Protein Embeddings Predict Binding Residues in Disordered Regions

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Short Title: Embeddings Predict Binding in Disorder

Abstract

The identification of protein binding residues helps to understand their biological processes as protein function is often defined through ligand binding, such as to other proteins, small molecules, ions, or nucleotides. Today's methods predicting binding residues often err for intrinsically disordered proteins or regions (IDPs/IDPRs). Here, we presented a novel machine learning (ML) model trained to predict binding regions specifically in IDPRs. The proposed model, IDBindT5, leveraged embeddings from the protein language model (pLM) ProtT5 to reach a balanced accuracy of 57.2±3.6% (95% confidence interval). This was numerically slightly higher than the performance of the state-of-the-art (SOTA) methods ANCHOR2 (52.4±2.7%) and DeepDISOBind (56.9±5.6%) that rely on expert-crafted features and/or evolutionary information from multiple sequence alignments (MSAs). IDBindT5's SOTA predictions are much faster than other methods, easily enabling full-proteome analyses. Our findings emphasize the potential of pLMs as a promising approach for exploring and predicting features of disordered proteins. The model and a comprehensive manual are publicly available at https://github.com/jahnl/binding_in_disorder.

Key words: protein disorder, protein function, protein binding, protein binding prediction, machine learning, protein language model.

Abbreviations used: AA, Amino Acid; **AI**, Artificial Intelligence; **API**, Application Programming Interface, **BFD**, Big Fantastic Database; **CAID**, Critical Assessment of protein Intrinsic Disorder; **CNN**, Convolutional Neural Network; **CV**, Cross Validation; **FN**, False Negative; **FNN**, Feed-forward Neural Network; **FP**, False Positive; **HBI**, Homology-Based Inference; **HVAL**, HSSP Value; **IDP**, Intrinsically Disordered Protein; **IDPR**, Intrinsically Disordered Protein Region; **MCC**, Matthews Correlation Coefficient; **ML**, Machine Learning; **MSA**, Multiple Sequence Alignment; **NLP**, Natural Language Processing; **NN**, Neural Network; **PIDE**, Pairwise sequence Identity; **pLM**, protein Language Model; **ROC**, Receiver Operating Characteristic; **SOM**, Supporting Online Material; **TN**, True Negative; **TP**, True Positive

Introduction

Intrinsically disordered proteins (IDPs) [1], or local regions in these (IDPRs) are characterized by regions of amino acids (AAs) absent of regular secondary [2] or tertiary structure [3-6], exhibiting unique properties that enable them to maintain domain separation, facilitate interactions, and offer increased propensity for post-translational modifications, such as phosphorylation [3]. IDPs are involved in signal transduction, regulation, and specific binding with various partners depending on the cellular environment, including metal ions, inorganic molecules, small organic molecules, and other biomolecules [3, 7]. Understanding the binding residues in IDPs may provide important insights, including potential drug targeting [3] and may extend to biotechnological applications, offering opportunities for engineering proteins and designing biomaterials for diverse scientific and medical purposes [8].

The experimental identification of binding residues in IDPs poses significant challenges [9]. This is also reflected by the development of an avalanche of *in silico* methods for IDPs; tools geared toward well-structured proteins often fail on disordered proteins [9]. IDPs and well-structured proteins are not antipodes, instead there is a spectrum of transitions, including partial disorder, hybrid proteins, or conditional disorder, wherein the structure may change depending on environmental conditions [3]. This inherent complexity complicates the curation of gold standards for machine learning (ML) [3, 10]. The Critical Assessment of protein Intrinsic Disorder (CAID) project has been trying to provide sustained evaluations [11]. In 2018, the method *ANCHOR2* performed best [11, 12] by using biophysics-based energy functions balancing disorder tendency and interaction [12]. Two years later, methods outperformed ANCHOR2 [13, 14] through using homology-based inference (HBI) [10, 11], evolutionary information from multiple sequence alignments (MSAs) and expert-crafted, knowledge-based features as input for ML [10, 12, 13]. However, for disordered proteins, this information is often unavailable [15], and it has been shown that it may be suboptimal to apply MSAs and hand-crafted features to IDPs and IDPRs [9].

Protein language models (pLMs) present a novel approach for representing protein sequences without explicitly using MSAs. Drawing inspiration from Natural Language Processing (NLP), pLMs utilize the sequential order of input to learn the underlying principles of sequence features in an unsupervised and hypothesis-free manner [16, 17]. The advantage of this approach lies in its independence from manually validated data, allowing for substantial scalability of generic Large Language Models (LLMs) [16]. Prominent examples for pLMs are ProtT5 [16], ESM-2 [18], SeqVec [19] and Progen [20], all successfully applying transformer architectures on protein sequences. Since the introduction of transformer-based pLMs, it has been shown that the protein embeddings, i.e., numeric representations generated with such pre-trained models (practically the values from the last hidden layers [16]), are predictive of many aspects of protein structure and function, performing on-par or outperforming MSA-based methods while only using sequence as input [16, 18, 21-29].

Inspired by the success of MSA-free pLM embeddings particularly for binding residue prediction [21], we introduce *IDBindT5* (Fig. 1), a novel method predicting binding residues in disordered regions (IDPRs) from single sequence input. We trained IDBindT5 on carefully curated and redundancy-reduced data sets derived from *MobiDB* [30], which collects data on protein disorder and interactions from several other databases, such as *DisProt* [7] and *IDEAL* [31]. Leveraging ProtT5 embeddings as input, IDBindT5 predicts binary scores indicating whether a residue in an IDPRs is likely to bind.

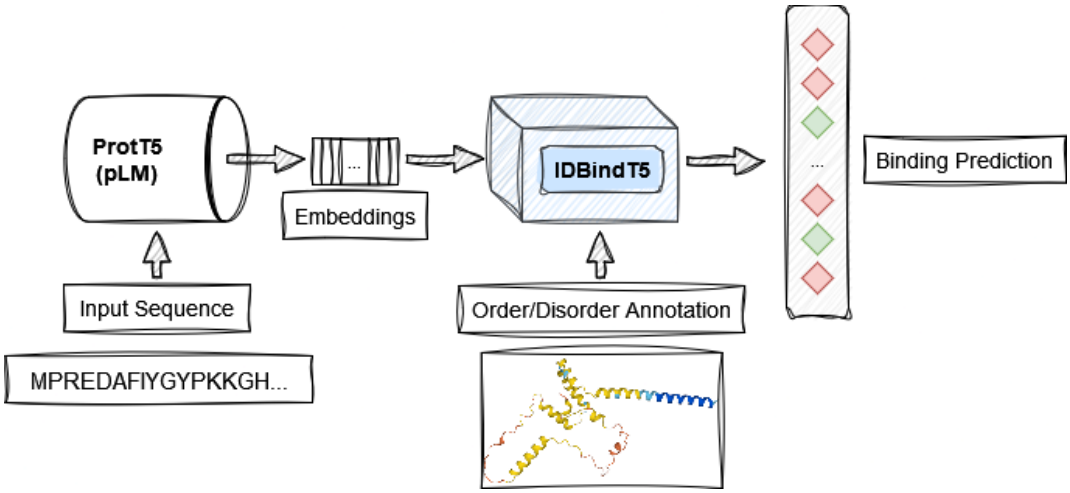

Fig. 1: Workflow of IDBindT5. To predict whether or not a residue in a disordered region (IDPR) is binding, *IDBindT5* takes numerical representations of a protein sequence (embeddings) generated by the protein language model (pLM) ProtT5 [16] accompanied by either predicted or experimental per-residue annotation of (dis-)order as input. *IDBindT5* avoids dramatic explosion of free parameters and overfitting through a relatively simple feed-forward neural network (FNN, single hidden layer). The input consists of a binary vector for disorder/order (either from prediction or annotation; dimension $\mathrm{L} \times 1$, with L being the number of residues in a given protein), and the generated embeddings are of shape $\mathrm{L} \times \mathrm{m}$ (m depends on specific pLM, for ProtT5 $\mathrm{m} = 1024$). The output produced by *IDBindT5* is of shape $\mathrm{L} \times 1$, representing a per-residue binding prediction.

Results and Discussion

We propose the novel machine learning (ML) model IDBindT5, which predicts binding residues in intrinsically disordered protein regions (IDPRs). The feed-forward neural network (FNN) with a single hidden layer takes embeddings from the protein language model (pLM) ProtT5 [16] as input and outputs a binary per-residue binding prediction. For details on the datasets, the training and evaluation procedure please refer to *Methods*. Here, we present our most important findings from the model evaluation and comparison to the state-of-the-art (SOTA).

Choice of pLM relevant but not critical. We compared several pLMs as input embeddings for the downstream prediction task of binding within IDPRs. Comparing "identical" ML architectures (not fully identical due to the different dimensionality), the model based on ProtT5 [16] slightly outperformed the one based on ESM-2 [18] (details see Methods section): MCC(IDBindT5) = 0.210 ± 0.019 (95% CI, confidence interval) vs. MCC(FNN_all_ESM2) = 0.179 ± 0.019 (Supplementary Fig. SOM_F2 and Supplementary Table SOM_T3 in the *Supporting Online Material (SOM)*). This difference was numerically better, but not statistically significant within the 95% CI. Other performance measures largely confirmed the same trend (Supplementary Table SOM_T3). Thus, the choice of the pLM appeared, overall, not critical, confirming similar results for conservation prediction [24]. This also underscored the robustness of embeddings from different pLMs for subsequent supervised training.

Embeddings allow for simple downstream architecture. We developed several ML models. On the validation set, two tied for best performance: a CNN (Convolutional Neural Network) trained on disordered regions only (dubbed CNN_disorder) and IDBindT5 (Supplementary Fig. SOM_F2 and Supplementary Table SOM_T3), an FNN trained on both ordered and disordered residues. As the CNN can capture more information about the local residue environment than an FNN, this result suggested that the ProtT5 embeddings already captured that information. To reduce the odds of over-fitting and limit the runtime/energy consumption, we chose an FNN as our final model.

In contrast to a CNN, which was balanced on a per-protein level, an FNN also provided the option to incorporate per-residue level balance through over- or under-sampling on the per-residue level. Consequently, the CNNs differed more on the validation set between the two training datasets than the FNNs. Training a CNN on all residues as opposed to only on disordered residues reduced the F1 (Eqn. 7) by about 10%, for the FNNs, the corresponding difference was below 1% (Supplementary Table SOM_T3). Since CNN and FNN performed similarly on the validation set, we tested their consensus combination (average over raw output and optimization of threshold). Performance increased numerically, but not at levels of statistical significance (Supplementary Table SOM_T4).

IDBindT5 reached SOTA. After the above steps decided on the best model (IDBindT5) according to the validation set, we estimated performance through the test set (Fig. 2, Supplementary Table SOM_T4). Compared to the validation set, test set estimates of precision and recall were both significantly lower (Supplementary Tables SOM_T3 and SOM_T4), while balanced accuracy (Eqn. 6) and MCC (Eqn. 8) remained within the 95% confidence interval of each other (respective p-values via Welch's t-test: 0.580 and 0.790). The decrease in estimates for precision and recall from validation to test set were similar for the random baseline. Neither was "compensated" for by a change in the corresponding values for negatives. IDBindT5 clearly outperformed the random baseline.

In comparison to the SOTA models *ANCHOR2* [12] and *DeepDISOBind* [32], IDBindT5 performed favorably in our hands (Fig. 2, Supplementary Table SOM_T4). However, while IDBindT5 was numerically best in terms of balanced accuracy and MCC, no method stood out in a sense of statistical significance when applying a Welch test [33] (Supplementary Table SOM_T5). The recall of IDBindT5, however, was higher than those of the two SOTA methods and this was not at the expense of precision that remained also higher (Supplementary Table SOM_T4). All methods displayed a relatively low precision (<43%), suggesting that the reduction of false positives without loss of recall remains a main challenge for binding residue prediction in IDPRs.

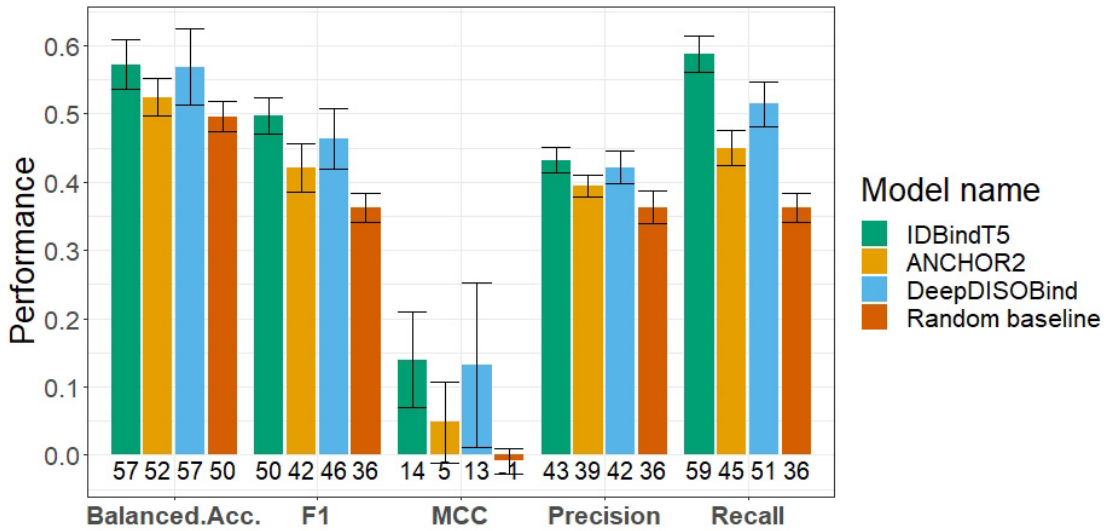

Fig. 2: Test set performance. Methods to predict binding regions in IDPRs (intrinsically disordered regions): *IDBindT5* (here), SOTA methods *ANCHOR2* [12] and *DeepDISOBind* [32], and a *Random baseline* (frequency of 38.8% positives and 61.2% negatives). Data set: test set (*Mobi195* with 195 proteins. The performance is captured by the four per-residue measures (scaled to [0,1]): precision (Eqn. 1), recall (Eqn. 2), balanced accuracy (Eqn. 6) and MCC (Eqn. 8). Error bars reflect the 95% confidence interval (CI) of 1.96*standard errors. Only IDBindT5 is significantly better than the random baseline for all measurements. While it also reaches the highest numerical values for all measures, not all differences are significant at 95% CI. Noteworthy is the superior recall value at top precision (more measures in Supplementary Table SOM_T4).

Given the small size of our test set, none of the SOTA methods consistently improved over the random baseline (randomly choosing 38% of the residues as positives) at levels that were statistically significant (Fig. 2). This might be due to the difference in training data used for the SOTA methods. For instance, both used different databases, and different details in redundancy-reduction.

IDBindT5 best and fastest. Users want methods to be as good as possible, and developers making their methods available in webservers want them to be energy-aware, i.e., to consume as few resources as possible. Thus, we compared the three best methods on *Mobi11k*, a subset of 11,114 human proteins (see Methods) using the same machine (CPU: 2x Intel Xeon Gold 6248, 400 GB RAM, 20 cores; GPU: 4x Quadro RTX 8000, 46 GB vRAM). The slowest method, DeepDISOBind needed 33 hours and 22 minutes, the fastest, ANCHOR2 took 21 minutes. Our method, IDBindT5, completed predictions within 2 hours and 10 minutes, providing a balance between predictive performance and runtime. IDBindT5, along with a comprehensive manual, is publicly available at https://github.com/jahnl/binding_in_disorder.

Wanted: additional experimental data on binding in disordered regions. Although bigger AI models are not always better in computational biology [16], without models with substantially more free parameters than three decades ago, neither pLMs nor breakthroughs on the level of AlphaFold2 [34] would have been feasible. Although the past rule-of-thumb of 10 of the minority samples (here the positives accounting for 38% of all points) per free parameter are more often ignored by orders of magnitude than not in the era of deep learning, modern AI is simply data hungry. In fact, this is the reason why generalized pLMs are so successful: they accumulate over 50-times the amount of data as the entire Wikipedia of the English language for Natural Language Processing [16, 19]. IDPs and IDPRs clearly do not fall into this category. In fact, pLM embeddings help through their power in transfer learning, i.e., by partially *understanding the* language *of life as written in protein sequences* [19], they allow the development of relatively simple ML models to predict disorder without using too much data [29]. Our application of pLMs to predict binding in IDPRs clearly pushed the envelope.

The inherent complexities of molecular interactions in IDPRs render experimental annotations of protein-protein interactions in such regions exceptionally daunting. Therefore, available data to train ML methods is sparse and necessitated strategic compromises for the development of IDBindT5. While IDBindT5 provides accurate and fast SOTA per-residue binding predictions in disordered regions, it does not distinguish between the type of binding. Although other methods are able to predict DNA and RNA binding and protein hubs, performance is often very limited with a large performance gap compared to binding site prediction in well-structured regions [12, 13, 32] which in itself suffers greatly from a lack of reliable experimental data [21, 35]. We decided to maximize the available data by using binary annotations (binding/non-binding).

The database MobiDB [30] collects curated disorder and interaction information from several other databases, including IDEAL [31], UniProt [36], DIBS [37], ELM [38], MFIB [39], and DisProt [7]. As MobiDB provides 78% more IDPs with curated information than DisProt (2853 vs. 1605, as of September 2022), it was the natural choice to train an ML method with the focus of generalizability. However, the type of the binding partner when downloading entries from MobiDB via its application programming interface (API) is not listed, so training a multilabel model predicting ligand types was not possible.

An additional compromise imposed by the available data was that the models were evaluated only on disordered regions. This choice was driven by the large data imbalance between negatives (anything in order plus non-binding residues in disorder) and positives (binding residues in disorder). This imbalance naturally favors methods that mainly distinguish ordered from disordered residues, even when considering metrics that take class imbalance into account. In order to avoid a bias towards these models, we only evaluated the ability to predict binding in disordered residues. Consequently, our method numerically improved over the SOTA, but at the cost of requiring additional input data, disorder annotations, which the reference methods either do not need or predict by themselves during runtime.

The challenges encountered in developing a method to predict binding residues in IDPRs underscored the critical need for improved annotations in protein-protein interactions, particularly within disordered regions. Unfortunately, we cannot foresee whether a data duplication will significantly improve performance. But overcoming some of today's data limitations might set the stage for future advancements that promise to deepen our understanding of molecular interactions within disordered regions, opening new avenues for research and discovery in the realm of structural and functional biology.

Methods

Datasets

We used three datasets: one for training and validation of our new method IDBindT5, one for testing and performance evaluation and comparison to the state-of-the-art (SOTA) methods ANCHOR2 [12] and DeepDISObind [32], and one to assess the prediction speed of all three methods.

Train: Mobi2k and Test: Mobi195. For ease of comparisons, we relied upon MobiDB [30] (version: October 17, 2022). To ensure the reliability of annotated proteins for the task of predicting the potential interaction between disordered residues and binding partners, we only selected proteins with manually curated disorder and binding annotations. The resulting data set comprised 2,816 proteins with 188,940 disordered residues. Of these disordered residues, 117,122 (62%) were categorized as negatives (disordered without binding annotation), and 71,818 (38%) as positives (disordered and binding). To manage memory consumption, we excluded proteins with over 10k (10,000) residues, i.e., excluded one single protein, namely titin (Q8WZ42 with 34,350 residues).

The following meticulous redundancy reduction steps ensured an unbiased and robust assessment of performance. First, we randomly selected 200 positive proteins (those with at least one binding region in disorder) and 200 negative proteins (devoid of any binding region in disorder) from the MobiDB dataset as a test set. To minimize sequence and structural similarity within the test set, we applied MMSeqs2 and UniqueProt [40-42]. First, we ran MMseqs2 [41] with default settings (e-value: 10, sensitivity: 7.5, minimum alignment length: 11) and calculated the HVAL (HSSP-value [40]). We reduced redundancy at HVAL=0 (corresponding to, e.g., <20% pairwise sequence identity (PIDE) for pairs of proteins aligned over 250 residues) for both positives and negatives. This left 168 positives and 151 negatives in the test set. Next, we reduced the remaining negatives again by MMseqs2 alignment against the positives using the same procedure. This resulted in 132 negatives. To facilitate comparisons with the SOTA methods ANCHOR2 [12] and DeepDISObind [32], we also redundancy-reduced the test set with respect to their training sets. This filter resulted in 98 positives and 115 negatives.

The proteins removed this way due to overlap with the development sets of other methods, we added to our training set. This gave 2,502 training set proteins. Next, we redundancy-reduced positives and negatives of the training set through CD-HIT [43] at 40% PIDE resulting in 777 positives and 1282 negatives. As before, we next redundancy-reduced the negatives against the positives (CD-HIT <40%). This left 1,176 negatives. For added security against data leakage, we again redundancy reduced the resulting training set against the test set using MMSeqs2-UniqueProt [40-42] at HVAL<0, resulting in 1762 proteins (679 positives and 1083 negatives) in the training set.

Lastly, to balance the ratios positives-to-negatives in training and testing set, we excluded 18 other positives (with 16,567 residues) from the test set and moved those to the training set, leading to the final training set, dubbed **Mobi2k**, with 1780 proteins (697 positives, 1083 negatives, in disorder: 64,228 binding residues, 101,381 non-binding residues, Supplementary Table SOM_T1). Next, we randomly split the training set into five equally sized folds for five-fold cross-validation (CV). We used two versions of this set for training: one with all residues, and one consisting of only residues in annotated disordered regions. The final test set, dubbed **Mobi195**, consisted of 195 proteins (80 positives, 115 negatives, in disorder: 6,657 binding residues, 11,644 non-binding residues, Supplementary Table SOM_T1). In each split, one fold served as validation set to optimize hyper-parameters,

including the choice of the best method. We estimated the test performance only on the best model identified by the validation set, i.e., avoided the frequent mistake of reporting test results for more than one of our models, typically the one performing best on the test set.

Mobi11k – speed assessment. To assess the runtime needed to apply our method, we generated a third, larger dataset. We filtered the human proteome in the MobiDB at <100% PIDE and we included sequences shorter than 5,000 residues with an annotation matching the sequence length and having at least 5% disordered residues predicted by MobiDB-lite [44]. This resulted in 11,114 human proteins with median sequence length of 489 residues.

Input pLM embeddings

As input, we compared embeddings from the following generic non-fine-tuned pLMs: (1) ESM-2 with 3 billion (B) parameters [18] (based on BERT [45] and trained on UniRef50 [36]), and (2) ProtT5-XL-U50 [16] with 3B parameters (for simplicity referred to as ProtT5; based on T5 [46], and trained on BFD [47] and Uniref50 [36]). We extracted the per-residue embeddings from the last hidden layer of the models of dimension d=1280 for ESM-2 and d=1024 for ProtT5 $\times L$, where L is the length of the protein sequence and 1280 or 1024 is the dimension of the hidden states/embedding space of ESM-2 or ProtT5. After extracting the embeddings from the last hidden layer of the model, the embeddings were expanded by one dimension containing a binary indicator whether the residue is located in an IDPR based on the manually curated information from MobiDB [30].

Prediction methods

As shown before [21-25], the rich information contained in embeddings allows to keep models for downstream prediction tasks relatively shallow (million(s) instead of billions of free parameters). We systematically combined the following architectures and parameters, creating different models: Architecture (Feed-forward Neural Networks (FNNs) and Convolutional Neural Networks (CNNs), balancing methods (different strategies for over- and under-sampling), training residue subset (all residues of a protein or disordered only), number of layers, kernel size (for CNNs only), dropout probability, batch size and learning rate. All models were implemented in PyTorch [48], applied early stopping with a patience (i.e., number of epochs without improvement in loss on the validation set) of five and used the Adam [49] optimizer. Non-linearity was introduced by using the ReLU activation function after each hidden layer (except for the last hidden layer). As loss function, we applied the binary cross entropy loss. The cutoff used to classify a residue as binding (output probability of the model > cutoff) or non-binding (output probability ≤ cutoff) was chosen individually for each model and fold, based on receiver operating characteristic (ROC) curves (Supplementary Fig. SOM_F1). The aim was to achieve a good precision while avoiding a large decrease in recall. All models exclusively input pLM embeddings and per-residue disorder annotations.

For each combination of parameters and architectures, we trained five models, one for each CV-fold. These were combined to an ensemble method by averaging their final output. Below, we describe a subset of the methods, chosen based on validation-set performance. Other models that we evaluated are listed in Supplementary Table SOM_T2. We chose the model with the numerically highest performance, dubbed IDBindT5 (Fig. 1), as our final model.

IDBindT5. The following architecture performed best in the cross-validation: FNN, input: ProtT5 (Fig. 1; 1025 units), hidden layer (612 units), and output layer (one unit), leading to a total of 1.7M (million) free parameters, trained with a batch size (here: number of residues) of

512, and a learning rate of 0.01. We trained the model using both ordered and disordered ("all") residues (Supplementary Tables SOM_T1, SOM_T2). The FNN architecture was better suited for balancing the dataset on residue-level and given the unbalanced dataset, we decided to under-sample the non-binding residues within and outside of IDPRs. Due to the different distributions in the CV-folds, we applied a different ratio for each so that both subsets reach the same abundance as the binding residues for each fold. Based on the predictive performance on the validation set, the prediction cutoffs for the five models of the different CV-folds were chosen based on the respective ROC curves as 0.55, 0.40, 0.50, 0.35 and 0.30 (Supplementary Fig. SOM_F1 c).

FNN_all_ESM2. We trained a model with the same architecture and training settings as IDBindT5 but switching the ProtT5 [16] embeddings for those of ESM-2 [18] with 3B parameters. Due to the larger vector size (2,560 input units for ESM-2), the free parameter count increased from 1.7M (ProtT5) to 9.8M (ESM2). The cutoffs for the five models of the different folds were chosen as 0.4, 0.35, 0.45, 0.4 and 0.35, respectively (Supplementary Fig. SOM_F1 d).

Random baseline. As random baseline we only considered the frequency of positives in the training set. Thus, we randomly predicted 38.8% of the disordered residues as binding.

AAindex_disorder. In addition to a random baseline, we introduced a baseline trained on classical biophysical amino acid (AA) features. *AAindex1* is a database of numerical properties of single amino acids, derived from the literature [50]. Instead of the features of the protein embedding, a vector of all 566 associated AAindex1 values was assigned to each residue. The model was then trained based on the configuration of the model *CNN_disorder* (Supplementary Table SOM_T2), which is a CNN of five one-dimensional convolutional layers (channels having the ranges 1025, 512, 256, 128, 64 and 1) using a kernel size of 5 and zero padding and predicting the binding labels for one disordered region at a time. Non-binding proteins were under-sampled and the learning rate was set to 0.002. The free parameter count is 2.3M. The cutoffs for the five models of the different folds were chosen as 0.30, 0.30, 0.25, 0.25 and 0.25, respectively (Supplementary Fig. SOM_F1 f).

Performance Measures

The following standard measures assessed performance (TP (true positives): correctly predicted as binding; FP (false positives): incorrectly predicted as binding; TN (true negatives): correctly predicted as non-binding; FN (false negatives): incorrectly predicted as non-binding). The resulting 2x2 confusion matrix enabled the computation of all non-statistical scores used for evaluation, namely:

$$Precision = \frac{TP}{TP+FP} \quad \text{(Eqn. 1)}$$

$$Recall = Sensitivity = \frac{TP}{TP+FN} \quad \text{(Eqn. 2)}$$

$$Negative\ Precision = \frac{TN}{TN+FN} \quad \text{(Eqn. 3)}$$

$$Negative\ Recall = Negative\ Sensitivity = \frac{TN}{TN+FP} \quad \text{(Eqn. 4)}$$

$$Specificity = \frac{TN}{TN+FP} \quad \text{(Eqn. 5)}$$

$$BalancedAccuracy = \frac{Recall+Specificity}{2} \quad \text{(Eqn. 6)}$$

$$F1\ Score = 2 * \frac{Recall*Precision}{Recall+Precision} \quad \text{(Eqn. 7)}$$

$$MCC = \frac{TP*TN-FP*FN}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}} \quad \text{(Eqn. 8)}$$

Standard boot-strapping [51] turned these values into statistical estimates. Toward this end, we applied each performance measure to batches of 100 disordered residues, and calculated the mean over the resulting distribution, to avoid protein length affecting the proportional impact of a particular prediction. We estimated the standard error after bootstrapping 1,000 batches (Eqn. 9) then we applied a 95% confidence interval (CI) [51, 52].

$$Standard\ Error = \sqrt{\frac{\sum(x_i-\langle x\rangle)^2}{n}} \quad \text{(Eqn. 9)}$$

The difference between distributions, whose 95% CIs did not overlap, was considered as statistically significant. To compare models whose 95% CIs overlapped and consequently showed no significant difference, we performed Welch's t-test which does not assume equal population variance [33, 52].

Comparison to SOTA. As state-of-the-art methods (SOTA), we compared IDBindT5 to ANCHOR2 [12] and DeepDISOBind [32]; both stood out at CAID [11, 53]. We tapped into the webserver of each resource to obtain predictions for all proteins in our test set. While ANCHOR2 predicts only protein-protein interactions, DeepDISOBind also predicts interactions with nucleic acids [32].

Conclusions

We presented a new method, called IDBindT5, for predicting whether a residue in an intrinsically disordered protein region (IDPR) binds to any ligand. On our newly introduced test set, the predictor achieved a balanced accuracy of 57.2 ± 3.6%, a precision of 43.2 ± 1.9% and a recall of 58.7 ± 2.6%. IDBindT5's predictive performance can compete with the established state-of-the-art methods ANCHOR2 [12] and DeepDISOBind [32] (Fig. 2) albeit requiring neither alignments nor a complex ML architecture. Key to this is that IDBindT5 operates solely on embeddings from single sequences generated by the pre-trained pLM ProtT5 [16] and a disorder annotation as input. Consequently, in terms of prediction speed our model is more than 15 times faster than DeepDISOBind, enabling many predictions even on common notebook hardware and requiring less energy. Further, while all methods showed a relatively low precision, IDBindT5 was numerically best, confirming that while making precise predictions for binding residues in IDPRs continues to be a challenging task, the use of pLM embeddings as input is an approach worth building upon.

Data Availability

The source code, data sets, the trained models and a detailed manual on how to use our prediction tool are publicly available in the project's GitHub repository (https://github.com/jahnl/binding_in_disorder). ProtT5 embeddings can be generated using the *bio_embeddings* [16] pipeline or the Jupyter Notebook provided in the ProtTrans GitHub repository (https://github.com/agemagician/ProtTrans). Disorder annotations can be replaced by predictions from the LambdaPP webserver [54].

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Author contributions

L.R.J. implemented and evaluated the method and co-wrote the manuscript. C.M. supervised the project and co-wrote the manuscript. M.H. co-conceived and supervised the project. B.R. supervised and guided the work. All authors read and approved the final manuscript.

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Figure Legends

Fig. 1: Workflow of IDBindT5. To predict whether or not a residue in a disordered region (IDPR) is binding, *IDBindT5* takes numerical representations of a protein sequence (embeddings) generated by the protein language model (pLM) ProtT5 [16] accompanied by either predicted or experimental per-residue annotation of (dis-)order as input. *IDBindT5* avoids dramatic explosion of free parameters and overfitting through a relatively simple feedforward network (FNN, single hidden layer). The input consists of a binary vector for disorder/order (either from prediction or annotation; dimension $\mathrm{L} \times 1$, with L being the number of residues in a given protein), and the generated embeddings are of shape $\mathrm{L} \times \mathrm{m}$ (m depends on specific pLM, for ProtT5 $\mathrm{m} = 1024$). The output produced by *IDBindT5* is of shape $\mathrm{L} \times 1$, representing a per-residue binding prediction.

Fig. 2: Test set performance. Methods to predict binding regions in IDPRs (intrinsically disordered regions): *IDBindT5* (here), SOTA methods *ANCHOR2* [12] and *DeepDISOBind* [32], and a *Random baseline* (frequency of 38.8% positives and 61.2% negatives). Data set: test set (*Mobi195* with 195 proteins. The performance is captured by the four per-residue measures (scaled to [0,1]): precision (Eqn. 1), recall (Eqn. 2), balanced accuracy (Eqn. 6) and MCC (Eqn. 8). Error bars reflect the 95% confidence interval (CI) of 1.96*standard errors. Only IDBindT5 is significantly better than the random baseline for all measures. While it also reaches the highest numerical values for all measures not all differences are significant at 95% CI. Noteworthy is the superior recall value at top precision (more measures in Supplementary Table SOM_T4).