Abstract

The symbiotic nitrogen fixing metabolic capacity is known to present in several prokaryotic
bacterium across taxonomic groups. Experimental detection of nitrogen fixation in microbes requires species-specific environment, making it complex to achieve a widespread survey of this attribute. Rhizobia legume symbiosis is an attractive research field because of its importance in agriculture. Rhizobia interact with host legume plants in soil to develop root nodules, which convert atmospheric nitrogen into ammonia, a form of nitrogen used by plants as nutrients. Experimental identification of nitrogen fixing proteins (nifu) is labor- as well as time-intensive. In this work, we present a Support Vector Machine (SVM) based method for the prediction of nifu and nifu-like proteins. The SVM models were trained PSI-BLAST derived PSSM matrices. The best classifiers are based on compositional properties as well as PSSM and yield an overall accuracy of 98.16%. This work will aid rapid and rational identification of nifu, expedite the pace of experimental characterization of novel nifu proteins and enhance our knowledge about role of Rhizobia –legume interaction.

References


Index Terms

Computer Science          Hpc Applications

Keywords

Rhizobium   Legumes   Genes   Svm