Review of: "Evolution of new variants of SARS-CoV-2 during the pandemic: mutation-limited or selection-limited?"

David W. Ussery[1]

[1] University of Arkansas for Medical Sciences

Potential competing interests: No potential competing interests to declare.

I like the idea of having clearly testable hypothesis, along with predictions of what is expected. However, the link to the data used no longer works. I am curious how many of the 15 million SARS-CoV-2 genomes available were used in this analysis. Also, it was not clear to me what methods were used to clean the very noisy data (often times with lots of ‘NNNNN’s in the sequence, for example). There's also the problem of potential bias towards geographic locations where the virus is more heavily sampled, whilst other areas with perhaps more actual people infected are rarely sequenced.