Classification of Dengue Serotypes Using Protein Sequence Based on Rule Extraction from Neural Network

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Abstract

Dengue virus is a growing problem in tropical countries. It serves disease, especially in children. Some exiting clinical methods CIMSiM, DENSiM, ELISA, SPSS, SARIMA, PCR and RT-PCR need a volume of blood cells which cannot be obtained from children. Meanwhile, some existing machine learning algorithms are used to diagnose the dengue infection based on the date of dengue fever, days, current temperature, white blood cell count, joint muscles, metallic taste in mouth, appetite, abdomen pain, hemoglobin, mild bleeding, vomiting, headaches, rainfall, and relative humidity attributes. These methods are used to diagnose the dengue in later stages. Sometimes these methods could not identify the correct results. To overcome these problems, this paper proposes the stable method of classifying dengue serotypes based on amino acids in the protein sequences. It needs only skin cells or hair or nail which can be easily obtained from any person including children also. The proposed method classifies dengue serotypes using entropy-based feature selection and rule extracted from the neural network. Results of the experiments show that the proposed method for classifying dengue fevers with its serotypes.

Keywords

Dengue diagnosis   Protein sequence   Neural network   Classification

Rule extraction