Reviewer's report

Title: Role of loss of full length CtBP1 expression in malignant melanoma

Version: 2 Date: 19 September 2008

Reviewer: Stefan Wiemann

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In Article 4092593022190149, Frank describes the XplorSeq package of tools that he has implemented to aid in the analysis and annotation of metagenomic sequence data. In particular, this software is intended for users who do not have available sophisticated hard- and software environments but who rather rely on stand-alone solutions using their Macintosh computers. The author suggests phylogenetic analyses of environmental ribosomal RNA genes as a potential application and proposes that the new developments in high-throughput sequencing as well as the lack of sophistication of many users would increase the demand for software solutions like the one he is introducing. The package that he describes in this paper is applied to compile, manage, and phylogenetically analyze DNA sequences, and is supposed to be applicable also for high-throughput analyses of environmental rRNA gene sequences. Several programs that had originally been implemented in the UNIX OS have been compiled to run now on the Macintosh OS-X, making use of the Macintosh GUI. The software can be downloaded and is free for non-commercial users. The author reports an impressive list of publications where the authors have based their sequence analysis on the XplorSeq package.

1. Does the software address a novel task? Alternatively, if there is already software available that performs this task, does the software outperform it in terms of speed, reliability, efficiency, or breadth of application?

The implementation of software for sequence alignment, analysis, clustering, import & export is not really new, however, some of these solutions are either commercial (DNAStar) or have not been kept up-to-date (e.g., Staden package). The number of publications that are cited to have utilized the XplorSeq software tells me that there is a true need for such software and that this software has level of maturity that it can and is really applied.

2. Is it easy to use?

Yes. The Macintosh GUI should make this software easy to use.

3. Does it satisfactorily address the task or application the authors intend?

Yes

4. Is the software freely available for non-commercial use (note that this is a condition of publication)? And is the availability of the software and any restrictions on use clearly stated in the manuscript?
The URL is provided from where the software can be downloaded. The software is free for non-commercial users.

5. Does the manuscript clearly describe the problem the software is designed to address
   yes

6. Does the manuscript clearly describe how the software is implemented?
   yes

7. Does the manuscript clearly describe how the software performs and its advantages/limitations over existing applications?
   Yes. The revised version of the manuscript now also considers the limitations that are caused by the hardware it has been designed for.

8. Does the manuscript state the software's operating requirements
   Yes. With the benchmarking study displayed in table 3 potential users should be able to quite easily assess what computer hardware they should need for their own sequencing projects.

9. Are the discussion and conclusions of the manuscript well balanced and adequately supported by the data?
   yes

10. Do the title and abstract of the manuscript accurately convey what has been found?
    Yes

11. Is the writing acceptable?
    Yes, I am just not sure if the statement ‘can be applied to most any sequencing project’ is grammatically correct.

**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.

**Declaration of competing interests:**

I declare that I have no competing interests