Reviewer Report

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

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Reviewer name: Ian Korf

Reviewer Comments to Author:

The paper by Ludwig et al demonstrates that DENTIST offers a substantial improvement in closing genomic assembly gaps. The paper is well written with a clear and concise style. I liked the way they approached the experiments with a combination of simulated and real data for both the assemblies and reads. Specifically, I applaud how they generated gaps where they actually happen. The figures are generally effective. The only exception to this is Figure 4 with the black background and inconsistent ordering of competing software. In addition to winning the bake-off against other software, they did a very useful analysis of read depth (figure 6) and resources used (table 2). These help future users plan their projects. From a code perspective, I like that they have put their code on github. I don't think they need to have the supplemental file of command line parameters, as anyone who wants to use the software is going to go to the github anyway, which has a much more comprehensive explanation of usage.

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