Machine learning, an impetus approach for molecular functional annotation in plants

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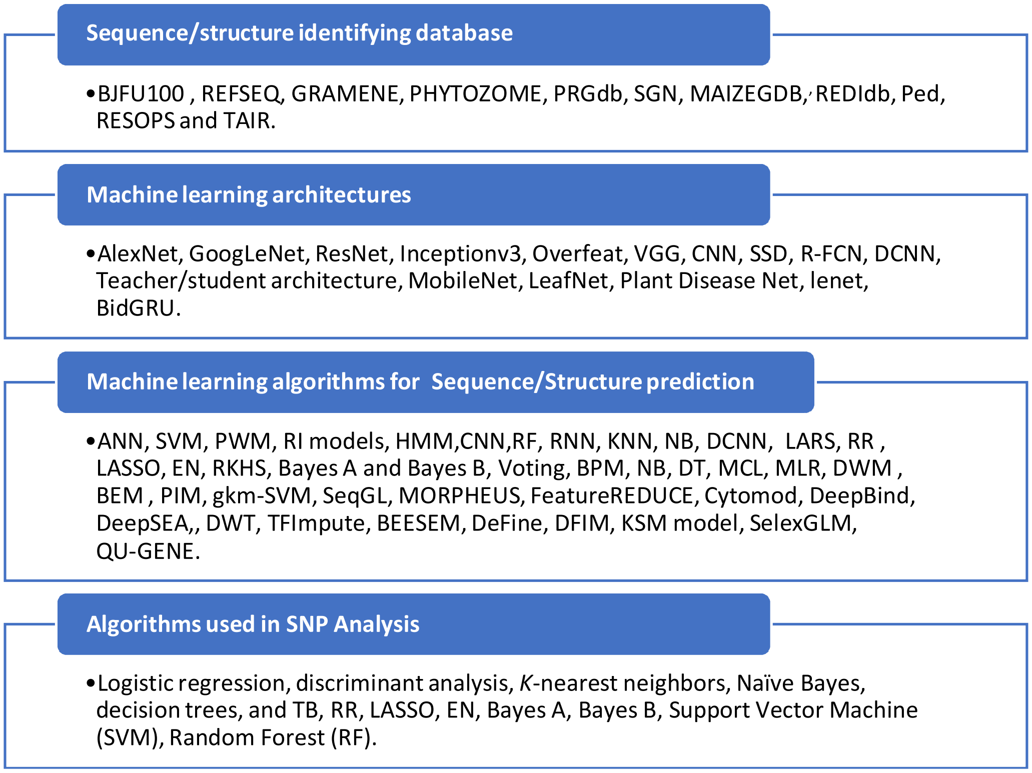
Traditional agriculture research programs have used classical breeding and molecular biology approaches for crop improvement. Besides, they are proved inadequate to deal collectively with a major number of problems. High throughput sequencing has shown a way towards overcoming those barriers along with storing and evaluating various big scale datasets on experimental basis. Artificial intelligence with Machine and deep learning techniques uses a training dataset as a calibrator for performing identification, classification, quantification and prediction. Different algorithms can interpret the same data to different desirable outputs; the output includes a simpler solution for the complex problems in link with a given dataset. Its application has moved research towards less biased and high precision results which are extensively accepted on a global level [1-3].

The sophisticated application of AI and machine learning is prevalent in genomics, transcriptomics, proteomics, metabolomics and systems biology[4]. The approach of Interpreting a given dataset with deep learning algorithms mentioned in figure 1 has been used for predicting translational initiation site recognition[5],signal peptide prediction[6], subcellular localisation[7], plant effectors[8], fungal effectors[9], promoter recognition[10], mRNA based alternative splicing[11], m5cap[12], poly A site[13], RNA editing[14], epistatic state[15], gene[16] and protein function and interaction[17],mutational analysis[18], epigenetic interaction[19], gene expression analysis[20], transcription factor binding[21], Chromatin signature[21], gene–environment interactions[22], SNP detection for QTL and interactome analysis[23-25].

Single nucleotide polymorphism is one of the major molecular markers for the indication of genetic diversity for crop improvement programs. It is majorly used for the assessment of genomic breeding values. Approaches like NGS are used to locate SNP in economic improvement traits, for the easy and early domestication of beneficial crops. However, the error-prone fashion of the available NGS analysis tools is still a big concern which can lead to false-positive results. Machine learning methods have paved a way towards more precise SNP screening from the sequenced data available in large natural population [23-25]. Fig.1 depicts the available machine learning algorithm used in SNP detection. In addition to it, “Integrated SNP Mining and Utilization” (ISMU) Pipeline [26] and “SNP machine learning” (SNP-ML)[27] are two of the ML based models presently in use for SNP based QTL analysis. Use of molecular marker datasets with machine learning algorithm holds promising results in genetic analysis and hybrid breeding [28].



Sequence/structure identifying database

- BJFU100 , REFSEQ, GRAMENE, PHYTOZOME, PRGdb, SGN, MAIZEGDB, REDIdb, Ped, RESOPS and TAIR.

Machine learning architectures

- AlexNet, GoogLeNet, ResNet, Inceptionv3, Overfeat, VGG, CNN, SSD, R-FCN, DCNN, Teacher/student architecture, MobileNet, LeafNet, Plant Disease Net, lenet, BidGRU.

Machine learning algorithms for Sequence/Structure prediction

- ANN, SVM, PWM, RI models, HMM,CNN,RF, RNN, KNN, NB, DCNN, LARS, RR , LASSO, EN, RKHS, Bayes A and Bayes B, Voting, BPM, NB, DT, MCL, MLR, DWM , BEM , PIM, gkm-SVM, SeqGL, MORPHEUS, FeatureREDUCE, Cytomod, DeepBind, DeepSEA,, DWT, TFImpute, BEESEM, DeFine, DFIM, KSM model, SelexGLM, QU-GENE.

Algorithms used in SNP Analysis

- Logistic regression, discriminant analysis, *K*-nearest neighbors, Naïve Bayes, decision trees, and TB, RR, LASSO, EN, Bayes A, Bayes B, Support Vector Machine (SVM), Random Forest (RF).

Figure 1- Machine Learning tools in Plant Biology.

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