

Viral Instant Mutation Viewer (VIMVer): a tool to speed up the identification and analysis of new SARS-CoV2 emerging variant

Vincent Wilde, Bruno Canard, Francois Ferron

▶ To cite this version:

Vincent Wilde, Bruno Canard, Francois Ferron. Viral Instant Mutation Viewer (VIMVer): a tool to speed up the identification and analysis of new SARS-CoV2 emerging variant. ViBioM 2022, Mar 2022, Valencia, Spain. online. hal-04387599

HAL Id: hal-04387599 https://amu.hal.science/hal-04387599

Submitted on 11 Jan 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.





AFMB Viral Instant Mutation Viewer (VIMVer):

a tool to speed up the identification and analysis of new SARS-CoV2 emerging variant vincent WILDE

Vincent WILDE¹, Bruno CANARD^{1,2}, François FERRON^{1,2}

1. Architecture et Fonction des Macromolécules Biologiques, CNRS and Aix-Marseille Université, UMR 7257, PolytechCase 925, 13009 Marseille, Franc
2. 2 European Virus Bioinformatics Center, Leutragraben 1, 07743 Jena, Germany



1st year PhD student vincent.wilde@univ-amu.fr

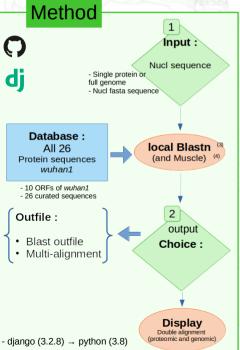
test run on LC633760.1 - delta variant (6



Introduction

Two years after its outbreak, COVID-19 still represents a major public health problem as it keeps spreading at an alarming rate through the rise of many pathogenic variants (1). The severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), responsible for the COVID-19 pandemic, has become one of the most studied viruses since its emergence. The divergence of these variants from the original strain has a real impact on the efficiency of the vaccination. In this context, our main goal is to understand the differences behind the mutations observed simultaneously in the proteome and the genome. To act accordingly, we developed an user-friendly web-service software (Viral Instant Mutation Viewer or VIMVer) which allows a fast identification of new mutations and displayed them in both the nucleotide and protein sequences in comparison to a reference sequence (wuhan-1). Given a SARS-CoV-2 nucleotide sequence (as a newly sequenced genome), our software will instantly extract, analyze and visualize mutations on the genome and the proteome with the proper numbering and

positioning. Furthermore, the lineage or the relative position to known lineage of the variant of interest is available on the link to Phylogenetic Assignment of Named Global Outbreak LINeages (Pangolin COVID-19) (2). We believe this tool will help many in their daily process to analyze their data. The source code is released under public license and can be adapted for further development.



available source code (gitHub)

Obiectives Live Demo



Available only during the seminar from 23rd to 25th of March 2022

Conclusion & Perspectives

Detect and characterize mutations and thus

Integrate and synthesize data or results from

secondary and tertiary structure analyses

Collaborate with wet-lab experimental structural

- VIMVer will be soon available to the general public
- Interactive alignment

doi:10.1073/pnas.2104241118.

- Extend the Database with more variants of SARS-CoV-2, and with even more viral species.
- Connect this project to another annotation database for viral sequences: VaZvMolo (5)

(1), Rochman, Nash D., et al. "Ongoing global and regional adaptive evolution of SARS-CoV-2," Proc. Natl. Acad. Sci. U.S.A., vol. 118, no. 29, 20 July 2021.

(2) Rambaut, A., Holmes, E.C., O'Toole, Á. et al. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. Nat Microbiol 5 1403-1407 (2020), https://doi.org/10.1038/s41564-020-0770-5 (3). "BLAST: Basic Local Alignment Search Tool." 17 Mar. 2022, blast.ncbi.nlm.nih.gov/Blast.cgi

(4). Edgar, Robert C. "MUSCLE: multiple sequence alignment with high accuracy and high throughput." Nucleic Acids Res., vol. 32, no. 5, 2004, p. 1792 (5). Ferron, François, et al. "VaZyMoIO: a tool to define and classify modularity in viral proteins." J. Gen. Virol., vol. 86, no. Pt, Mar. 2005, p. 3.

doi:10.1099/vir.0.80590-0. (6). "Severe acute respiratory syndrome coronavirus 2 TKYTK1734 2021 genomic - Nucleotide - NCBI." 17 Mar. 2022,

www.ncbi.nlm.nih.gov/nuccore/LC633760.1.

Results Input

CGATCATCAGCACATCTAGGTTTTGTCCGGGTGTGACCGAAAGGTAAGATGAGAGACCTTGTCCCTC TTAATGAGAAAATATACGTCCAACTCAGTTTGCCTGTTTTACAGGTTCGCGACGTGCTCGTACGTGC TAGAAGTTGAAAAAGGCGTTTTGCCTCAACTTGAACAGCCCTATGTGTGTCATCAAACGTTCGGATGCT GGTGAGACACTTGGTGTCCTTGTCCCTCATGTGGGCGAAATACCAGTGGCTTACCGCAAGGTTCTTCT CGAGCTTGGCACTGATCCTTATGAAGATTTTCAAGAAAACTGGAACACTAAACATAGCAGTGGTGTTA CGTGAACTCATGCGTGAGCTTAACGGAGGGGCATACACTCGCTATGTCGATAACAACTTCTGTGGCCC ACAACTGGACTTTATTGACACAGAGGGGGTGTATACTGCTGCCGTGAACATGAGGATGAAATTGCTT

GACACCTTCATGGGGAATGTCCAAATTTTGTATTTCCCTTAAATTCCATAATTCAATCATATCAAGACATTCAACCAA TTGAAAAGAAAAAGCTTGATGGCTTTATGGGTAGAATTCGATCTGTCTATCCAGTTGCGTCACTAA NATGCAACCAAATGTGCCTTTCAACTCTCATGAAGTGTGATCATTGTGGTGAAACTTCATGGCAGACC TGATTTTGTTAAAGCCACTTGCGAATTTTGTGGCACTGAGAATTTGACTAAAGAAGGTGCCACTACT

AGCATAGTCTTGCCGAATACCATAATGAATCTGGCTTGAAAACCATTCTTCGTAAGGGTGGTCGCAC



NC 045512.2:265..805:540 [ORF1ab:leader protein] nucl score length identity 540 540 100.00%

NC 045512.2:805..2719:1914 [ORF1ab:nsp2] nucl core length identity 908 1914 99.90% Mutant

Display

Protein Nucleotide