## **LIST OF SYMBOLS**

k Number of nearest neighbors

d Euclidian distance

H<sub>1</sub> Hydrophobicity

H<sub>2</sub> Hydrophilicity

M Side chain mass

n Number of training data sets

mtry Size of random subset of features

*ntree* Number of trees in the random forest

 $X_1, X_{2,} ... X_{1497}$  Sequence derived properties

c<sub>k</sub> Class variable

S Feature subset

m membership coefficient of fuzzy k-NN

 $\sum$  Summation

## **LIST OF ABBREVIATIONS**

AAC Amino acid composition

ACC Accuracy

ANN Artificial neural network

CART Classification And Regression Tree

CF Correlation factors

CTD Composition, transition and distribution of properties

DC Dipeptide composition

DNA Deoxyribonucleic acid

FCBF Fast correlation based filter

GPCRs G-protein coupled receptors

k-NN k-nearest neighbors.

MCC Matthew's correlation coefficient

MLP Multi-layer perceptron

MRMR Minimum redundancy and maximum relevancy

NCBI National center for biotechnology information

PAAC Pseudo amino acid composition

PDB Protein data bank

RNA Ribonucleic acid

ROC Receiver operating characteristics

SD Sequence order descriptors

SVM Support vector machine

SVM-RFE Support vector machine based recursive feature elimination

## LIST OF KEYWORDS

Bioinformatics

Enzymes

Receptors

Ion Channels

Protein function prediction

G-protein coupled receptors

Sequence derived properties

Random forest

Rotation random forest

Weighted k-nearest neighbor

Fuzzy k- nearest neighbor

Voltage gated ion channels

Ligand gated ion channels

Feature selection

Prediction

Pattern classification

Minimum redundancy and maximum relevancy