

Mathematical Analysis of the competition among different Variants of SARS-CoV-2 in European Countries

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Countries across Europe suffered different waves of COVID-19 during the pandemic [1]. Such countries experienced similar variants of the SARS-CoV-2 virus as the pandemic evolved over time, including pre-Alpha, Alpha, Delta, and Omicron, with various lineages such as BA1, BA2, BA5 and BQ.1.

We employ a mathematical modeling approach based on non-interactive epidemics of the different variants to analyze the transmissibility of these variants in Europe over a period of more than two years, from late 2020 to early 2023. Weekly sequencing data from 28 European countries were used to estimate the difference on the transmission rate $\Delta\beta$ between different variants of SARS-CoV-2, specifically between pre-Alpha vs Alpha, Alpha vs Delta, and Delta vs Omicron. Sub-lineages of Omicron (BA1, BA2, BA5 and BQ.1) were also analyzed within 16 European countries. An example of such analysis is shown in Fig.1 for the particular case of France. The number of samples analyzed in France is shown in the top panel, and the resulting variants are shown with a different color code. The fraction of each variant with respect the total is shown in middle panel, which permit us to define the substitution model and calculate the increase of the trasmissibility between two variants. Finally, the dynamics among the variants can be compared with the total number of cases and the corresponding reproductive number of the epidemics, see botton panel

The study found that the transmission rate of SARS-CoV-2 increases as the virus evolves, $\Delta\beta_\alpha < \Delta\beta_\delta < \Delta\beta_o$. Furthermore, the transmission rate tends to be higher in smaller countries than in larger ones, thats why multiple substitution, spatially, and temporally separated are also studied.

Analyzing the transmission rates of different variants can provide insights into factors that influence the spread of the virus and it can be compared with hospitalization rates to

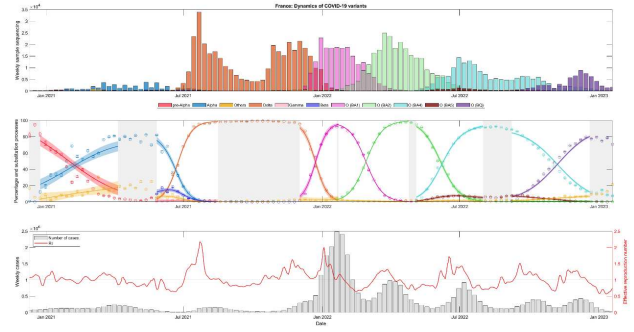


Fig. 1. Dynamical evolution of the differnt variants of SARS-CoV-2 in France over time. Weekly sample sequencing of the differnt variants (top); real percentage data of eahc variant compared witht the mathematical substitution model (middle); and weekly total cases together with the associated effective reproduction number (bottom).

assess the decrease of the severity of the differnt variants [2].

[1] M Catal, S Alonso, E Alvarez-Lacalle, D Lpez, PJ Cardona, C Prats *Empirical model for short-time prediction of COVID-19 spreading*, Plos computational biology **16** (12), e1008431 (2010).

[2] M Catal, E Coma, S Alonso, C Andrs, I Blanco, A Antn, AE Bordoy, P.J. Cardona, F. Fina, E. Martr, M. Medina, N. Mora, V. Saludes, C. Prats, D. Prieto-Alhambra, E. Alvarez-Lacalle *Transmissibility, hospitalization, and intensive care admissions due to omicron compared to delta variants of SARS-CoV-2 in Catalonia: A cohort study and ecological analysis*, Frontiers in public health, 2490 (2022).