### Viral Miniproject

**Aim:**

The study will use bioinformatics approaches. In this project, participants will be required to use the provided files described in the manuscript to perform data preprocessing, variant calling, alignment, assembly and phylogenetic analysis as described by the manuscript. Participants will use any pipeline used in the study, interpret the output files, critique it, compare with other available pipelines or even come up with a better pipeline.

Manuscript:

Casimiro-Soriguer, C. S., Perez-Florido, J., Fernandez-Rueda, J. L., Pedrosa-Corral, I., Guillot-Sulay, V., Lorusso, N., Martinez-Gonzalez, L. J., Navarro-Marí, J. M., Dopazo, J., & Sanbonmatsu-Gámez, S. (2021). Phylogenetic Analysis of the 2020 West Nile Virus (WNV) Outbreak in Andalusia (Spain). Viruses, 13(5), 836. <https://doi.org/10.3390/v13050836>

**Objective:**

* Come with a detailed report answering the following:
* Describe all components of the pipeline used in the manuscript.
* Was it easy to utilize the pipeline? If not why?
* How can you compare it with other pipelines such as Galaxy?