Abstract

Phylogenetic analysis is one of the most reliable and important analyses in bioinformatics. Currently, many phylogenetic analysis tools can be used for the visualization and interpretation of biological data. However, a lot of technical expertise is required in order to use these tools. It is challenging for biologists to have to deal with this issue.

This study therefore compared three multipurpose phylogenetic analysis tools and informed on their features so as to help the user choose the appropriate tool for their research and resources, especially those who want to do research in bioinformatics in Africa.

Phylogenetic analysis was done on whole genome sequences obtained from NCBI repositories using MEGA, SeaView and Geneious separately. Subsequently, a detailed comparison table based on features for each tool was generated. What makes our study unique is that we used the African SARS-CoV-2 genomes which have rarely been used for studies describing the evolution of coronaviruses.

After the benchmarking, we recommend tools based on the user's resources and objectives. MEGA and SeaView would be the best option for a researcher with no technical bioinformatics knowledge and looking for a free tool. Geneious is as easy to use as MEGA and SeaView, and it additionally gives more options and information. On the other hand, it requires a lot of time and it is not free to use.

We have highlighted the relevant molecular and genetic evolutionary analysis tool based on the user's resources.