

# DNA-Binding Protein Classification: Comparison between various Traditional MLs vs Deep Learning Models

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## Introduction

DNA-binding proteins (DBPs) are crucial for the regulation of cellular functions, making their accurate identification important for genome studies (Si et al. 2011). Yet traditional lab methods for such a task are costly, time-consuming, and worst of all inaccurate (Fu et al. 2018). If we are able to harness Machine Learning (ML) to perform this task, we could expect great savings in cost and increases in accuracy.

## Literature Review

Various ML models have been used for DBP classification, using features such as structural, functional, evolutionary, and physicochemical properties from protein sequences with some encoding techniques (Sun et al. 2024; Jia, Huang, and Zhang 2021; Song et al. 2014). Classifiers such as Support Vector Machines (SVMs) are observed to perform with high accuracy alongside models such as Random Forests (RFs), XGBoost and Artificial Neural Networks (ANN). However, DBP classification remains challenging, where

- DBPBoost (Sun et al. 2024) has high computational costs due to the complexity of the improved differential evolution algorithm.
- KK-DBP (Jia, Huang, and Zhang 2021) is susceptible to overfitting with multiple features using Random Forest classifier.
- nDNA-prot (Song et al. 2014) struggles with handling class imbalance.

## Our Aim

Building on previous research, we aim to identify the most reliable model for DBP classification by selecting and comparing key feature extraction methods—namely global and local amino acid distribution & composition, physicochemical properties, and Natural Language Processing techniques like embeddings and integer encoding. Our goal is to evaluate these features and classifiers (both traditional and deep learning) - to determine the best combination of features and model for accurate, reusable, and reliable DBP identification.

## Methodology

Training and testing is done on the datasets `Train.fasta` and `Test.fasta` which include training and testing data respectively. Various classifiers and feature extraction methods based on natural language processing and biological scientific knowledge have been employed (Figure ).

## Exploratory Data Analysis & Data Pre-processing

There are around 53,000 and 17,000 protein sequences in the training and testing datasets respectively. Ratio between class 1 (positive binding) to class 0 (negative binding) is approximately 2 : 1 in both training and testing datasets. To deal with class imbalance, Synthetic Minority Over-sampling Technique (SMOTE) is used to generate synthetic samples for the minority class by interpolating between existing minority instances. SMOTE is applied for our traditional MLs (TF-IDF, physicochemical properties) while class weight is applied for Deep Learning to correct class imbalance.

Moreover, while hundreds of amino acids exist, only 20 of them are commonly found in proteins. Thus, dataset is filtered to retain protein sequences that contain the unknown amino acid X or the rare amino acid U. Glycine, G is used to replace these uncommon and unknown amino acids because glycine has negligible impact on the physicochemical properties of the protein (Ahern, Rajagopal, and Tan 2023).

Besides, in NLP feature extractions, amino acids are treated as character-level tokens. As more than 95% of protein sequences has length shorter than 1200 characters (Figure A.6), a maximum length of 1200 is applied during embedding and tokenization methods. Sequences shorter than 1200 will be padded while those longer than 1200 will be truncated.

## Feature Extraction & Selection

Statistical amino distribution & composition and scientific physicochemical properties features are used for traditional ML. Sequence-based character-level features in protein extracted from embedding and amino-acid integer encoding are used for Deep Learning models.

**Amino Acid Distribution** Local frequency of each of common 20 amino acids is studied here using this formula:

$$f(a, p) = \frac{N_a}{N_p}$$

where  $N_a$  is the number of amino acid  $a$  in a protein sequence  $p$  of length  $N_p$ . Overall, we obtain a matrix of size  $N \times 20$  with  $N$  being the number of sequences.

Logistic Regression is used to study the significance of mean local distribution of 20 amino acids in classifying the binding property of protein via the p-value. However, all p-values of 20 amino acids distribution are higher than 0.3, which is much higher than the usual threshold of 0.05 (Figure A.2), suggesting that local distribution of 20 amino acids are insignificant in predicting the binding response. Therefore, a comparative bar graph is plot to compare the mean local distribution of 20 amino acids between those of class 0 and those of class 1. (Figure A.1). Amino acids with a mean distribution difference greater than 0.03 between the classes were retained in the model due to their stronger association with binding properties compared to the rest.

**Term Frequency-Inverse Document Frequency (TF-IDF)** TF-IDF is used to capture the distribution of amino acids within sequences and their uniqueness across the dataset (Tasnim et al, 2024). The formula is:

$$\text{TF-IDF}(c, p) = \text{TD}(c, p) \times \log\left(\frac{N}{n_c}\right)$$

where  $\text{TD}(c, d)$  is the frequency of amino acid  $c$  in a protein sequence  $d$ ,  $N$  is total number of protein sequences in the training dataset, and  $n_c$  is the total number of sequences containing amino acid  $c$ .

**Physicochemical Properties** The main physicochemical properties that affect binding include hydropathy and net charge. Additionally, we examined other properties that may affect binding like instability index, average flexibility, isoelectricity, and molecular weight (Gromiha and Nagarajan 2013). The built-in Biopython library is used to retrieve physicochemical properties information (Figure A.4). We add physicochemical feature columns and save the datasets as `DNA_Train.csv` and `DNA_Test.csv` to avoid recalculating these features.

**Pseudo-Amino Acid Composition (pseAAC)** Unlike traditional amino acid composition, which only counts the frequency of each amino acid, pseAAC incorporates additional factors such as sequence order, physicochemical properties, and correlations between amino acids, which normal AAD does not use (Chou 2001). The builtin propy library is used to generate the feature vectors (Figure A.5).

**Embedding** Character-level embedding converts protein sequences into numerical vectors. We used `tokenize()` to map each of the 21 amino acids (20 common, 1 unknown 'X') to a unique integer. Padding and truncation is applied on each sequence to keep to a uniform length of 1200.

**Amino Acid Integer Encoding** A unique integer from 1 to 20 is assigned to each of 20 common amino acids. For rare U and unknown amino acids X, they will be mapped to 0. Zero padding and truncation is applied to standardize sequence length of 1200.

## Machine Learning & Deep Learning Classifiers

Traditional MLs classifiers selected for DBP classification tasks include: Logistic Regression (LR), Naive Bayes (NB), K Nearest Neighbors (KNN), Random Forest (RF), Decision Tree (DT), and Support Vector Machine (SVM) because they are usually used for binary classification tasks. Notably, KNN is fine-tuned to find the best  $k$  in a range of 1 – 250 that yields best MCC. RF and DT are also limited to a max depth of 10 to avoid overfitting.

Convolution Neural Network (CNN) which include a simple CNN and more sophisticated architecture ProtCNN which is designed for protein sequence classification are used as classifiers for Deep Learning models. Large Language Model using pre-trained ProtBert, which is more specialised for protein sequences are also employed.

**Logistic Regression** (LR) is our baseline for it being commonly used for Binary Classification tasks.

## Evaluation Metrics

Accuracy, Sensitivity, Specificity, AUC/ROC, and MCC are used as evaluation metrics. Due to class imbalance, MCC is more desirable to ensure classification is reliable. While accuracy provides a general measure of a model's performance, in cases of class imbalance, it can be misleading. Thus, Sensitivity (true positive rate) and Specificity (true negative rate) are more critical for our classification task.

## Results

### Traditional MLs with Amino Acid Distribution & Composition Features

Table 1 shows the results of using traditional MLs with AAD features. RF on both the full and selected AAD, and SVM for the full AAD, produced the highest MCC (0.43) with relatively high sensitivity, specificity, and AUC. Choosing only selected AAD causes greatest change in performance when LR and SVM is used, evident by a huge jump in sensitivity and specificity. Overall, traditional MLs with amino acid distribution as features do not have strong classification ability for DBP.

### Traditional MLs with Physicochemical Features

Table 1 shows the results of using traditional MLs with physicochemical properties. MCC is consistently low for all models, suggesting poor predictive ability for DBP in such an imbalanced training dataset. Nevertheless, SVM performs best when physicochemical properties are used as features due to the highest MCC and AUC. In contrast, NB performs the worst. Thus, coupled with the fact of high p-value, physicochemical properties alone are not effective in affecting protein-DNA interactions and binding.

Feature	LR	NB	KNN	SVM	DT	RF
Full AAD	Sensitivity 0.64	Sensitivity 0.74	Sensitivity 0.92	Sensitivity 0.74	Sensitivity 0.75	Sensitivity 0.74
	Specificity 0.64	Specificity 0.60	Specificity 0.42	Specificity 0.71	Specificity 0.66	Specificity 0.71
	Accuracy 0.64	Accuracy 0.65	Accuracy 0.59	Accuracy 0.72	Accuracy 0.69	Accuracy 0.72
	MCC 0.27	MCC 0.32	MCC 0.34	MCC 0.43	MCC 0.39	MCC 0.43
	AUC 0.70	AUC 0.74	AUC 0.80	AUC 0.80	AUC 0.78	AUC 0.81
Selected AAD	Sensitivity 0.18	Sensitivity 0.69	Sensitivity 0.58	Sensitivity 0.34	Sensitivity 0.79	Sensitivity 0.79
	Specificity 0.92	Specificity 0.66	Specificity 0.78	Specificity 0.92	Specificity 0.62	Specificity 0.67
	Accuracy 0.67	Accuracy 0.67	Accuracy 0.72	Accuracy 0.72	Accuracy 0.68	Accuracy 0.71
	MCC 0.16	MCC 0.33	MCC 0.36	MCC 0.32	MCC 0.39	MCC 0.43
	AUC 0.69	AUC 0.74	AUC 0.76	AUC 0.76	AUC 0.78	AUC 0.81
TF-IDF	Sensitivity 0.73	Sensitivity 0.63	Sensitivity 0.91	Sensitivity 0.70	Sensitivity 0.55	Sensitivity 0.57
	Specificity 0.63	Specificity 0.62	Specificity 0.37	Specificity 0.72	Specificity 0.68	Specificity 0.80
	Accuracy 0.66	Accuracy 0.62	Accuracy 0.55	Accuracy 0.72	Accuracy 0.64	Accuracy 0.72
	MCC 0.34	MCC 0.24	MCC 0.30	MCC 0.41	MCC 0.22	MCC 0.37
	AUC 0.75	AUC 0.68	AUC 0.76	AUC 0.78	AUC 0.61	AUC 0.77
pseAAC	Sensitivity 0.68	Sensitivity 0.76	Sensitivity 0.86	Sensitivity 0.68	Sensitivity 0.54	Sensitivity 0.54
	Specificity 0.62	Specificity 0.62	Specificity 0.41	Specificity 0.74	Specificity 0.67	Specificity 0.82
	Accuracy 0.64	Accuracy 0.64	Accuracy 0.56	Accuracy 0.72	Accuracy 0.63	Accuracy 0.73
	MCC 0.28	MCC 0.30	MCC 0.27	MCC 0.4	MCC 0.20	MCC 0.37
	AUC 0.70	AUC 0.73	AUC 0.71	AUC 0.78	AUC 0.60	AUC 0.76

Table 1: Comparison of performance metrics between various traditional MLs using AAD features.

Logistic Regression	Naïve Bayes		KNN		SVM		Decision Tree	Random Forest	
Sensitivity	0.62	Sensitivity	0.44	Sensitivity	0.79	Sensitivity	0.74	Sensitivity	0.69
Specificity	0.72	Specificity	0.83	Specificity	0.56	Specificity	0.63	Specificity	0.66
Accuracy	0.69	Accuracy	0.70	Accuracy	0.64	Accuracy	0.67	Accuracy	0.67
MCC	0.33	MCC	0.29	MCC	0.33	MCC	0.35	MCC	0.33
AUC	0.73	AUC	0.69	AUC	0.75	AUC	0.75	AUC	0.74

Table 2: Comparison of performance metrics between various traditional MLs using physicochemical properties.

## Traditional MLs with pseAAC

Table 1 shows the results of using traditional MLs with AAD features. Overall performance of all models using pseAAC is average. Yet, RF stood out, achieving the highest accuracy of 0.73 and a specificity of 0.82, but low sensitivity of 0.54. In contrast, Logistic Regression performed the worst across all metrics, particularly in sensitivity. Another notable drawback was the long computational time of  $\sim 1$  day.

## CNN Models with Encoding Techniques

Table 3 shows the results of using Deep Learning (CNN) and NLP feature extraction techniques. Embedding is a better feature extraction technique with 2 – 6% higher in accuracy, sensitivity, and specificity, with a 5% higher in MCC. In addition, ProtCNN performs better with higher score in all metrics than normal CNN. Overall, Integer Encoding and ProtCNN together performs the best.

## LLM ProtBert with Encoding

Table 3 shows the results of using a pretrained Large Language Model (LLM) of ProtBert and NLP feature extraction techniques, similar to that of CNN. However, our results were not ideal and extensive tuning is required to ensure it produces workable results.

Encoding Technique	CNN		ProtCNN		ProtBert
Embedding	SEN	0.75	SEN	0.78	SEN 0
	SPE	0.80	SPE	0.82	SPE 1
	ACC	0.85	ACC	0.87	ACC 0.67
	MCC	0.60	MCC	0.63	MCC 0
Integer Encoding	AUC	0.83	AUC	0.86	AUC 0.50
	SEN	0.70	SEN	0.72	
	SPE	0.78	SPE	0.79	
	ACC	0.82	ACC	0.83	-
	MCC	0.55	MCC	0.58	
	AUC	0.81	AUC	0.84	

Table 3: Comparison of Performance between CNN, ProtCNN, and ProtBert using embedding and integer encoding techniques.

## Discussion

Among all traditional MLs using biological features, LR consistently performs worst in all aspects except when using physicochemical properties. In contrast, RF is more recommended to be used with AAD due to the comparatively higher sensitivity, accuracy, MCC, and specificity.

Deep learning algorithms, including CNN and ProtCNN, show consistently higher performance metrics compared to traditional models, with remarkably high for MCC.

From a biological understanding, features like AAD and physicochemical properties has a good interpretability to predict DBP. However, our results show they are less effective in computational sense. In long protein sequences, DNA-binding sites constitute only a small portion of the overall structure (Sigrist et al. 2009). When analyzing the overall amino acid frequency, the significance of the binding sites, which contains sequential order of amino acid diminishes (Alberts et al. 2002).

NLP techniques that numerically encode amino acids, while less biologically interpretable, often outperform biologically driven features in predictive accuracy. This may be due to tokenization, truncation, and embedding processes that retain sequence-specific information in a vector. Since amino acid order and sequence endings are crucial for DBP-sites (Ahern, Rajagopal, and Tan 2023), NLP's capacity to preserve this order likely contributes to high performance, particularly in models like ProtCNN, which is specifically adapted for protein data. However, while DL models, especially ProtCNN, perform well, it may still require extensive fine-tuning to fully capture DBP-specific nuances than traditional MLs. Similarly, LLM-ProtBert also requires extensive tuning to achieve its full potential. Thus, the concern of high computational load may offset the strong predictive ability when applied in real-life settings, particularly with large datasets like ours, where fine-tuning is essential for achieving top performance in DL framework.

We recommend using ProtCNN with embedding for feature extraction, as it delivers reliable results even with large, imbalanced datasets. However, when computational resources are limited, RFs with AAD offer a faster alternative, though this approach should be applied carefully.

To further evaluate the model's performance, we could have done cross validation. However, since our data is already split into a training and testing portion, taking a portion of training data to train the model then apply this on the test model is not ideal. Along with the high computational demands of this task, we were not able to perform cross validation for our dataset.

## Impact of DBP classification by ML models

ML models, especially DL, are transforming DBP classification by providing efficient alternatives to human expertise. Although human experts can identify binding sites with high accuracy, their approach is time-consuming and less scalable (Alipanahi et al. 2015). Therefore, proper implementation of a ML model has the tremendous benefit of saving human time and effort, along with cost savings.

However, the adoption of ML for DBP classification presents several challenges:

- **Privacy:** Utilizing pre-trained databases for DBP classification risks genomic data leakage (Gymrek et al. 2013).
- **Fairness:** Models can produce biased results when applied to diverse datasets, leading to skewed outcomes (Mehrabi et al. 2021).
- **Interpretability:** Interpretable models allow researchers to uncover and validate biological mechanisms. Conversely, favoring opaque models can obscure the understanding of factors driving binding (Molnar 2023).
- **Job Impact:** Automation enables researchers to concentrate on more critical tasks, potentially shifting job requirements toward managing and validating advanced ML systems in bioinformatics (Autor 2015).

## Conclusion

In summary, ProtCNN with embedding is optimal for DBP classification with sufficient computational resources. For faster computation with less complexity, AAD with RF is suitable. However, our findings reveal a disconnect between biological features and binding ability in DBP classification. To balance interpretability, reliability, and computational efficiency, it's essential to combine machine learning with laboratory validation.



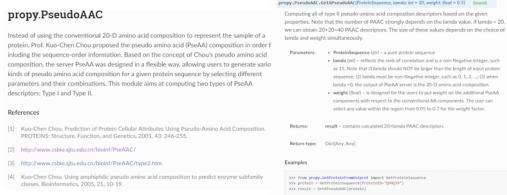


Figure A.5: propy package function which generates feature vectors for classification.

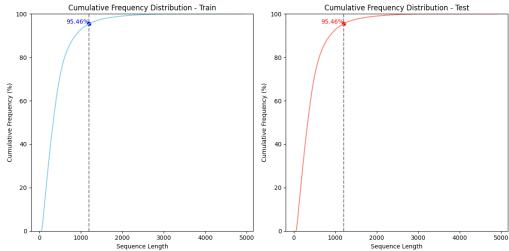


Figure A.6: Cumulative frequency distribution of sequence lengths. Note that 95% of all sequences have length  $\leq 1200$ .

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