Reviewer Report

Title: DENTIST â€“ using long reads for closing assembly gaps at high accuracy

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Reviewer name: Leena Salmela

Reviewer Comments to Author:

Overview:
The paper presents a new tool called DENTIST for closing gaps in short read assemblies using PacBio CLR data. Although new assemblies are nowadays most often done with PacBio HiFi data resulting in contiguous and accurate assemblies, closing the gaps of an existing short read assembly with long read data is a cost effecitve and therefore attractive alternative for species for which short read assemblies are already available. The new tool is shown to be more accurate than previous tools and of comparable sensitivity.
Suggestions for revision:
1) The authors should clearly indicate in the Introduction that their tool is tested on PacBio CLR reads. It would also be good to specify in the abstract that the reads were CLR reads and not HiFi reads.
2) In the Discussion, the authors recommend to "polish" the final gap closed assembly with Illumina reads. It would be interesting to see how much this improves the accuracy of gap closing. I would assume that the improvement on the gap sequences would be smaller than on other regions of the assembly because the gap sequences typically cover repetitive regions.
3) Last paragraph of section "Closing the gaps", page 14: DENTIST has three modes. Here it is indicated that the third mode (only use scaffolding information for conflict resolution and freely scaffold the contigs using long reads) would be the best mode for contig-only assemblies. It seems to me that also the second mode would be appropriate for this as it also closes gaps between scaffolds (or contigs in case of lack of scaffold information). Is this so?

Level of Interest

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