

Reviewer Report

Title: Fast-SG: An alignment-free algorithm for hybrid assembly

Version: Original Submission **Date:** 25 Dec 2017

Reviewer name: Daniela Puiu

Reviewer Comments to Author:

I have read the article and I found it well written and informative, especially for the genome assembly community. While the idea of generating synthetic mate-pairs is not new, you implemented it in the new context of long reads and unique kmers .

I have also managed to download, install and run Fast-sg, and reproduce some of results described in the article. However I had difficulties installing and running ScaffMatch, Integrating it in your package and creating a seamless interface between the two programs would be highly recommended.

Level of Interest

Please indicate how interesting you found the manuscript: An article of importance in its field

Quality of Written English

Please indicate the quality of language in the manuscript: Acceptable

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