Accepted Manuscript

A novel alignment-free vector method to cluster protein sequences

Lily He, Yongkun Li, Rong Lucy He, Stephen S.-T. Yau

PII: S0022-5193(17)30263-1
DOI: 10.1016/j.jtbi.2017.06.002
Reference: YJTBI 9098

To appear in: *Journal of Theoretical Biology*

Received date: 17 February 2017
Revised date: 4 May 2017
Accepted date: 2 June 2017

Please cite this article as: Lily He, Yongkun Li, Rong Lucy He, Stephen S.-T. Yau, A novel alignment-free vector method to cluster protein sequences, *Journal of Theoretical Biology* (2017), doi: 10.1016/j.jtbi.2017.06.002

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

ACCEPTED MANUSCRIPT

Highlights

- We find the use of three physicochemical properties, hydropathy index, polar requirement and the chemical composition of the side chain, is helpful for phylogenetic analysis using protein sequences
- We propose a 24 dimensional feature vector to characterize the distribution of amino acids in protein sequences.
- Our results indicate that the new tool is fast in speed and accurate for classifying proteins and inferring the phylogeny of organisms.

ACCEPTED MANUSCRIPT

Download English Version:

https://daneshyari.com/en/article/5760077

Download Persian Version:

https://daneshyari.com/article/5760077

Daneshyari.com