Reviewer’s report

Title: Predicting metabolite-disease associations based on KATZ model

Version: 1 Date: 27 Aug 2019

Reviewer: Olga Lazareva

Reviewer's report:

Dear author,

Thank you for your replies, but unfortunately, there are still few objections which do not let a reader to see the proposed method in a context of existing methods and to understand how powerful is the suggested method.

"3) In the Background section authors stated:

"some relevant methods about predicting have been delivered for genomics such as gene-disease correlations [9-11], transcriptomics like circRNA-disease associations [12, 13] and proteomics such as identification of essential proteins [14-16], but the computational methods for predicting metabolite-disease associations can be counted on the fingers of a hand." This is a very vague statement regarding competing methods. It is unclear whether those methods exist or not and if they exist, they should be mentioned explicitly.

Reply: Thanks for your comments. These methods in metabolomics has been existed but are very few compared with other fields. And the first method paper in this field as an example has been mentioned in paper."

REPLY: It is still unclear for a reader how is your method different, better or worse.

"5) section "Comparison with other methods":

Benchmarking of the results should be done with respect to the existing methods while authors just mention something about a classic random walk method and page rank that they have implemented themselves and did not give source code.

Reply: Thanks for your comments. Random walk has been applied in the first paper in this field and we use our data sets in random walk to compare with our method."
REPLY: Did you use the implementation from Hu et. al? If so it should be stated, otherwise more details on your implementation of benchmarking methods are needed. For instance, Hu et. al had 2 hyperparameters in their random-walk based method. Did you use the same values for your random-walk based comparison method?

"7) no information about computational complexity or run-time. This information is also missing in benchmarking with other algorithms.

Reply: Thanks for your comments. Because the size of our data sets is larger, we don't calculate the computational complexity and we will consider it in the future work. In our paper, we set AUC as a judging standard to compare with other methods and don't consider it, either. We will consider it in the future work, too."

REPLY: Lack of publicly available source code and even approximate estimate on how long the computations might take, makes it is very difficult for other members of the community to use the suggested method.

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An article of limited interest

Quality of written English
Please indicate the quality of language in the manuscript:

Not suitable for publication unless extensively edited

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