Reviewer Report

Title: Label3DMaize: toolkit for 3D point cloud data annotation of maize shoots

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Reviewer name: Luis Diaz-Garcia

Reviewer Comments to Author:

The authors describe a software called Label3DMaize to segment and annotate point cloud data. The software offers different types of segmentation methods, some of them faster than others. In terms of processing speed, Label3DMaize is faster than other platforms. The subject is of clear importance since highly precise phenotypes can be computed from 3D representations. Moreover, 3D representation allows the measurement of hard-to-measure or complex phenotypes.

Some comments:

- 1) This software runs in Matlab, which is vaguely mentioned in the Additional files section. I consider it is important to mention this in the main text because this will impact the accessibility of the software for many potential users.
- 2) The 3D point cloud data used in this study was generated by a system (MVS-Pheno) that the same authors developed just recently (the paper was published early 2020). MVS-Pheno is a commercial software it seems. My main concern is the dependency of Label3DMaize on data generated through MVS-Pheno. Is this going to work on data generated on a different system? If so, additional tests showing that must be included in the present study.
- 3) Both the introduction and the discussion sections are a little heavy; there is a constant reuse of ideas, which becomes repetitive and tedious to read. I suggest reducing the text considerably.
- 4) Lines 48-49. The authors say that multiple MVS platforms have been developed, but they just mention one reference (reference 16).
- 5) Examples of previous work regarding 3D point cloud data are presented in the Introduction section, which provides the reader a good context. However, it seems that the examples are presented one after another without a proper link.
- 6) Clearly, this is a relevant tool that could benefit researchers studying plant morphology as well as breeders. However, I don't think this study fits well within the scope and requirements of GigaScience (e.g. lack of novelty, more tests are required, why not using this in a different species with similar plant structure?, high dependency in other tools, etc...).
- 7) Section 4.3 could be integrated within other Discussion subsections.

 That said, I would consider that the work is not suitable for publication in its present form.

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Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

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