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Classification of Dengue Gene Expression Using Entropy-Based Feature Selection and Pruning on Neural Network(Conference Paper)

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Abstract

Dengue virus is a growing problem in tropical countries. It serves diseases, especially in children. Different diagnosing methods like ELISA, Platelia, haemocytometer, RT-PCR, decision tree algorithms and Support Vector Machine algorithms are used to diagnose the dengue infection using the detection of antibodies IgG and IgM but the recognition of IgM is not possible between thirty to ninety days of dengue virus infection. These methods could not find the correct result and needs a volume of the blood. It is not possible, especially in the children. To overcome these problems, this paper proposes classification method of dengue infection based on informative and most significant genes in the gene expression of dengue patients. The proposed method needs only gene expression for a patient which is easily obtained from skin, hair and so on. The classification accuracy has been evaluated on various benchmark algorithms. It has been observed that the increase in classification accuracy for the proposed method is highly significant for dengue gene expression datasets when compared with benchmark algorithms and the standard results. © 2018, Springer International Publishing AG, part of Springer Nature.

Author keywords

Classification | Dengue diagnosis | Dengue infection | Feature selection | Neural network | Pruning

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