

## Reviewer Report

**Title: PhageGE: An interactive web platform for exploratory analysis and visualisation of bacteriophage genomes**

**Version: Revision 1**      **Date: 7/15/2024**

**Reviewer name: Andre Mu**

### Reviewer Comments to Author:

I thank the authors for addressing most of the concerns from the first review; especially incorporating the multi-fasta upload function. I think it's important to state upfront in the abstract what phageGE can do (i.e., phylogenetic analysis, visualisation of phylo tree, predict phage lifecycle, and comparative analysis of phage genome annotations). Please include a link to the phageGE webpage in the abstract. Spelling mistakes throughout the manuscript - as an example L288: comprehensive.fna and .fasta are the same format. i.e., fna is a type of FASTA file. fna specifies that the fasta file specifically contains nucleotides (instead of amino acids). change "biologist friendly" to "User friendly" - this is more a philosophical/psychological change. I think bioinformatics on the command-line should be accessible and something biologists can develop. I think calling GUI programs "biologist-friendly" will deter more biologists from learning bioinformatics.

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