Reviewer Report

Title: SwiftOrtho: a Fast, Memory-Efficient, Multiple Genome Orthology Classifier

Version: Revision 1 Date: 7/16/2019

Reviewer name: Robert Davey

Reviewer Comments to Author:

The authors have addressed my concerns, and appear to have covered those of the co-reviewers. The extra supplemental information on the tool comparisons is welcome. I only have minor grammatical changes to pass on:

Lines 46-47: "first perform all-vs-all sequence alignment, then constructs gene families by the sequence similarity or conserved gene neighborhood" : "first performs all-vs-all sequence alignment, then constructs gene families by sequence similarity or conserved gene neighborhood"

L67-68: "However, these tools require high performance computers to analyze large-scale data." : "However, these tools tend to require high performance computers with large memory available to analyze large-scale data"

L102-103: "Spaced seed" should be plural in both cases.

L127: "First, SwiftOrtho sorts the data and store it on hard drive." : "Firstly, SwiftOrtho sorts the data and stores it on the filesystem"

L419: "[of, For] Bac set" : "[of, For] the Bac set"

L421: "impractical to apply OMA to large-scale data set." : "impractical to apply OMA to a large-scale data set in most computational environments"

L424: "Bac set" : "the Bac set"

L430-431: "on Bac set" : "on the Bac set"

L433: "in all-vs-all homology search step" : "in the all-vs-all homology search step"

L436: "of orthology inference" : "of the orthology inference"

L437: "to Bac set" : "to the Bac set"

L440-441: "In sum, these results show that SwiftOrtho is a top performer on large-scale data." : "In summary, these results show that SwiftOrtho is the most computationally efficient on large-scale data."

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