

Comparative Study of Machine Learning Models in Protein Structure Prediction

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Abstract -As physical and chemical properties of protein guide to determine quality of the protein structure, it has been used rigorously to distinguish native or native like structure from other predicted structures. In this work, by using six physical and chemical properties we explore the machine learning models and the properties are total empirical energy, secondary structure penalty, total surface area, pair number, residue length and Euclidean distance to predict the RMSD (Root Mean Square Deviation) of a protein structure in the absence of its true native state. There are total 1056 modelled decoys structure having 3078 native structures. The Real Coded Genetic Algorithm (RCGA) is used to determine feature importance and robustness is measured by the K-fold validation of the best predictive model.

The experiments results shows that the random forest model outperforms the other machine learning approaches in RMSD prediction. This work achieved the prediction of RMSD faster and inexpensive.

Keywords—Protein structure prediction, Machine learning, Random forest, RCGA.

Results: The performance result shows that in the prediction of RMSD, the RMSE (Root Mean Square Error) is 0.48; correlation is 0.90; R2 is 0.82; and accuracy is 97.02% (with ± 2 error) respectively on the testing data.

1 INTRODUCTION

for carrying out several biological functions Protein sequences are translated into 3D tertiary forms. Prediction of high resolution protein structure has become one of the “biggest problems“ in modern biology. Physical and Chemical properties of amino acids and their solvent environment are the key determinants in folding a protein sequence into its unique tertiary structure. These factors essentially generate various types of energy contributors such as electrostatic, van der Waals, salvation/desolvation, which create folding pathways.

ab initio approaches for structure determination employ these physical and chemical factors to generate a structure or an ensemble of structures from the sequence as plausible candidates for the native. In an alternative approach, called homology modeling, one uses experimentally known protein structures as templates based on sequence similarity. Because of the insufficient experimental data and lack of knowledge about the true folding path way of proteins to the native ,may

prediction models generate low quality structures .These low quality structures might be look similar to high resolution structure having all the quality assessment criteria but in reality they could be 10-15 °A away from their true native states (Fig. 1). It would be highly desirable to have a predictive model, which can tell how far a structure is from the native in the absence of its experimental structure.

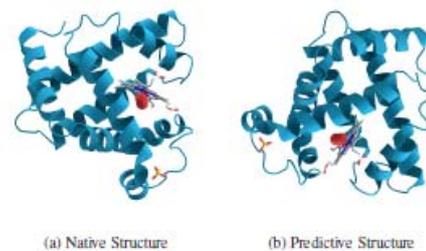


Fig. 1: The RMSD of predicted structure from its native is 10.3 Å (PDB ID: 1IF4).

Machine learning models have been mostly used in protein structure prediction such as 2D and 3D structure prediction (Rost and Sander, 1993; Rost *et al.*, 1993), fold recognition (Cheng *et al.*, 2005b; Kim *et al.*, 2003), solvent accessibility prediction, disordered region prediction (Obradovic *et al.*, 2005; Cheng *et al.*, 2005a), binding site prediction (Travers, 1989), trans membrane helix prediction (Krogh *et al.*, 2001), protein domain boundary prediction (Bryson *et al.*, 2007), contact map (Fariselli *et al.*, 2001; Baldi and Pollastri, 2002), functional site prediction, model generation (Simons *et al.*, 1997) and model evaluation (Wallner and Elofsson, 2007; Qiu *et al.*, 2007). In this work, we have explored the machine learning models with physical and chemical properties to predict the RMSD (Root Mean Square Deviation) of a modeled protein structure in the absence of its true native state. Physical and Chemical properties namely total empirical energy, secondary structure penalty, total surface area, pair number, residue length and Euclidean distance are used. There are total 1056 modelled decoys structures having 3078 native structures. The modelled structures are taken from protein structure prediction center (CASP-5 to CASP-10 experiments), public decoys structures database (Public-Decoy, 2010) and native structure from protein data bank (RCSB).) the feature importance is determined by the Real Coded Genetic Algorithm (RCGA) .machine learning model shaving the features

and names Decision Tree, random forest, Linear model and Neural Network for the prediction of RMSD protein structure. By the whole experiments, it is observed that random forest model outperforms the other machine learning approaches in prediction of RMSD. Further, K-fold cross validation is used to measure the robustness of the best predictive model. Finally, for the benchmarking of model correctness, the performance of best predictive model is compared with top-performing ProQ2 (Ray *et al.*, 2012) . The benchmark method is single model method. ProQ2 is based on Support Vector Machine. Rest of the paper is organized as follows. A brief overview of the considered features, data set, methodology, RCGA algorithm, and machine learning models are presented in Section 2. Model evaluation is presented in Section 3. Section 4 describes experiments, results and discussion. Finally, conclusion is presented in Section 5.

2 FEATURES AND METHODS

2.1 Data set and its features

There are total 1056 modelled structures having 3078 native structures. The modelled structures are fetched from protein structure prediction center (CASP-5 to CASP-10 experiments), public decoys structures database (Public-Decoy, 2010) and native structure from protein data bank (RCSB). Table 1 describes the physical and the chemical properties used in this study. A sample of the data set is shown in Table 2. Table 3 shows the correlation between each feature. There is no correlation of energy with euclidean distance, pair number, residue length and area. There is high correlation between (i) euclidean distance and pair number, (ii) residue length and pair number, and (iii) residue length and area

Table 1. Description of the features.

Feature	Information
Area	Total surface area.
ED	Euclidean distance.
Energy	Total empirical energy.
SS	Secondary structure penalty.
RL	Residue length
PN	Pair number

Table 2. Sample dataset.

RMSD	Area	ED	Energy	SS	RL	PN
0.00	8243.0	4939.6	-3391.1	86	75.00	165.00
8.03	7918.2	11984.2	-2273.2	29	153.00	102.00
6.77	9354.8	11535.1	-2422.5	66	67.00	186.00
13.26	15664.1	129761.0	-5820.4	146	104.00	368.00
0.00	8836.1	12198.8	-2926.1	80	66.00	101.00
6.76	12629.3	41461.0	-6206.8	146	61.00	116.00

Table 3. Correlation between each feature.

	Energy	SS	ED	PN	RL	Area
Energy	1.000	0.003	0.001	0.001	0.002	0.002
SS	0.003	1.000	0.514	0.572	0.670	0.656
ED	0.001	0.514	1.000	0.953	0.838	0.803
PN	0.001	0.572	0.953	1.000	0.913	0.837
RL	0.002	0.670	0.838	0.913	1.000	0.942
Area	0.002	0.656	0.803	0.837	0.942	1.000

2.2 Feature Measurement

We have explained an overview of the physical and the chemical properties used in this research.

2.2.1 Root Mean Square Deviation (RMSD)

The RMSD is calculated using the superposition between matched pairs of C α in two protein sequences. This superposition is computed using the Kabsch rotation matrix (Betancourt and Skolnick, 2001). The RMSD is calculated as:

$$RMSD = \sqrt{\frac{\sum_i^N (d_i * d_i)}{N}}$$

where, d_i is the distance between matched pair i , N is the number of matched pairs. RMSD is calculated using the freely available program at (RMSD, 2011).

2.2.2 Total surface area (Area)

Protein folding is done by various driving forces, which holds minimization of its total surface area. Degree of these external forces depends on the surface of protein exposed to the solvent, which convey the strong dependency of free energy on solvent accessible surface area (SASA) (Durham *et al.*, 2009). SASA has been used as one of the important properties to assess the quality of protein structures. Hydrophobic collapse is considered as a major factor in protein folding and this can be estimated as a loss of SASA of non-polar residues. Each amino acid shows a different affinity to be found on the surface of the protein based on the functional groups present in its side chain (Janin, 1979). Some questions arise with regard to the usage of SASA: (i) should it be the total area or is it the area of the non-polar residues, (ii) what is the standard fixed value of SASA for a native structure and (iii) is the rule of minimum area applicable to non-globular proteins. Here, total SASA have been calculated using Lee & Richards (Janin, 1979) method.

2.2.3 Euclidean distance (ED)

Spatial positioning of C α atoms decides the overall conformation of a protein. Recently, neighborhood profiles of C α atoms for each pair of residues have been characterized and observed to be invariant in 3618 native proteins suggesting certain geometrical constraints in their positioning (Mittal and Jayaram, 2011). The authors consider four aliphatic non polar residues Alanine (ALA), Valine (VAL), Leucine (LEU) and Isoleucine (ILE); collectively they formed 6 unique pairs among each other. Cumulative inter-atomic distance of their respective C β atoms were calculated for each residue pair. Euclidean distance is calculated by taking the cumulative difference of C α and C β . Euclidean distance between two protein sequences p and q is given as:

$$E_d = \sqrt{\sum_{t=0}^n (q_t - p_t)^2}$$

where, n is sequence length.

2.2.4 Total empirical energy (Energy)

The total empirical energy is the absolute sum of electrostatic force, van der Waals force and hydrophobic force (Arora and Jayaram, 1997; Naranget al., 2006). Molecular dynamics simulation package AMBER12 (Götz et al., 2012) is used to compute total empirical energy. It is computed as given below:

$$E_{elec}^{ij} = \frac{332 * qi * qj}{r_{ij}}$$

$$E_{vdW}^{ij} = \frac{C_{12}^{ij}}{r_{ij}^{12}} - \frac{C_6^{ij}}{r_{ij}^6}$$

$$E_{hyd}^{ij} = \frac{M_{12}^{ij}}{r_{ij}^{12}} - \frac{M_6^{ij}}{r_{ij}^6}$$

where, r_{ij} is the distance between pair of atoms i and j , $\epsilon\sigma^{12}$, $C_6^{ij} = 2\epsilon\sigma^6$, σ is the van der Waals radii, ϵ is the well $M_{12}^{ij} = \epsilon R^{12}$, $M_6^{ij} = \epsilon R^6$, R is the distance variable and ϵ is 1. Finally total empirical energy is given as:

$$|E_{total} = \sum_{i=1}^{n-1} \sum_{j=i+1}^n (E_{elec}^{ij} + E_{vdW}^{ij} + E_{hyd}^{ij})$$

2.2.5 Secondary Structure penalty (SS) Secondary structure prediction has reached to 82% accuracy (Sen et al., 2005) over the last few years. Therefore deviation from ideal predicted secondary structures can be used as a measure to quantify the quality of a structure. Secondary structure penalty is measured from the secondary structure sequence. It is computed as the absolute difference of the STRIDE (Frishman and Argos, 1995) and the PSIPRED (Jones, 1999) scores. STRIDE is used to assign three secondary structure classes, i.e., helix, sheet and coil to each residue in the protein models based on coordinates. PSIPRED is used to predict the probability for the same secondary structure classes.

$$S_{stride}(P) = S_{helix}(P) + S_{sheet}(P) + S_{coil}(P)$$

$$S_{psipred}(P) = F_1(P) + F_2(P) + F_3(P)$$

$$SS = abs(S_{stride}(P) - S_{psipred}(P)) \quad (2)$$

where, P is the protein sequence ; Sstride(P) and Spsipred(P) are the STRIDE and PSIPRED scores respectively; Shelix(P), Ssheet(P) and Scoil(P) are the STRIDE score for helix, sheet and coil of protein sequence P respectively; F1(P) is the predicted probability from PSIPRED for the secondary structure of the central residue in the sequence window; F2(P) is the correspondence between predicted and actual secondary structure over a 21-residue window; F3(P) is the secondary structure assigned by STRIDE ,binary encoded into three classes over a 5-residue window.

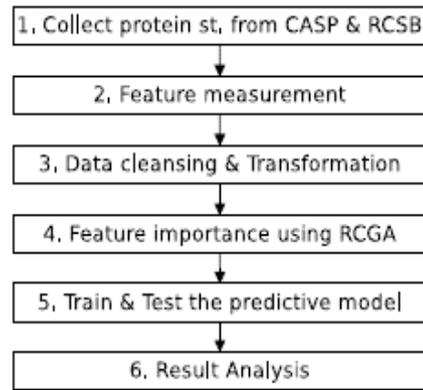


Fig. 2: Methodology used.

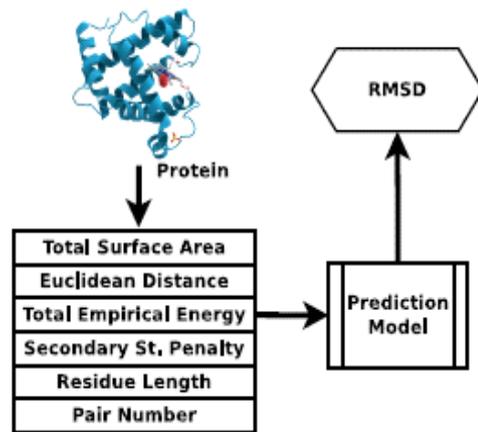


Fig. 3: Prediction model.

Pair number is the total number of aliphatic hydrophobic residue pairs in the protein structure and it is calculated by counting the total number of pairs between the Cβ carbons in the protein structure.

2.2.7 Residue Length (RL)

Residue length is the total number of Ca carbons in the protein structure.

2.3 Methodology

The methodology is explained in Fig. 2. In the very previous step, the modelled protein structures are taken from protein structure prediction center (CASP-5 to CASP-10 experiments), public decoys database (Public-Decoy, 2010) and native structure from protein data bank (RCSB). The feature measurement, as discussed in section 2.2, of protein structures is carried out in second step. In the next step the removal of duplicates and missing value entries from dataset were carried out. There are total 1056 decoys structures having 3078 native structures. In the fourth step, the Real

Coded Genetic Algorithm (RCGA) is used to measure the importance of each feature. Feature selection makes the prediction of model efficient and accurate. In the last step, the four machine learning approaches (refer, Table 5) were trained and tested on the data set with their default parameters. Fig. 3 describes the prediction model. Finally, the evaluation of the model is done on Root Mean Square Error (RMSE), Coefficient of Determination (R²), Correlation and Accuracy and K-fold cross validation is used to measure robustness of the best predictive model.

2.4 Real Coded Genetic Algorithms (RCGA)

Real Coded Genetic Algorithms (RCGA) is one of the most popular optimization method among the evolutionary algorithm (EAS). It's a population based stochastic search approach and in general can be regarded as a searching method from multiple positions and directions. It is used for the biological evolution in nature selection and it consists three operations – reproductions, crossover and mutation. Multiple good solution are carried out by the reproduction operations. The crossover operation blends genetic information operation between solution to generate new candidate solution. And the mutation operation convergence to a suboptimum solutions.

Due to it's good results in solving optimization problems, it has been widely applied in science, economics and engineering fields.

The crossover operation is considered as important in the evolutionary algorithm as it guides the search by producing new considered solution.

In past, the performance of RCGA has been developed by many difference kinds of crossover operators. From technical point of view, the crossover operators developed are mainly on the base of the line segment connection and distribution analysis of parent solutions, e.g., mean-centric and parent centric approaches. As observed in previous studies however, these featured approaches might bring out some problems. We searched firstly, there could be some areas where the crossover operation cannot generate offspring as the size of population so it's relatively small as compared to the whole search space, and/or the distribution of the initial given population does not uniformly scatter over the search space. Secondly, these crossover operators do not work well on the problems when the optimum is located at or near the boundaries of the search space. Moreover, due to the inherent nonlinearities, complex constraints and apparent interaction among decision variables, most RCGAs can unavoidably experience the problem of excessive complexity in implementation and the difficulties in locating true global optimal for some practical applications.

2.4.1 Feature Importance using RCGA

The RCGA is used to find the importance of each features. It defines the weight to each feature according to the objective function defined in eq. (3). As consider crossover rate (CR) and mutation rate (MR) are set to be 0.9 and 0.01

Table 4. Importance of each feature using RCGA.

Runs	Energy	RL	PN	SS	ED	Area
1	0.256	0.184	0.172	0.150	0.123	0.115
2	0.250	0.190	0.169	0.153	0.120	0.118
3	0.253	0.187	0.172	0.150	0.123	0.115
4	0.249	0.182	0.174	0.148	0.125	0.122
5	0.251	0.184	0.177	0.156	0.117	0.115
Avg.	0.252	0.185	0.173	0.151	0.122	0.117
Ranking	1	2	3	4	5	6

Respectively. Uniform crossover operator is used for crossover and arithmetic mutation (adding or subtracting a small number) is used as mutation operator. After five different runs, the weight obtained for each feature is described in Table 4. We can see in the above table the average weight of energy is highest and area is lowest that also signifies the importance of each feature in the dataset. As the weight given to each feature is significant so all the features are selected for the experiment

$$Objfun = \min \left(\sum_{i=1}^T \sqrt{\left(R_i - \sum_{j=1}^n w_j \cdot P_{i,j} \right)^2} \right) \quad (3)$$

where, T is the total number of instances in training data set, R is the RMSD, P is physical and chemical properties, n is the number of properties (6 in this case) and w is the weight given to each feature defined in the range of [0,1].

2.4.2 Machine learning models

In this work, we used four machine learning models (refer, Table 5) for prediction of RMSD of protein structure. The models are available in R open source software. R is licensed under GNU GPL. In precisely the models is presented below:

1. Decision Trees: This model is an extension of C5.0 classification algorithms described by Quinlan.
2. Random forest: It is based on a forest of trees using random inputs.
3. Linear Models: It uses linear models to carry out regression, single stratum analysis of variance and analysis of covariance.
4. Neural Network: Training of neural networks using back propagation, resilient back-propagation with or without weight or the modified globally convergent version.

3 MODEL EVALUATION

We have many ways to measure performance of the prediction, where some are more suitable than the others depending on the application considered. A brief discussion on the performance measures is explained below. The formula used for all the machine learning models is given by:

$$RMSD_Area + ED + Energy + SS + RL + PN$$

Table 5. Machine learning models used

Model	Package	Tuning Parameter(s)	Ref.
Decision Trees	C50	winnnow, model, trials	(Quinlan, 1986)
random forest	randomForest	mtry	(Liaw and Wiener, 2002)
Linear Model	stats	None	(Chambers, 1977)
Neural Network	neuralnet	layer2, layer1, layer3	(Riedmiller and Braun, 1993)

3.1 Root Mean Squared Error

RMSE is a popular formula to measure the error rate of a model. However, it can only be compared between models whose errors are measured in the same units. It is calculated as follows:

$$RMSE = \sqrt{\frac{\sum_{i=1}^n (p_i - a_i)^2}{n}} \tag{4}$$

Where ,a is actual value, p is predicted value and n is the total number of instances.

3.2 Coefficient of Determination (R2)

The coefficient of determination (R2) summarizes the explanatory power of the model and is computed from the sums-of-squares terms.

$$R^2 = \frac{SSR}{SST} = 1 - \frac{SSE}{SST} \tag{5}$$

where,

Sum of Squares Total: $SST = \sum (y - \bar{y})^2$

Sum of Squares Regression: $SSR = \sum (\hat{y} - \bar{\hat{y}})^2$

Sum of Squares Error: $SSE = \sum (y - \hat{y})^2$

where, y is the observed data, \bar{y} is the mean of the observed data, \hat{y} is the actual data and $\bar{\hat{y}}$ is the mean of the actual data. R^2 describes the proportion of variance of the dependent variable explained by the model. If the model is perfect, SSE is zero, and R^2 is 1. If the model is a total failure, SSE is equal to SST, no variance is explained by regression and R^2 is zero.

3.3 Accuracy

The accuracy is calculated as percentage deviation of predicted RMSD with actual RMSD.

$$Accuracy = \frac{100}{n} \sum_{i=1}^n q_i$$

$$q_i = \begin{cases} 1 & \text{if } abs(p_i - a_i) \leq 2 \\ 0 & \text{otherwise} \end{cases} \tag{6}$$

Where , a is actual value, p is predicted value and n is the total number of instances.

3.4 Correlation

Correlation describes the statistical relationships between actual and predicted values. It is defined as follows:

$$Corr = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^n (x_i - \bar{x})^2 \sum_{i=1}^n (y_i - \bar{y})^2}} \tag{7}$$

where, x is the actual value, y is the predicted value, \bar{x} is the mean of the all actual values, \bar{y} is the mean of the all

predicted values and n is the number of instances. Correlation lies in the range of [0,1] and is considered to be good if its value tends towards 1.

3.5 K-Fold Cross Validation

K-fold cross validation is used to measure accuracy of the predictive model. The original sample is randomly partitioned into k equal size subsamples. Of the k subsamples, a single subsample is retained

as the validation data for testing the model and the remaining k-1 subsamples are used as training data. The cross-validation process is then repeated k times (the folds) with each of the k subsamples

used exactly once as the validation data. Further, the k results from the folds are can be averaged to produce a single estimation. The advantage of this model over repeated random sub-sampling is

that all observations are used for both training and validation, and each observation is used for validation exactly once. Here, 10-fold (k=10) cross validation is used to measure the robustness of the best

selected model. 3.6 Benchmark of local model correctness For the benchmarking of model correctness performance of the random forest model is compared with top-performing ProQ2 (Ray *et al.*, 2012) . Both the benchmark methods are single-model method. ProQ2 is based on Support Vector Machine.

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For the benchmarking of model correctness performance of the random forest model is compared with top-performing ProQ2 (Ray *et al.*, 2012) . The benchmark method is single-model method. ProQ2 is based on Support Vector Machine.

4 RESULTS

In this section, we observe the prediction results of all the four machine learning models on the training and testing dataset. The machine learning models might be suffer from over fitting due to the possibility of criterion used for training the model is not the same as the criterion used to judge the efficacy of a model. Here, to avoid the over fitting , all four machine learning models are run on their default parameters and the distribution of data in training and testing set are 70% and 30% respectively for all the models.

Table 6 shows a comparative performance of all the models in the prediction of RMSD on RMSE, Correlation, R2 and Accuracy. The performance results show that the random forest model outperforms

the machine learning models in the prediction of RMSD of the protein structure in the absence of its true native state.

The RMSE is used to measure the differences between values predicted by a model and the values actually observed. The RMSE is calculated using equation 4. The random forest have the lowest

RMSE of 0.26 in the training dataset and 0.48 in the testing dataset. The correlation describe the statistical relationships

between actual and predicted values and it is calculated using eq. (7). The

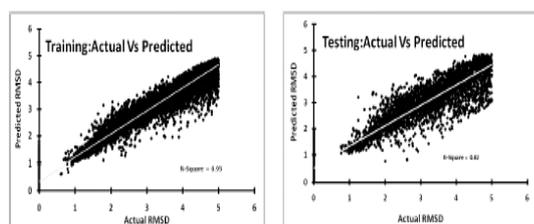
random forest have the highest correlation of 0.98 in the training dataset and 0.90 in the testing dataset.

R2 summarizes the explanatory power of the model between the prediction for each observation and the population mean. The R2 is calculated using eq. (5). The random forest have the highest R2 of

Table 6. Performance comparison of all four models on training and testing data set.

Table 6. Performance comparison of all four models on training and testing data set.

Model	Training dataset				Testing dataset			
	RMSE	Correlation	R ²	Accuracy%	RMSE	Correlation	R ²	Accuracy%
Decision Tree	1.20	0.50	0.25	79.55	1.16	0.51	0.26	82.46
RandomForest	<u>0.26</u>	<u>0.98</u>	<u>0.96</u>	<u>99.89</u>	<u>0.48</u>	<u>0.90</u>	<u>0.82</u>	<u>97.02</u>
Linear Model	1.43	0.25	0.06	65.51	1.44	0.22	0.05	65.97
Neural Network	1.39	0.31	0.10	70.19	1.46	0.06	0.00	67.15



- Actual vs Prediction RMSD for training dataset
- Actual vs Prediction RMSD for testing dataset

Fig. 4: Scatter plot of Actual vs Predicted values of RMSD on training and testing dataset using random forest

0.96 of in the training dataset and 0.82 in the testing dataset. Fig. 4 shows R2 in training and testing dataset. Accuracy is the degree of consistency of a calculated or measured quantity to its true (actual) value, where as precision is an experiment value, which measures the reliability of an experiment.

The accuracy is calculated using eq. (6) with acceptable error of ± 2 . The random forest have the highest accuracy of 99.89% in the training dataset and 97.02% in the testing dataset. Here, k-fold ($k=10$) cross validation is used to measure the robustness of the random forest. Fig. 5 shows the RMSE, correlation, R2 and accuracy for 10 folds in prediction of RMSD. Cross validation results show a uniform performance in all model evaluation parameters. Fig. 4 shows the scatter plot between actual and predicted RMSD for training and testing dataset using random forest. To prove the effectiveness of the predictive model, the performance of random forest is compared with top-performing ProQ2 and the performance is found to be quite impressive (refer, Table 7).

CASP Target ID	RMSD Prediction		
	Actual	ProQ2	RF
T0654_Multicom-Construct_Ts2	3.44	<u>2.95</u>	1.67
T0688_Bilab-Enable_Ts1	3.2	2.81	2
T0714_Multicom-Novel_Ts2	1.68	1.58	1.43
T0651_Native	0	4.5	<u>0.04</u>
T0653_Native	0	2.99	<u>0.18</u>
T0671_Native	0	3.01	1.06
T0684_Native	0	3.45	1.07
T0690_Native	0	3.45	<u>0.01</u>

Table 7. Performance validation on the existing decoys sets in the prediction of RMSD using random forest.

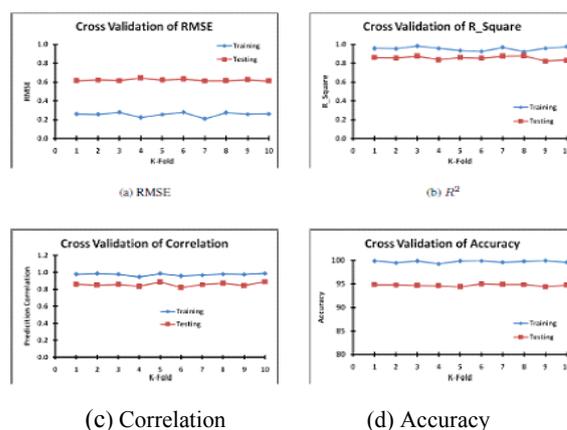


Fig. 5: 10-fold cross validation of RMSE, R2, Correlation and Accuracy on training and testing data set in the prediction of RMSD using random forest.

5 CONCLUSION

In this work, we explore four machine learning methods with six physical and chemical properties to predict the RMSD of protein structure in the absence of its true native state. The exact quality of a model is expressed in terms of how the model scoring the expected values from a given set of high resolution experimental structures. Here, the methods machine learning don't include any other information from other models or alternative template structures. All the models are evaluated on RMSE, correlation, R2 and accuracy. By the experiments, it is found that random forest method outperforms the machine learning methods in the prediction of RMSD. The K-fold cross validation is used to measure the robustness of random forest. Finally, for the benchmarking of model correctness, the performance of random forest model is compared with top-performing ProQ2. The benchmark method is single-model method and it is found that the random forest prediction accuracy is quite impressive. We believe that the more physical and chemical properties and other computational methods can be combined with machine learning methods produces even better results. The data set used in the study is available at <http://bit.ly/PSP-ML>

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