

**General Claimed:**

(A) proposed a DNA-binding protein prediction method that utilizes both sequence based evolutionary and structure based features of proteins to identify their DNA-binding functionality

(B) used SVM-RFE (Recursive Feature Elimination) method to extract an optimal set of features.

(C) trained a prediction model using SVM with linear kernel.

(D) achieves accuracy: jackknife test: **90.18%**, 10-fold cross-validation test: **88.87%**, Independent dataset: **80.64%**

**Features Used:**

1. Features generated from PSSM file:

Feature Name	Feature Vector Size
1. Amino acid composition	20
2. Dubchak features	105
3. PSSM Bigram (represents the transition probabilities of two adjacent amino acid residue positions)	400
4. PSSM 1-lead Bigram ( transition probabilities of the amino acid residue positions at 1 distance or separation )	400
5. PSSM Composition	20
6. PSSM Auto-Covariance	200
7. PSSM Segmented Distribution (used Fp = 5, 10, 25.)	200

Total = 1,345

2. SPIDER (used Spider2) based features:

Feature Name	Feature Vector Size
1. Secondary Structure Occurrence( count or frequency of three types of motifs structural motifs in proteins: $\alpha$ -helix (H)	3
2. Secondary Structure Composition( secondary structure motif occurrence normalized by the length of the phage protein length )	3
3. Accessible Surface Area Composition, Torsional Angles Composition, Structural Probabilities Composition	12
4. Torsional Angles Bigram	64
5. Structural Probabilities Bigram	9
6. Torsional Angles Auto-Covariance	80
7. Structural Probabilities Auto-Covariance	30

Total = 201

**Overall Feature Vector Size: 1345 + 201 = 1546**

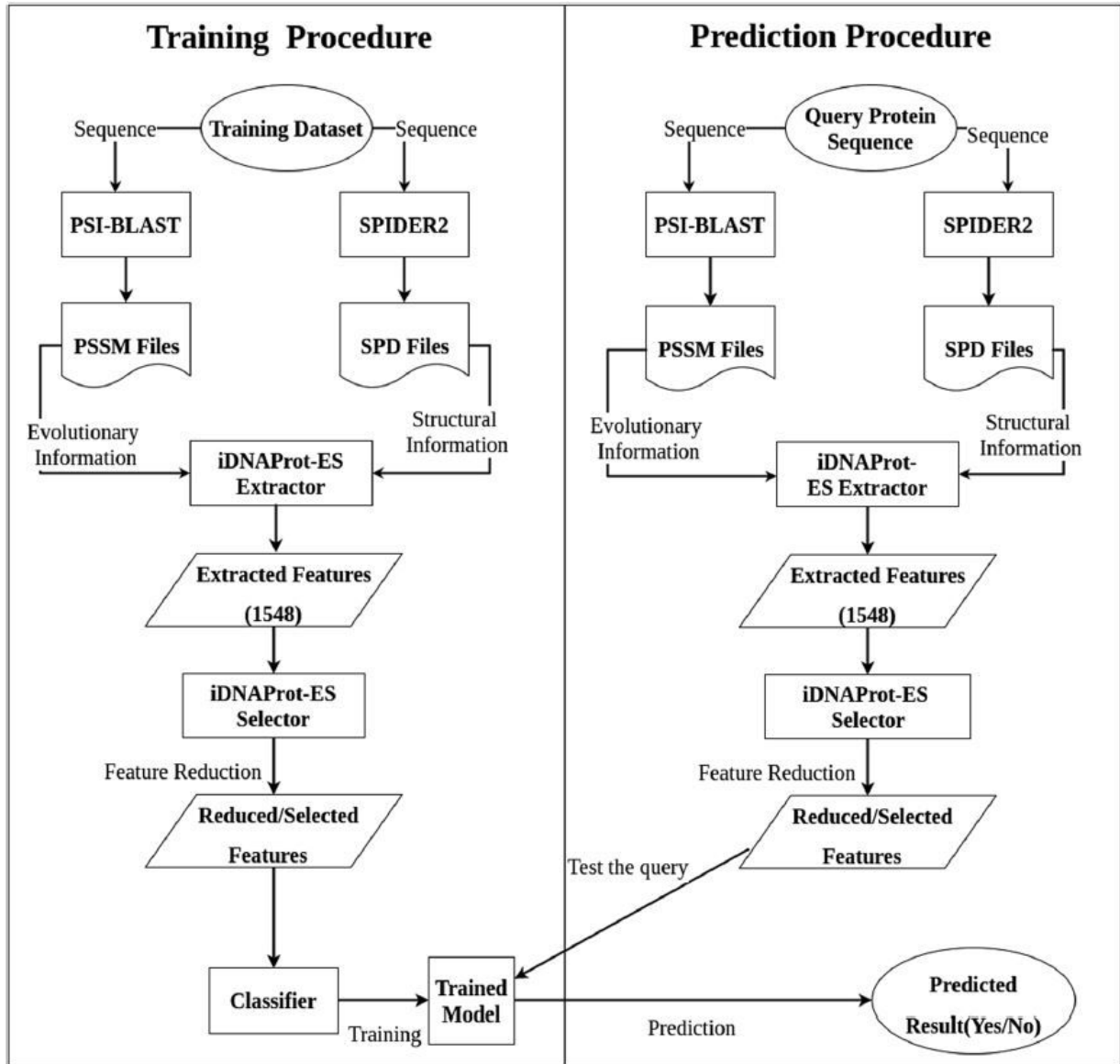


Figure: System flow diagram of iDNAProt-ES showing the training and prediction procedure.

#### Performance Measures:

(A) Jackknife on the benchmark dataset:

Accuracy (90.18%), SE (0.9038), SP(0.9000), MCC (0.8036), auROC(0.9412)

(B) 10-fold cross validation on the benchmark dataset:

ACC(88.87%), SE(0.8945), SP(0.8826), MCC(0.7788), auROC(0.9391), auPR(0.8828)

(C) Independent dataset:

Accuracy (80.64%), SE (0.8131), SP(0.8000), MCC (0.6130), auROC(0.8434)