Review of: "Microbiome Maps: Hilbert Curve Visualizations of Metagenomic Profiles"

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First, I would like to declare that I am not a computer scientist or a mathematician so I cannot comment on some of the algorithmic decisions made by the authors.

The authors describe a tool, which they call Jasper, that utilises Hilbert Curve to visualise genomes in metagenomic samples. Overall, the manuscript is very well written, easy to read, clear and to the point. I find that the advantages that the authors ascribe to their method to be genuinely interesting and of potential relevance and value to the community. I find myself interested in using the tool in the future and perhaps even recommending it. The website associated with the tool is well designed and has sufficient content.

I have a few comments:

- It is helpful to have line numbering for specific commenting
- Overall, the authors do not comment on how they consider abundance values reported from different metagenomic profiling tools. I would urge the authors to have a look at a recent review by Sun et al (2021) [1]. This review describes a somewhat concerning problem of reporting microbial abundances in metagenomics samples
- "*While the Karken2 software does it for 16S datasets*". This is not strictly true. Kraken2 is WGS metagenomic profiler that can also accommodate some 16S datasets. In fact the standard Kraken2 database is RefSeq (Bacteria, Archaea & Viruses). Refer to the publication [2] as well as the GitHub repo (https://github.com/DerrickWood/kraken2/wiki/Manual#standard-kraken-2-database).
- I am bit disappointed that the authors only provide a MacOS version of their tool (not clear in the manuscript). I would have been nice to have a Linux version or a webserver.
- "*Note that unlike other HCV techniques, microbiome maps do not depict genomic positions….from a reference collection*": not clear. Please elaborate.

References

1. ^*Zheng Sun, Shi Huang, Meng Zhang, Qiyun Zhu, et al. (2021).Challenges in benchmarking metagenomic profilers. Nat Methods, vol. 18 (6), 618-626. doi:10.1038/s41592-021-01141-3.*

2. ^*Derrick E. Wood, Jennifer Lu, Ben Langmead. (2019).Improved metagenomic analysis with Kraken 2. Genome Biol, vol. 20 (1). doi:10.1186/s13059-019-1891-0.*