**Reviewer Report** 

Title: NanoPipe - a web server for nanopore MinION sequencing data analysis

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**Reviewer name: Keith Robison** 

**Reviewer Comments to Author:** 

This application note describes a useful, web-oriented pipeline for several major nanopore data use cases.

Given the straightforward nature of the manuscript, I'm going to devote most (if not all) comments about the software itself in the hopes the authors find these useful

A rather serious disagreement between the text and the web software is the set of reference genomes; the github archive appears to have no reference genomes. The manuscript claims 12 database and the 7 offered on the website don't fully overlap that set.

I tried uploading a small set of E.coli reads and an E.coli reference (one of the manuscript-promised, noton-server cases!) but I seem to be permanently parked behind two other jobs.

The website has a "View Testcase" button -- that yields an error message screen .

Similarly the github package does not appear to contain a useful test case or any code to check the installation except running the package -- so if anything goes wrong it could be difficult for a novice to determine which of the long list of dependencies (11 Perl modules, 9 Python modules, 2 other tools)

The authors might also consider distributing as a docker container and/or conda package with all dependencies covered.

Streamlining the process of creating a new target database would be desirable -- the "install.txt" file gives a 5 step protocol -- two of which should be combined ( "Create the target database" & amp; "target.fasta". The lastdb step really should be wrapped in something that checks the new database information for consistency

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