

## Reviewer Report

**Title:** Libra: scalable k-mer based tool for massive all-vs-all metagenome comparisons

**Version:** Revision 2      **Date:** 12/5/2018

**Reviewer name:** Rachid Ounit

### Reviewer Comments to Author:

Authors have fixed the formatting/issues for the formulas, and provided references for the sentence referring to the microbial dark matter.

Authors claim: "advanced tools such as k-mer based classifiers that rapidly assign metagenomic reads to known microbes miss "microbial dark matter" that comprises a significant proportion of metagenomes" How significant is this proportion? Please provide a range, and I recommend to provide reference(s) for that said range.

Also note that I did not find the references for the list of tools mentioned in supplemental material, but I assume the editor will follow up on this.

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Please indicate the quality of language in the manuscript: Choose an item.

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