



Document details - Protein sequence in classifying dengue serotypes

1 of 1

[Export](#) [Download](#) [More...](#)

Advances in Intelligent Systems and Computing

Volume 713, 2019, Pages 97-108

2nd International Conference on Advanced Computing and Intelligent Engineering, ICACIE 2017; Ajmer; India; 23 November 2017 through 25 November 2017; Code 216249

Protein sequence in classifying dengue serotypes(Conference Paper)

Pandiyarajan, P., Thangairulappan, K.

^aDepartment of Computer Science, Ayya Nadar Janaki Ammal College, Sivakasi, Tamil Nadu 626124, India

^bResearch Centre in Computer Science, V.H.N. Senthikumara Nadar College, Virudhunagar, Tamil Nadu 626001, India

Abstract

Dengue is the growing disease. It serves, especially in children. Different diagnosing methods like ELISA, Platelia, haemocytometer, RT-PCR, decision tree algorithms and recommender system with fuzzy logic are used to diagnose the dengue by blood specimen. But these methods identify severe cases after five to ten days of the person infected by dengue. Some other methods require saliva and urine samples instead of blood specimen when a volume of blood samples cannot be obtained from person, especially from children. But from this sample, the correct result could not be identified. To overcome these problems, this paper proposes dengue diagnosis method based on amino acids or components in the protein sequence as it needs only skin cells or hair or nail which can be collected easily from the patients. The proposed method not only diagnoses the dengue but also identifies serotypes using statistical analysis of protein sequence. The experimental results prove that the proposed method identifies dengue and its serotypes correctly by amino acids and components of protein sequences. The proposed method is capable of finding deficiency or dominance of amino acids or components in the dengue-infected protein sequence by assessing entropy, relative and weighted average values of amino acids or components. © Springer Nature Singapore Pte Ltd. 2019.

Author keywords

[Dengue serotypes](#) [Diagnosing methods](#) [Protein classification](#) [Protein sequence](#)

Indexed keywords

Engineering controlled terms: [Amino acids](#) [Blood](#) [Data mining](#) [Decision trees](#) [Diagnosis](#) [Fuzzy logic](#) [Intelligent computing](#) [Proteins](#) [Statistical methods](#)

Engineering uncontrolled terms: [Blood specimens](#) [Decision-tree algorithm](#) [Diagnosing methods](#) [Diagnosis methods](#) [Protein Classification](#) [Protein sequences](#) [Serotypes](#) [Weighted averages](#)

Engineering main heading: [Classification \(of information\)](#)

Cited by 0 documents

Inform me when this document is cited in Scopus:

[Set citation alert >](#)

[Set citation feed >](#)

Related documents

Find more related documents in Scopus based on:

[Authors >](#) [Keywords >](#)

ISSN: 21945357

ISBN: 978-981131707-1

Source Type: Book Series

Original language: English

DOI: 10.1007/978-981-13-1708-8_9

Document Type: Conference Paper

Volume Editors: Pati B., Panigrahi C.R., Pujari A.K., Bakshi S., Misra S.

Publisher: Springer Verlag

SciVal Topic Prominence ⓘ

Topic:

Prominence percentile:



About Scopus

[What is Scopus](#)

[Content coverage](#)

[Scopus blog](#)

[Scopus API](#)

[Privacy matters](#)

Language

[日本語版を表示する](#)

[查看简体中文版本](#)

[查看繁體中文版本](#)

[Просмотр версии на русском языке](#)

Customer Service

[Help](#)

[Tutorials](#)

[Contact us](#)

ELSEVIER

[Terms and conditions](#) ↗ [Privacy policy](#) ↗

All content on this site: Copyright © 2024 Elsevier B.V. ↗, its licensors, and contributors. All rights are reserved, including those for text and data mining, AI training, and similar technologies. For all open access content, the Creative Commons licensing terms apply. We use cookies to help provide and enhance our service and tailor content. By continuing, you agree to the use of cookies ↗.

