor before combining them with selection factors. Specifically, when evaluating paired heavy-light chain sequences, the per-site neutral mutation rates $p_{j,c}(t, X)$ for light chain sites are multiplied by this adjustment factor, while heavy chain rates remain unscaled.

Model implementation, training, and evaluation

This model was implemented in PyTorch 2.5 [49]. Models were trained using the RMSprop optimizer, with 4 cycles, each consisting of branch length optimization then neural network optimization.

We used the following software: Altair [50,51], BioPython [52], Matplotlib [53], pandas [54], pytest [55], Seaborn [56], and Snakemake [57].

LLM model score computation

ESM2 scores were calculated using the FLAb paper methodology, separately evaluating heavy and light chains then averaging the pseudo-perplexities, while AbLang2 directly evaluated paired heavy-light sequences. ProGen2 scores were computed following the same FLAb methodology of separately evaluating heavy and light chains then averaging perplexities.

Koenig evaluation

We obtained the Koenig et al. deep mutational scanning data from the FLAb benchmark repository [8] (commit 67738ee, April 17, 2024). For DASM evaluation, we used the wild-type G6.31 heavy and light chain sequences as input to predict selection factors for each possible amino acid substitution at each site. The model's log selection factors were compared against the experimental log enrichment ratios via Pearson correlation. We evaluated performance separately for heavy and light chains across both binding and expression datasets.

Shanehsazzadeh evaluation

We obtained the Shanehsazzadeh et al. binding affinity data from the FLAb benchmark repository [8] (commit 67738ee, April 17, 2024). We subset to the "zero-shot" component of the dataset. For DASM evaluation, we partitioned the data by heavy chain amino acid length (119 and 120 residues) due to the diverse nature of the designed sequences. For each length group, we computed a site-by-site consensus sequence to serve as the reference sequence for model predictions. The aggregate log selection factor for each variant was calculated as the sum of log selection factors for each position that differed from the consensus sequence. Model performance was evaluated through Pearson correlation analysis between the aggregate log selection factors and experimental binding affinities.

MAGMA-seq evaluation

We combined data from two complementary studies using the MAGMA-seq methodology: Petersen et al. [14] providing CDR-targeted mutagenesis data around mature influenza antibodies and Kirby et al. [15] providing UCA to mature antibody evolution trajectories for SARS-CoV-2 antibodies. All sequence variants were assigned to their corresponding antibody systems using reference matching with sequence similarity thresholds. To ensure data quality, experimental replicates were aggregated using geometric mean in $\log_{10}$ space, and high-variance measurements (coefficient of variation > 0.5) were filtered out as in the original papers. After deduplication and quality filtering, the unified dataset contained 1,128 sequences across 6 antibody systems: 4 Kirby UCAs and 2 Petersen mature antibodies. The 1_20 antibody system was dropped from the Kirby data as it only had 7 assigned sequences. Reference sequences were used as inputs for DASM score calculations. Model performance was evaluated using Pearson correlation with binding affinity ($-\log_{10} K_D$).

Data availability

Models and inference code can be found at `https://github.com/matsengrp/netam`, including a simple means of accessing the pretrained model demonstrated in the `notebooks/dasm_demo.ipynb` notebook. Our reproducible experiments

are available at `https://github.com/matsengrp/dasm-experiments`. Relevant preprocessed data has been uploaded to Zenodo at `https://doi.org/10.5281/zenodo.17322891`.

Reproducing figures

The following figures were made in notebooks, which can be found in the `notebooks/dasm_paper` directory of the experiments repository.

- Figure 1 is made in `nt_process_in_llms.ipynb`.
- Table 1 and Figures 3, S1, S2, S3, and S4 are made in `koenig.ipynb`.
- Figure S5 is made by the Snakemake pipeline and in `perplexity.ipynb`.
- Table 2 and Figure S6 are made in `shanehsazzadeh.ipynb`.
- Table S1 is made in `data_summaries.ipynb`.
- Table S2 values are from `https://github.com/matsengrp/dasm-experiments/pull/2`.

Figure S9 is made in `multihit_model_exploration.ipynb` in the `https://github.com/matsengrp/thrifty-experiments-1` repository.

Our repository file `data/whitehead/MAGMA_PIPELINE_STRUCTURE.md` describes how Figure S7 and Table 3 are made.

Table 4 is made by `timing_direct_gpu.py` and `make_timing_table.py`.

Competing interests

The authors have no competing interests to disclose.

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Supplementary Materials

purpose	name	samples	clonal families	PCPs	median mutations
train	`JaffePairedCC`	4	50,776	209,599	7
train	`TangCC`	21	45,267	651,899	2
train	`VanwinkleheavyTrainCC`	149	21,269	124,985	4
train	`VanwinklelightTrainCC1m`	330	2,658	1,000,000	2
test	`RodriguezCC`	51	3,592	38,050	5

Table S1: Data used in this paper. CC means that PCPs with mutated cysteines are excluded from the data. `JaffePairedCC` is paired data from [59] sequenced using 10X. `TangCC` data is heavy chain data from [58, 60] and was sequenced using the methods of [60]. `VanwinkleheavyTrainCC1m` is a subset of the heavy chain data from [61] sequenced using Takara 5'RACE BCR kit. `VanwinklelightTrainCC1m` is a 1M subset of the light chain data from [61] sequenced using Takara 5'RACE BCR kit. `RodriguezCC` data is the 5′ RACE heavy chain data from [17] and is used only for testing. The "samples" column is the number of individual samples in the dataset; in these datasets, each sample is from a distinct individual. "Clonal families" is the number of clonal families in the dataset. "PCPs" is the number of parent-child pairs in the dataset. "Median mutations" is the median number of mutations per PCP in the dataset. tab:data

	Binding		Expression	
Model	Heavy	Light	Heavy	Light
ESM2-650M	−0.001	0.308	0.418	0.524
ESM2-3B	−0.025	0.283	0.418	0.469

Table S2: Comparison of ESM2 model sizes on the Koenig benchmark. The larger ESM2-3B model (2.8B parameters) performs slightly worse than the 650M variant, particularly on light chain predictions. tab:esm2scaling

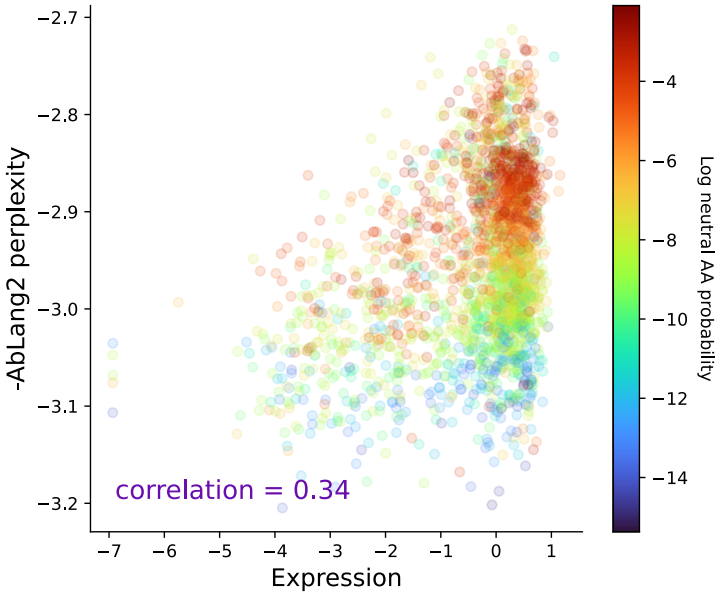

Figure S1: Conflating mutation and selection hinders functional prediction. This plot is analogous to the rightmost panel of Figure 1c, but colored by mutability according to the Thrifty [9] model. fig:koenigAblangSHM

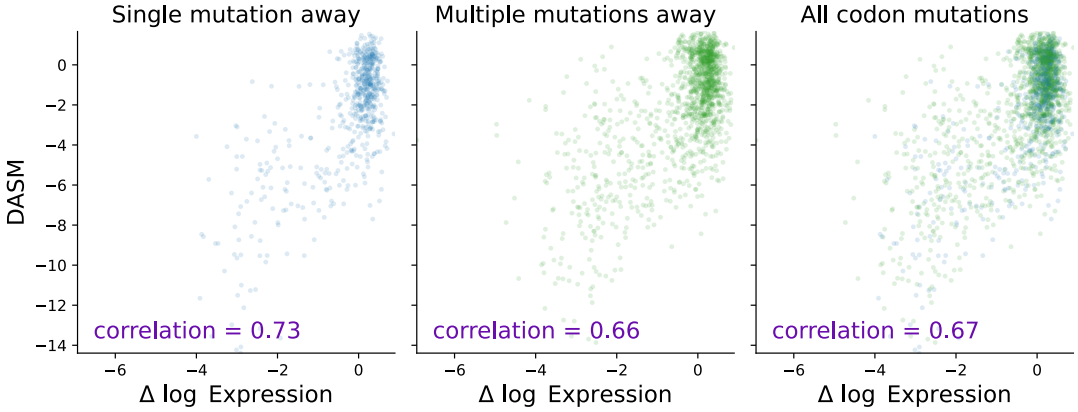

Figure S2: DASM removes codon bias in light chain functional predictions. Equivalent plot as Figure 3 but for light chain. fig:koenigDASMExpressionLight

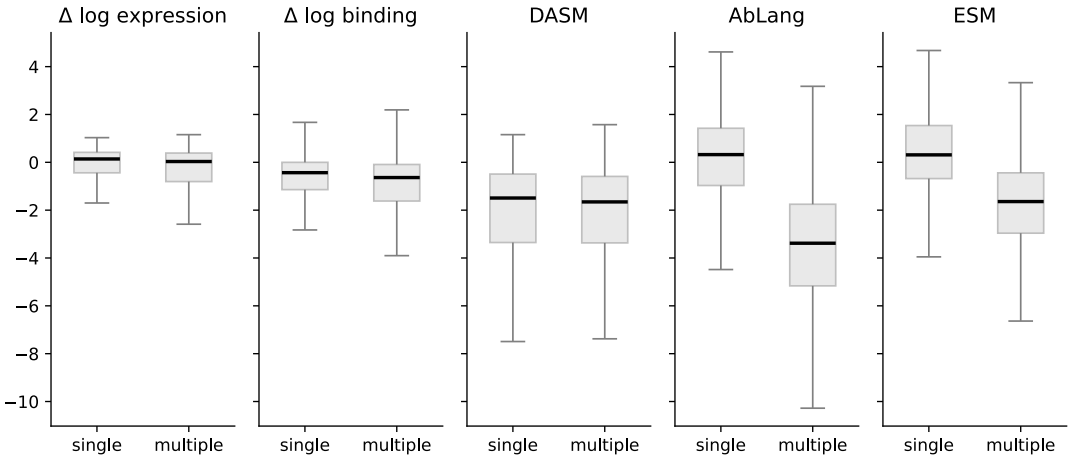

Figure S3: DASM selection factors are similar between codon neighbor amino acids and non-neighbors (compare Figure 1a), in contrast to other models. Comparison done on the heavy chain of the Koenig [16] wildtype sequence. fig:KoenigNeighborComparison

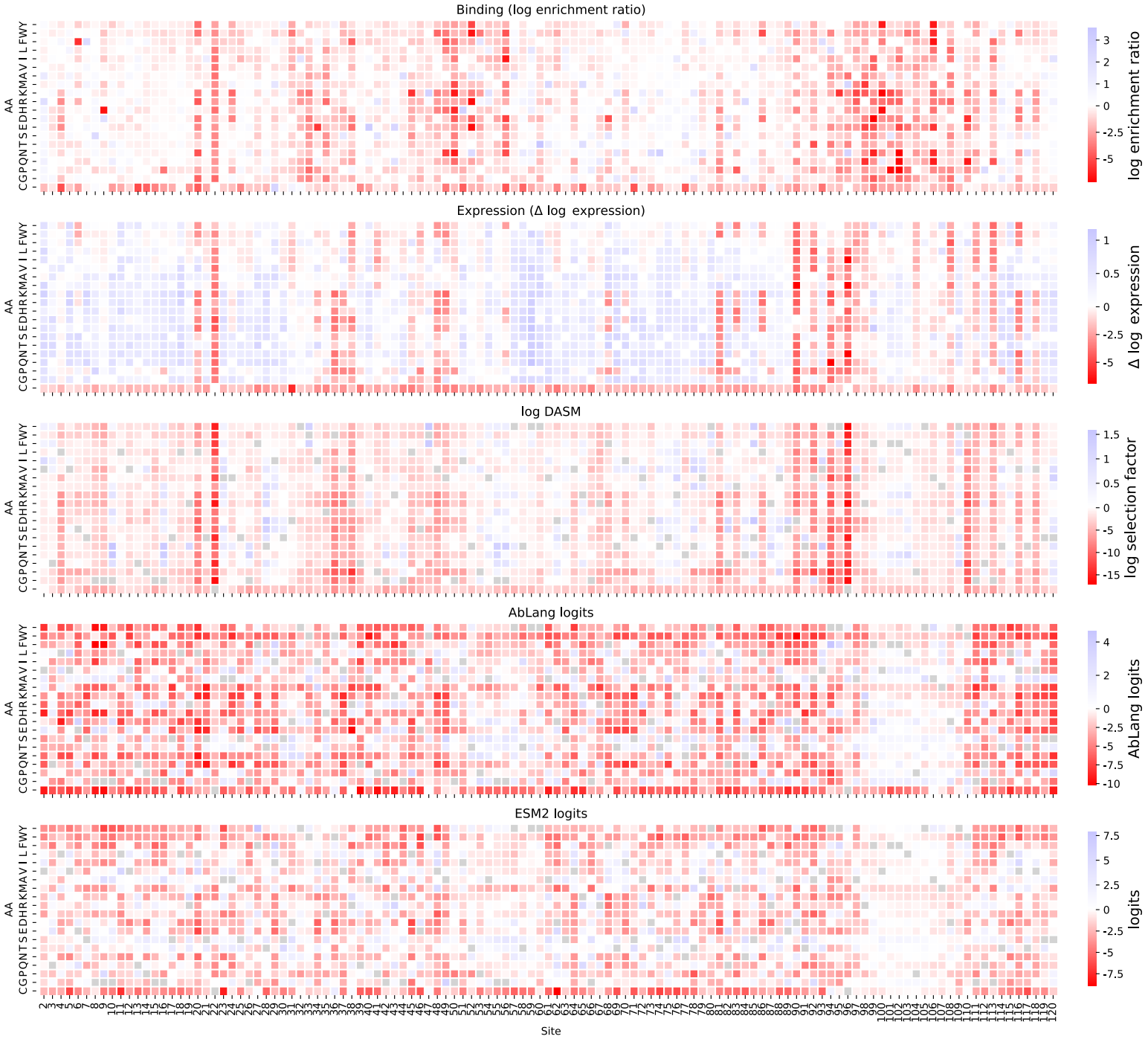

Figure S4: Heatmap showing the heavy-chain data of [16] along with model predictions.

fig:koenigHeavyHeatmap

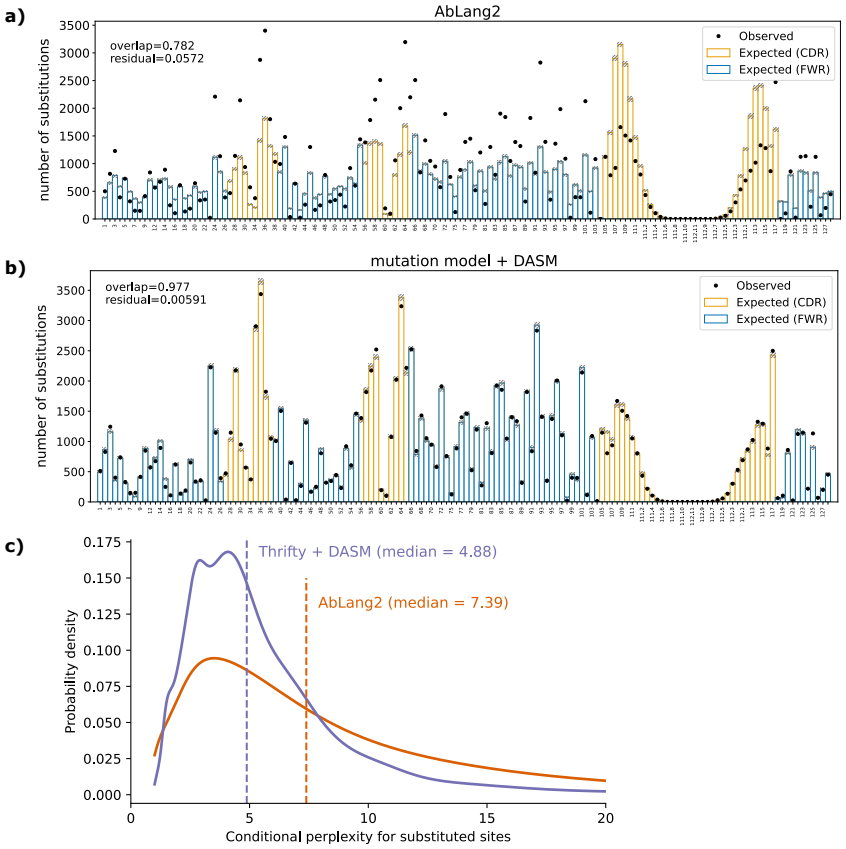

Figure S5: The DASM with the Thrifty neutral model accurately assesses probabilities of natural affinity maturation paths. **a**, **b**: The DASM is better than AbLang2 at predicting the location of nonsynonymous mutations observed in PCPs withheld from model training. **c**: The DASM achieves lower conditional perplexity (median 4.88 vs 7.39) when predicting amino acid identity at mutated sites, with fewer extreme outliers. The conditional perplexity is the perplexity of the child amino acid, conditioned on there being a mutation at that site. Note that due to the inherent stochasticity of affinity maturation, there is a lower limit to this conditional perplexity that is substantially greater than 1. fig:pcpr-predictions

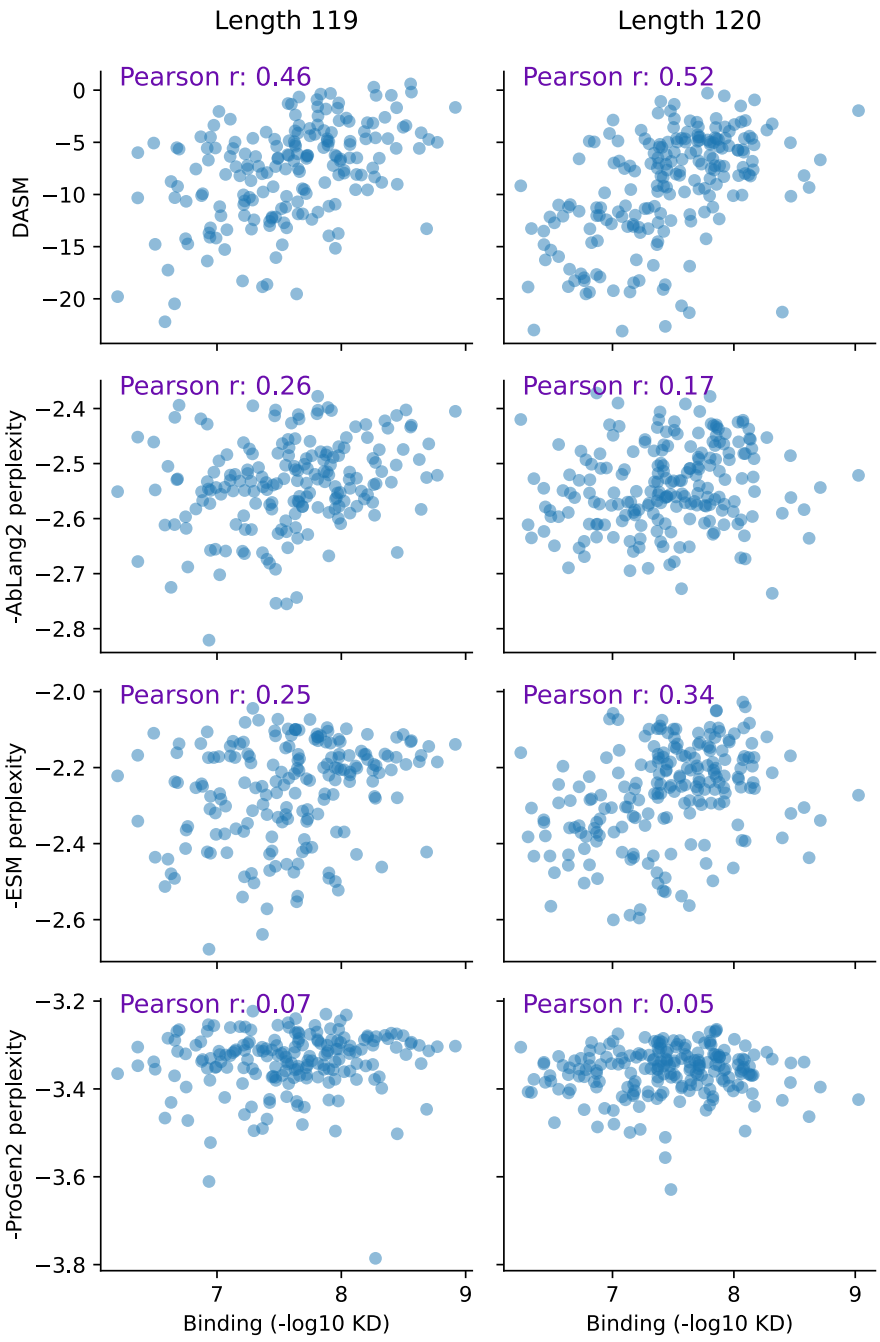

Figure S6: Scatterplots for the data of [28] zero-shot data set, partitioned by sequence length.

fig:shane

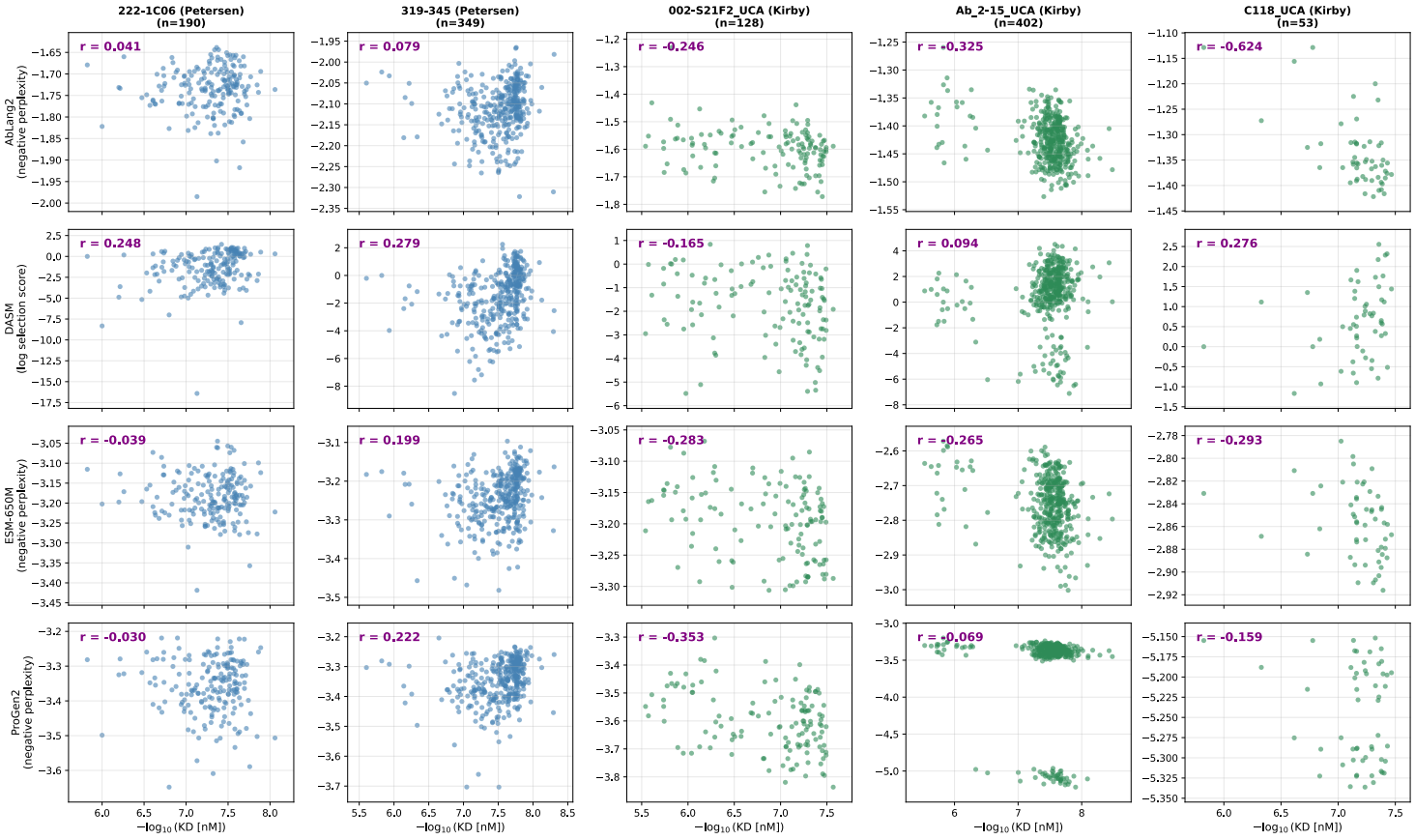

Figure S7: Model predictions versus experimentally measured binding affinity for five antibodies using the MAGMA-seq protocol. "Petersen" data are from an experiment probing the rules of recognition for influenza neutralizing antibodies [14] and "Kirby" data are from combinatorial libraries applying combinations of mutations on the path from naive to mature [15]. Each row shows a different model (DASM, ESM2, AbLang2, ProGen2) and each column shows a different antibody lineage.

fig:magmaScatter

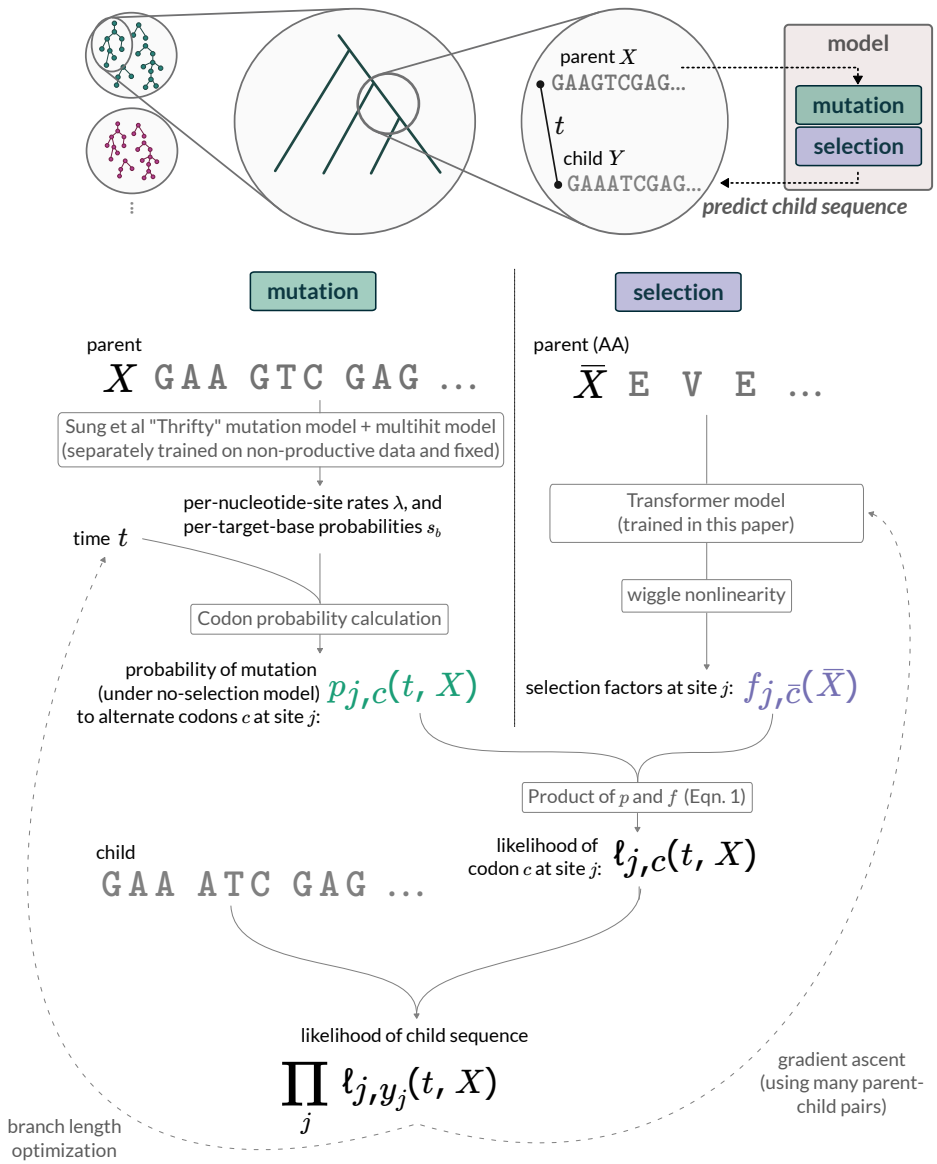

Figure S8: The model is trained to predict the probability of a child sequence given the parent sequence. It is divided into mutation and selection components. Mutation: given a parent sequence X, probability of mutation to alternate codons after time t is calculated using a model of SHM [9] and a "multihit model" (see Methods) and then aggregated into codons as in [19] to obtain $p_{j,c}(t, X)$. Selection: given an amino acid translation $\bar{X}$ of the parent, the transformer-encoder gives per-site selection factors $f_{j,\bar{c}}(\bar{X})$. These are then multiplied (1) and summed to give the probability of the observed child sequence at every site. This gives a likelihood for a parent-child pair. The algorithm maximizes the likelihood across branch lengths t for each parent-child pair as well as across the parameters of the transformer model for all parent-child pairs in the dataset (dashed lines).

fig:bigMethods

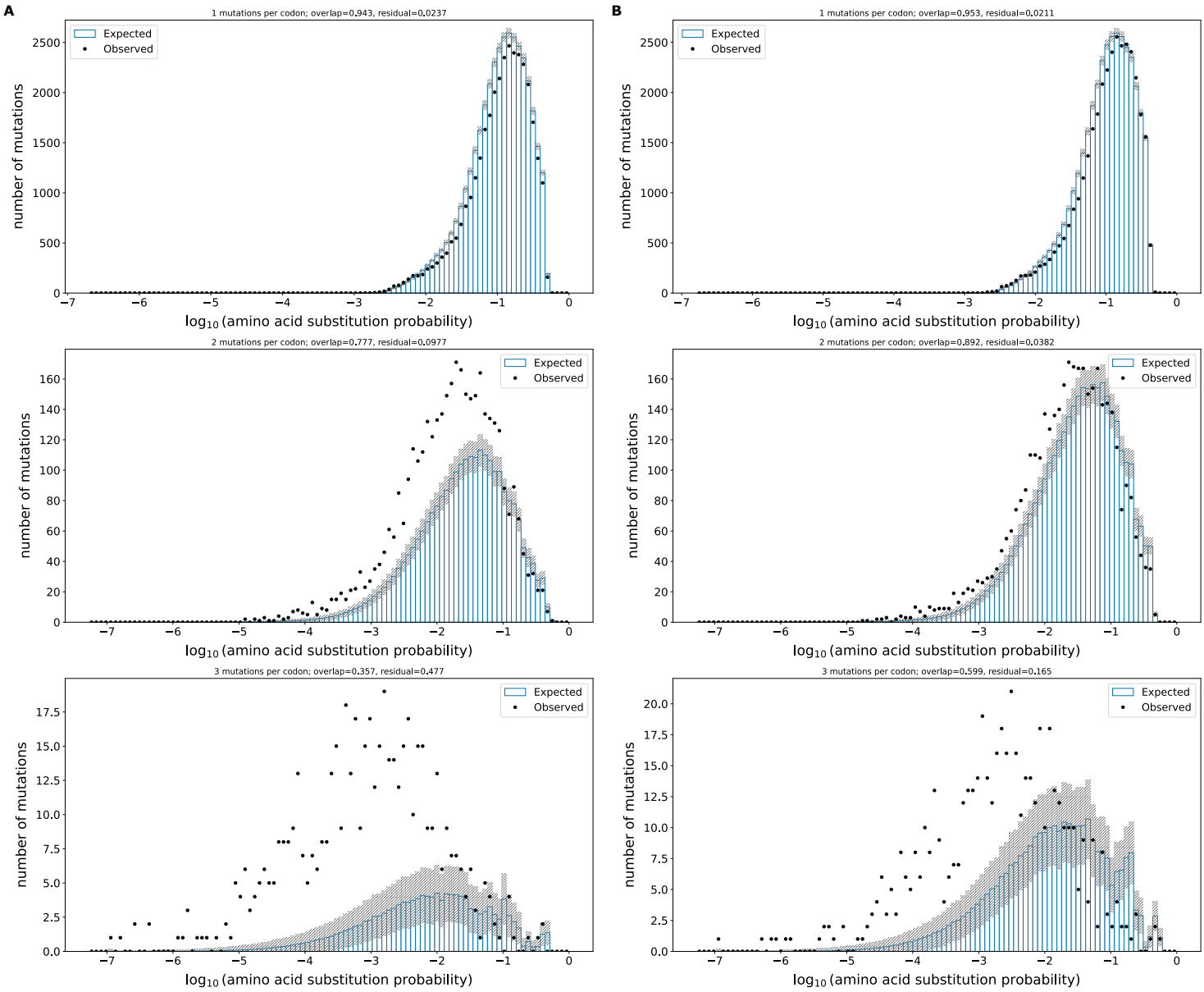

Figure S9: Models that allow for multiple hits per codon (right column) show better model fit than without (left column) on the out-of-frame data from [58] as prepared in [9]. These observed-versus-expected plots compare the observed number of mutations to the computationally predicted number across bins of mutation probability. For each bin, the expected number of mutations is calculated as the sum of mutation probabilities for all sites in that bin, while the observed count represents the actual mutations found in those sites. The overlap metric quantifies the area of overlap between observed and expected distributions divided by their average area, while the residual metric measures the normalized root-mean-square difference between observed and expected counts. These plots are faceted by the number of mutations per codon.

fig:hc