**Reviewer Report**

**Title: PIRATE: A fast and scalable pangenomics toolbox for clustering diverged orthologues in bacteria**

**Version: Original Submission** **Date:** 5/7/2019

**Reviewer name: Andrew Page**

**Reviewer Comments to Author:**

This is a well written paper describing a new pan-genome method called PIRATE.  They compare it to the state of the art and provide many improvements, so it will be of great use to the microbial bioinformatics community.  In particular they use Dimond to speed up comparisons, and do a much better job with paralogs and assembly errors compared to Roary (my tool).  The software is easy to install via Conda, and it accepts a very commonly used annotation file format (GFF3 files from PROKKA), all things that are often overlooked in papers, so good work.
Just a few minor comments:
You should consider adding the GC content of the 3 species under test since there is a nice range.
PopPunk (Lees et al.) has recently come out and would be a relevant citation:
https://genome.cshlp.org/content/29/2/304
Could you add the inflation factor for MCL and how you arrived at it, because it can have a big impact on the end results.

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**Quality of Written English**

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