

Other Mountain Stones Can Attack Jade: The 5-Steps Rule

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ABSTRACT

Since the 5-steps rule was proposed in 2011, it has been widely used in many areas of molecular biology, both theoretical and experimental. It can be even used to deal with the commercial problems and bank systems, as well as material science systems. Just like the machine-learning algorithms, it is the jade for nearly all the statistical systems.

1. INTRODUCTION

Since it was proposed in 2011, the “5-steps rule” or “5-step rules” has been widely used in molecular biology, both theoretical and experimental. Its original source was usually referred by citing a review paper for celebrating the 50th anniversary year of Journal of Theoretical Biology [1].

Interestingly, no such a clear-cut term as “5-step” can be found in the entire aforementioned paper. Why? This is because: it is the idea of the “5-steps rule” that would become crystal clear after carefully reading through the whole paper. Accordingly, the paper [1] is actually the cradle of the “5-steps rule”.

2. THE ESSENCE OF 5-STEPS RULE

In order to quantitatively predict, or develop a useful predictor for, a molecular biology system, the following five guidelines should be observed: 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. The predictors established in compliance with these steps 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 predictors; 5) very convenient to be used by the majority of experimental scientists.

3. RESULT AND DISCUSSION

It is without exaggeration to say that the “5-steps rule” has been used at a very deeper levels of many molecular biology systems, as clearly and remarkably indicated by a series of the following reports: 1) “prediction of S-sulfenylation Sites” [2], 2) “identify phosphohistidine sites in proteins” [3], 3) “identify tyrosine sulfation sites” [4], 4) “prediction of S-sulfenylation sites” [5], 5) “exploring DNA-binding proteins” [6], 6) “reveal active compound and mechanism of shuangsheng pingfei san on idiopathic pulmonary fibrosis” [7], 7) “exploring DNA-binding proteins” [6], 8) “predict splice junctions with interpretable bidirectional long short-term memory networks” [8], 9) “identify hydroxylation sites in proteins” [9], 10) “identifying S-palmitoylation sites in proteins” [10], 11) “identifying S-prenylation sites in proteins” [11], 12) “identification of piRNA and their functions” [12], 13) “predicting secondary sequence information” [13], 14) “therapeutic treatment against Parkinson’s disease” [14], 15) “identifying DNA N(6)-methyladenine sites in rice genome” [15], 16) “identifying enhancers” [16], 17) “identifying molecular functions of cytoskeleton motor proteins” [17], 18) “identifying cancer targets” [18], 19) “identifying DNase I hypersensitive” [19], 20) “identifying DNA 6 mA modifications” [20], 21) “identify lysine crotonylation sites” [21], 22) “identifying RNA N6-methyladenosine” [22], 23) “detecting formylation sites” [23], 24) “identification of DNA N6-methyladenine sites” [24], 25) “calcium pattern assessment in patients with severe aortic stenosis” [25], 26) “identifying FL11” [26], 27) “prediction and analysis of quorum sensing peptides” [27], 28) “evaluate the stability of tautomers” [28], 29) “prediction of lysine formylation” [29], 30) “identifying nuclear receptors and their families” [30], 31) “identifying proteases and their types” [31], 32) “classifying anti-cancer peptides” [32], 33) “generating protein physicochemical descriptor” [33], 34) “modelling feedback in lung cancer” [34].

It is instructive to point out that in the systems of molecular biology there exist many multi-label ones where each of the individual constituents or samples considered may need two or more labels for distinction. For this kind of multi-label systems, two kinds of metrics are needed: one is the global set of metrics to indicate the global accuracy of the prediction method or predictor developed, while the other is the local metrics to indicate its local accuracy [35]. For the concrete mathematical formulations of the two sets of metrics, as well as their biological implications, refer to a recent paper [36].

4. CONCLUSION AND PERSPECTIVE

The “5-steps rule” has played substantial roles in stimulating in-depth studies of molecular biology, both theoretical and experimental. It is indeed a remarkable and profound milestone for molecular biology.

Although at the present the reports in this regard from theoretical scientists are more than those from experimental scientists, it is anticipated that, with more experimental data available in future, this kind of reports from experimental scientists will be increasing as well. Particularly, the combined reports between experimental and theoretical approaches, or their compliments to each other, will increasingly appear, as indicated by some very impressive papers [35-41] and a series of very recent papers (see, e.g., [42-56]).

CONFLICTS OF INTEREST

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

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