Reviewer's report

Title: Logic Minimization and Rule Extraction for Identification of Functional Sites in Molecular Sequences

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Reviewer: Jesus Aguilar-Ruiz

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In this paper, authors propose a logic minimization algorithm to build rules that can be used to predict Transcription Factor Binding Sites (TFBS) in DNA and =O-glycosylation sites in proteins, that means, to identify functional sites in molecular sequences.

COMMENTS TO BE REVISED

The analysis presented in this paper is appropriate to the journal:

- The Background section determines the context of the problem and it is well written. However, authors could include a short view of the state-of-the-art in the prediction methods in general, instead of the two benchmark methods used in the performance analysis.

- In section Methods, authors claim that the point of balance between time and effort needed to process the inputs will depend on each user. It would be interesting that authors could provide the complexity of the algorithm instead of an estimation.

- In section Results and Discussion, the dataset and results are well described. As a minor comment, when authors explain that they use 10 training sets, I suppose that they use 10-fold cross validation, isn’t it?

In general the paper is appropriate to the journal, well written and of interest.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.