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ICS 675
Paper Review Comments
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Paper Review Comments

Questionnaire: Fill out the review questions.

    a.   Technical Content and Accuracy

Answer: 1   2   3   4   5   6   7   **8**   9   10

Paper didn't get into the algorithms and the time consumption of the algorithms. As a reader, I would guess this application is pretty time-consuming. It might be helpful if the authors can add some algorithm related information. They will give people a better idea of how difficult to add or delete a virus strand into this taxonomic system. Also, if we decide this is a slow application, there might be ways to improve it.

    b.   Significance of the Work

Answer: 1   2   3   4   5   6   7   8   9   **10**

The "current" taxonomic system of phages hadn't changed for the last three decades, and it is based the physical characteristics. As the genome sequencing technology revolutionaries, people are seeking for ways to extract the phylogeny information out of the genome information. It should be possible to categorize a species based on it genome information, which is more accurate and easier to obtain compare to a whole set of phenotypes of this species.

    c.   Appropriate Title, Introduction, and Conclusion

Answer: 1   2   3   4   5   **6**   7   8   9   10

The suggestion of changing the taxonomy system is good, but the conclusion that the proteomic tree reflex phages' evolutionary history is weak. Paper didn't provide much supporting for this conclusion. Although it states a subtle improvement of the algorithms should help, it didn't clarify the drawbacks of the original algorithm or what improvement would be helpful.

d.   Overall Organization

Answer: 1   2   3   4   5   6   7   8   **9**   10

The organization is decent. It is not hard to follow the author's logic. Paper starts with some background introduction, which leads to the problem formulation, solutions proposal, and then conclusions and discussions. I would rearrange the order for the two conclusions. The first one proposes to use the proteomic tree as the new taxonomy system because it's the main conclusion.

e.   Style and Clarity of the Paper

Answer: 1   2   3   4   5   6   7   8   **9**   10

The paper is overall pretty clear and follows the typical style of science papers.

f.   Originality of the content

Answer: 1   2   3   4   5   6   7   8   9   **10**

Based on the research of some related papers and reviews, this group of people was definitely the first who proposed proteomic tree as a revolutionized phage taxonomy system. Their work was compared with two other main groups that hold different opinions of this issue.

g.   Referee's Confidence in the Paper's Subject

Answer: 1   2   3   4   5   6   7   8   **9**   10

The authors might want to reconsider the last conclusion, where they think this system reflexes the evolutionary history, or they could provide some related work from them or other researchers that supports this conclusion. Also, more algorithm detail would be helpful. Overall I, as the referee, am confident in the paper's subject.

h.   As a referee, how do you rate your knowledge, ability, and confidence in reviewing this paper?

Answer: 1   2   3   4   5   6   7   8   **9**   10

I had to look up some research history, algorithm details, some following up study. But that was the amount of work I expect for any research paper. So, overall, I was able to understand the paper and try to criticize its content.

Comments: Comments to the Authors (must include summary of the paper and comments)

Answer: Paper presented a phage proteomic tree, which is based on the overall similarity of 105 completely sequenced phage genomes. The predicted proteomic tree was able to rule out the possibility of having a single genomic marker for phylogeny study of phages, and it is compatible of the "current" classifications of phages according to authority. Therefore the authors propose that the phage proteomic tree be used as the basis of a genome-based taxonomical system for phages.

The comments are basically covered in the previous section. It was valuable work addressing an essential taxonomy issue. The authors' goal is to set up a new standardization and fill in the missing link of the bacteria virus phylogeny problem. There are two comments of how improving the paper. One is that providing some support martial for the last conclusion might help. Two is that the readers might want to know more about the algorithms.

Comments: Comments to the committee

Answer: Please refer to the first section.