Chapter 43
Using Blockchain Technology, Artificial and Natural Neural Network in Bioinformatics

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ABSTRACT

Blockchain technology has come up with solutions for the issues faced in the current healthcare system. Stakeholders and researchers can share electronic health records to find the solution to diseases. This not only improves the health sector, but it also provides information about other diseases. To maintain the security and privacy of the patient, a healthcare data gateway storage platform was created based on the blockchain technique. To overcome the problem, this article proposes a dengue diagnosis method based on nucleotides in the gene sequence, it needs only skin cells, hair, or a nail which can be collected easily from the patients. The proposed method not only diagnoses dengue, but also classifies serotypes using wavelet coefficients of EIIP indicator sequences.

INTRODUCTION

Blockchain technology has come up with solutions for the issues faced in the current healthcare system. Stakeholders and researchers can share electronic health records to find the solution to diseases. This not only improves the health sector, but it also provides information about other diseases. To maintain the security and privacy of the patient, a healthcare data gateway storage platform was created based on the blockchain technique. To overcome the problem, this article proposes a dengue diagnosis method based on nucleotides in the gene sequence, it needs only skin cells, hair, or a nail which can be collected easily from the patients. The proposed method not only diagnoses dengue, but also classifies serotypes using wavelet coefficients of EIIP indicator sequences. Although infection with one serotype grants a lifelong protection antigen against that serotype, it does not necessarily safeguard against a secondary infection with some other serotype. Some clinical diagnostic methods are used to diagnose the later stages of Dengue infections. These methods are based on the detection of IgG and IgM antibodies in the blood.

After the infection, IgM becomes unrecognized between thirty and ninety days. Among these periods, the treatment of normal viral fever is given to dengue patients. This leads to severe of dengue infections. The recognition of IgG alone is not enough to confirm the dengue infection without the presence of IgM. Generally, serotypes refer to the subdivision of a virus that is divided based on their surface antigen. Each serotype has its own characteristics and there is no cross production. The burden of dengue in the world is to classify dengue serotypes hence this paper suggests a useful and stable method based on Discrete Wavelet Transformation (DWT) for classifying dengue serotypes of using dengue gene sequence. Using Block chain Technology, Artificial and Natural Neural Network in Bioinformatics.

REVIEW OF LITERATURE

Numbers of different disease prediction models are used in medical diagnosis systems which are using data mining and machine learning techniques like Bayesian classification, decision tree, regression model, neural network, single best model and ensemble model. The different machine learning techniques (supervised, semi supervised, unsupervised, deep learning and reinforcement) and classification algorithms (Decision tree, kNN, Artificial Neural Network) are used in diagnosing different diseases such as Heart, dengue and cancer (Razia, prathyusha, Krishna & sumana, 2017).

(Raval, Bhatt, Kumbar & Salesin, 1994) have observed the current scenario of medical diagnosis system using different data mining techniques. The Prediction model was proposed using feedforward neural network for obtaining the optimal result of swine flu diagnosis. A clustering method (Kaur,Gupta & Bhathal, 2017) was proposed for diagnosis of dengue in a human by using the factors like period of fever, fever temperature, rashes or red spots, nausea or vomiting, Low heart rate and fatigue collected from dengue patients, meanwhile many dengue patients are suffered by fever temperature, muscle and joint pain and rashes or red spots. An appropriate method (Saberkar, Shami, Heravi & Sedaagh, 2013) was proposed for finding protein coding regions, which convert DNA into numerical sequences by EIIP (Electron Ion Interaction Pseudo potentials of nucleotides) values of nucleotides and are applied to discrete wavelet transformation for eliminating the high frequency noise and extracted the period-3 components from gene sequence as per the fixed threshold value of coding regions using Goertzel algorithm. From this method, the discrete wavelet transformation is also used for identifying protein coding and non-coding regions of patient's gene sequences. A novel GUI tool (Ali, Humayur, Azam, Munir, Riziwar, Mahmood & Adnan, 2017) was developed for classification of dengue based on genotype and the information in sequences of patients. It classifies a patient's genotype using Naïve Bayes classification algorithm. The results obtained from this method are useful for drug designers. (Rocha, Guilarde, Argolo, Tassaraa, Da Silveria, Junqueira, Turchi, Feres & Martelli, 2017) have studied that DENV I serotype was more prone to present with several clinical and laboratory features as compared with DENV IV patients together with spontaneous bleeding (DENV I: 33.0% and DENV IV: 20.0%), intense abdominal pain (DENV I: 29.7% and DENV IV: 14.1%), neurological symptoms (DENV I:6.7% and DENV IV: 2.2%) and thrombacy topenia (DENV I: 33.7% and DENV IV:18.2%). The immune status measurement of DENV I and DENV IV was same for 202 patients. They have shown that DENV I and DENV IV are more or less same in an antibody response patterns and severity of the diseases. (Guzman, Halstead, Artob, Buchg, Farrar, Gubler, Hunsperger, Krooger, Margolis, Martinez, Nathan, Palegrino, Simmons, yoksan & Peeling, 2010) have reviewed the various methods of identification of dengue. They have also discussed dengue virus pathogenesis, clinical signs and immunological response, laboratory diagnosis of dengue

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