Using Similarity Software to Evaluate Scientific Paper Quality Is a Big Mistake

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ABSTRACT

Using similarity software to examine the quality of scientific papers is a nuisance. The significance of a scientific paper should be decided by the acknowledged experts. The practice of using the computer program to decide scientific papers must be rescinded or voided.

1. INTRODUCTION

The problem by using the similarity software to evaluate the quality of scientific papers is as follows. 1) For the classic laws, theorems [1], and rules [2], it is not allowed to change even one word. 2) In contrast, by using different words with essentially the same contents or ideas as the classic ones, so as to claim new findings or discovery to steal the credit. Unfortunately, the similarity software is unable to detect this kind of cheatings. 3) In many music tunes composed by Bach Johann Sebastian and Wolfgang Amadeus Mozart (two of the most productive and influential composers for all time), their similarities are extremely high, but their tunes have been highly appreciated until now and even forever.

2. DISCUSSION

To develop a really useful prediction method or predictor for a biological system, one needs to go through the following five steps: 1) select or construct a valid benchmark dataset to train and test the predictor; 2) represent the samples with an effective formulation that can truly reflect their intrinsic correlation with the target to be predicted; 3) introduce or develop a powerful algorithm to conduct the prediction; 4) properly perform cross-validation tests to objectively evaluate the anticipated prediction accuracy; 5) establish a user-friendly web-server for the predictor that is accessible to the public. Papers written in compliance with the guidelines of the 5-steps rules, also named by many as "Chou's 5-steps rule" [3-35], have the following notable merits: 1) crystal clear in logic development, 2) completely transparent in operation, 3) easily to repeat the reported results by other investigators, 4) with high potential in stimulating other sequence-analyzing methods, and 5) very convenient to be used by the majority of experimental scientists.

Also, one of the most challenging problems in computational biology today is how to effectively for-

mulate the sequence of a biological sample (such as protein, peptide, DNA, or RNA) with a discrete model or a vector that can considerably keep its sequence order information or capture its key features. The reasons are as follows. 1) If using the sequential model, *i.e.*, the model in which all the samples are represented by their original sequences, it is hardly able to train a machine that can cover all the possible cases concerned, as elaborated in [2]. 2) All the existing computational algorithms can only handle vector but not sequence samples. However, a vector defined in a discrete model may completely lose the sequence-order information. To cope with such a dilemma for proteomics and genomics systems, the approach of pseudo amino acid composition components [36, 37] and pseudo K-tuple nucleotide components, called by many as "Chou's PseAAC" and "PseKNC" [23, 38-202], have been proposed.

3. CONCLUSION

Using similarity software to evaluate scientific paper quality is completely meaningless. The practice of using the computer program to decide scientific papers must be rescinded or voided. The significance of a scientific paper should be decided by the acknowledged experts as well as by whether it is in compliance with the "5-steps rule", as indicated by some very impressive papers [203-210] and a series of very recent papers (see, e.g., [211-226]).

CONFLICTS OF INTEREST

The author declares no conflicts of interest regarding the publication of this paper.

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