

Topological Surveillance of Recurrent Mutations in SARS-CoV-2

CoVtRec report as of 29 January 2023

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Abstract

The appearance of new variants of the coronavirus SARS-CoV-2 in the current COVID-19 pandemic underlines the importance of being able to quickly identify mutations that could confer some adaptive advantage to the virus, such as immune evasion or higher infectivity. Here we apply CoVtRec, a fast and scalable early warning system based on Topological Data Analysis, for the identification and surveillance of emerging potentially adaptive mutations in the ongoing evolution of SARS-CoV-2. CoVtRec is based on a new topological approach to the study of recurrent mutations in large genomic datasets developed in [1].

Results

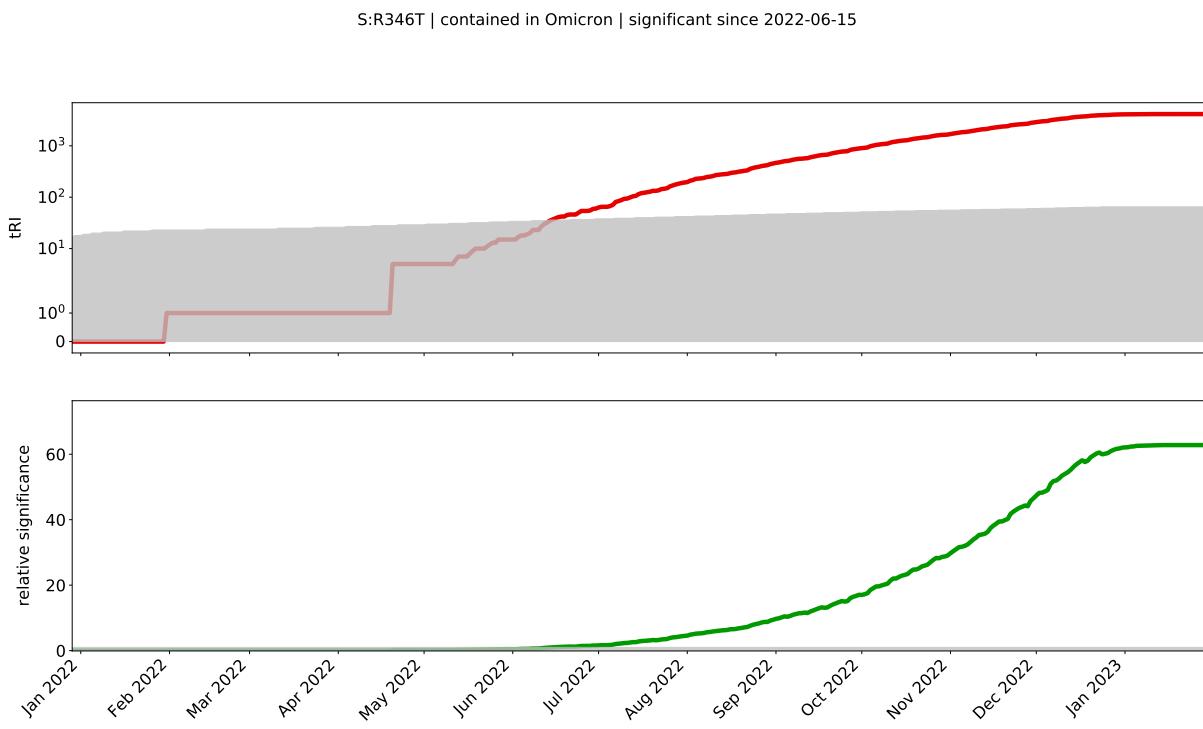
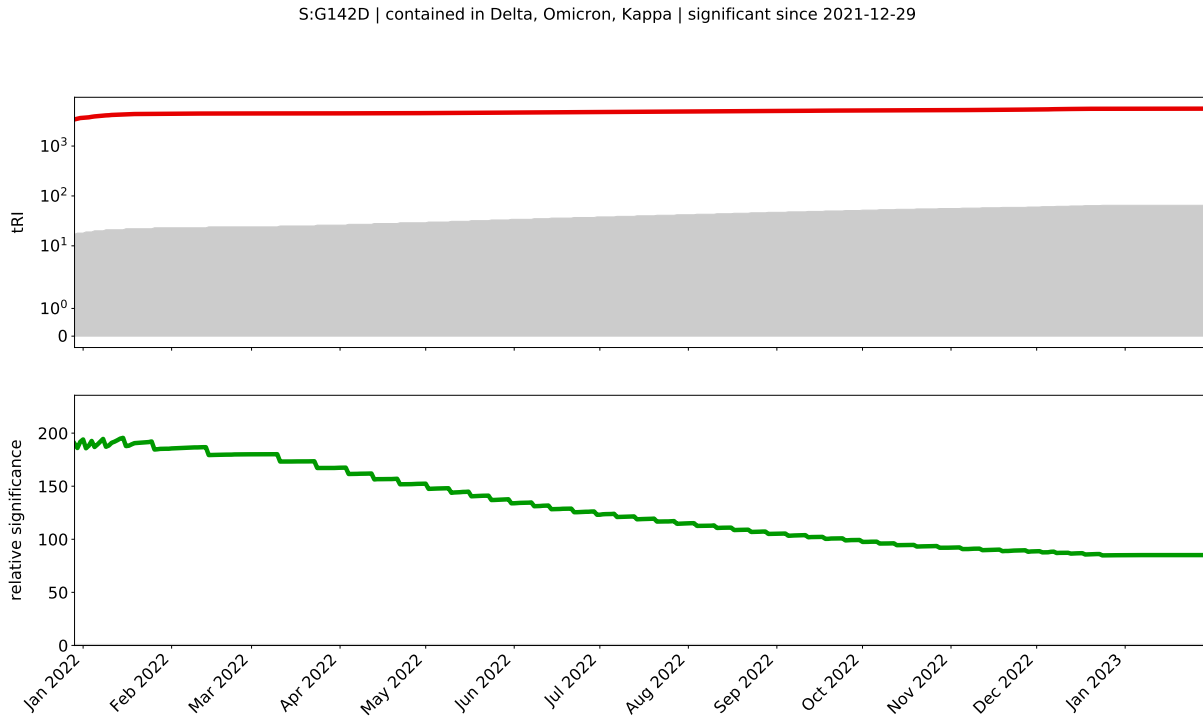
We analyzed topological signals for the ongoing convergent evolution of the coronavirus SARS-CoV-2 on the Spike gene from 29 December 2021 until 29 January 2023. To that end, we performed a topological recurrence analysis for a curated alignment of 13,250,133 high-quality SARS-CoV-2 Spike gene sequences shared via GISAID, the global data science initiative [2, 3]. For each Spike mutation we computed its topological recurrence index (tRI) and the corresponding time series analysis chart. The topological recurrence index is a topological measure for the potential adaptiveness of a given mutation (see [1, 4] for details).

We present a list featuring the top ten amino acid variations on the Spike gene that show strongest topological recurrence index as of 29 January 2023 (see [Table 1](#)). Here signals with $tRI \geq 66$ are statistically significant ($p < 0.05$). It was demonstrated in [1] that these mutations are potentially adaptive in the current phase of the pandemic and might therefore appear in future variants. We also present time series analysis charts (see [Figure 1](#)) showing (i) the development of the topological signal as well as its significance over time, (ii) major lineages containing the mutation, and (iii) the date from which on the topological signal became significant.

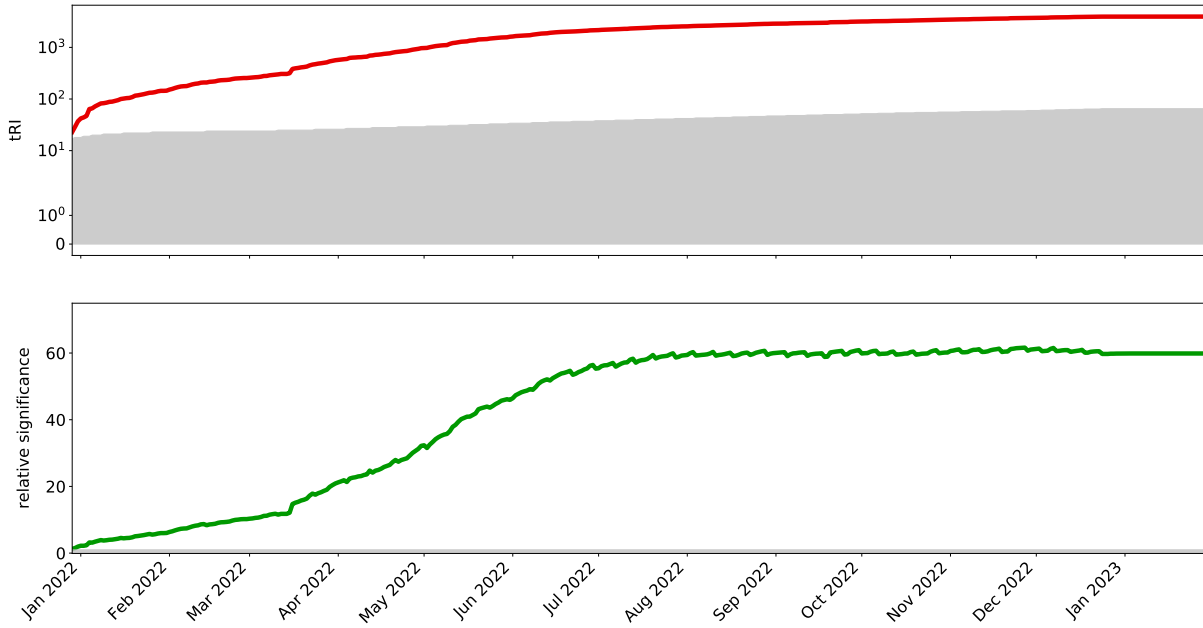
SAAV	tRI	relative significance	notable variants
G142D	5616	85.1	Delta, Omicron, Kappa
R346T	4144	62.8	Omicron
N440K	3951	59.9	Omicron
L5F	3551	53.8	Iota
R408S	3165	48.0	Omicron
T95I	2838	43.0	Delta, Omicron, Iota, Kappa, Mu
A1020S	1690	25.6	
N658S	1628	24.7	
T76I	1625	24.6	Lambda
K417N	1548	23.5	Beta, Omicron, Mu

Table 1. The top ten amino acid changes on the Spike gene showing strongest topological recurrence index as of 29 January 2023. For a given mutation, the table displays its topological recurrence index (tRI), its relative significance, and notable variants containing the mutation.

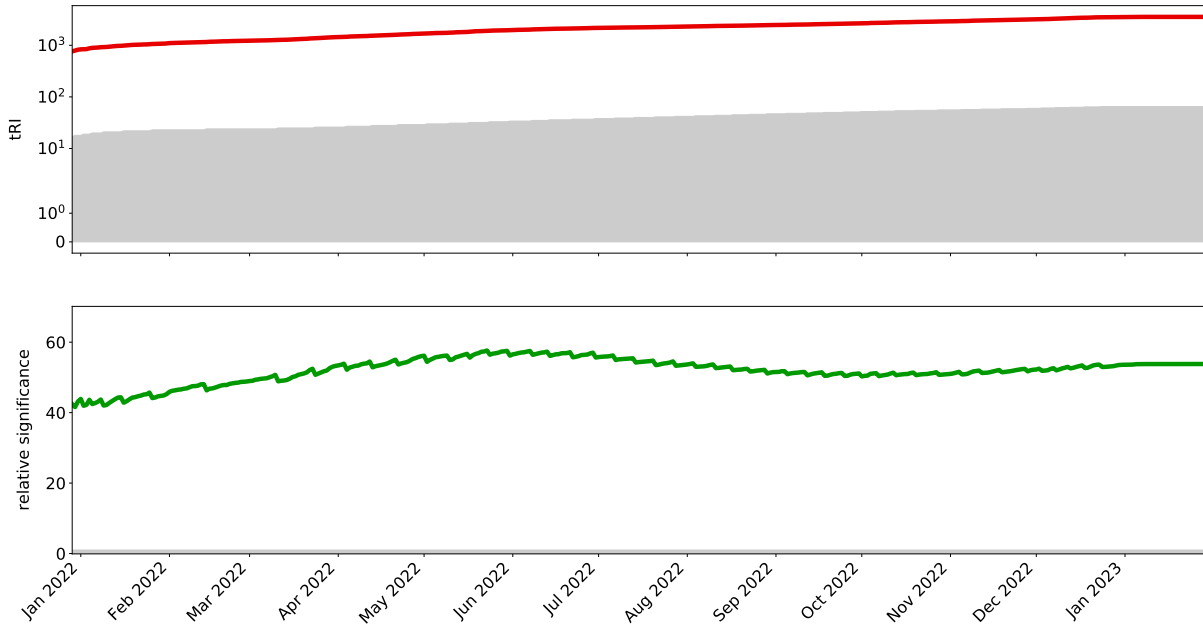
Figure 1. Time series analysis charts for the mutations listed in [Table 1](#). Each chart shows the topological recurrence index (red) and its relative significance (green) from 29 December 2021 until 29 January 2023. In each chart, in the upper diagram the shaded region marks the level of significance.



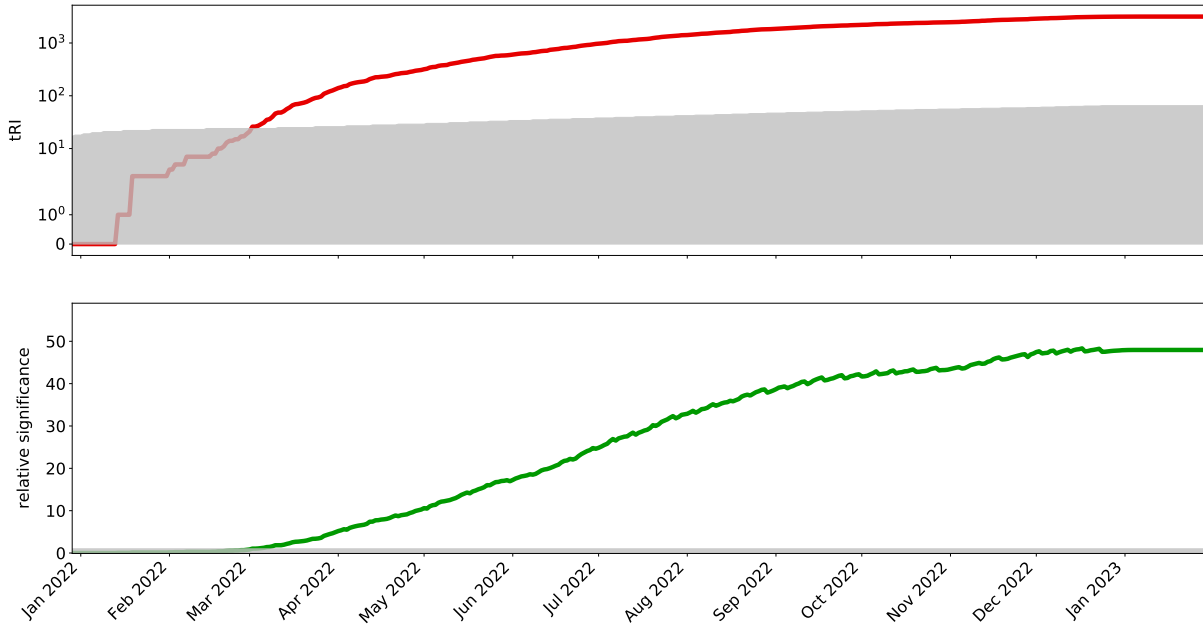
S:N440K | contained in Omicron | significant since 2021-12-29



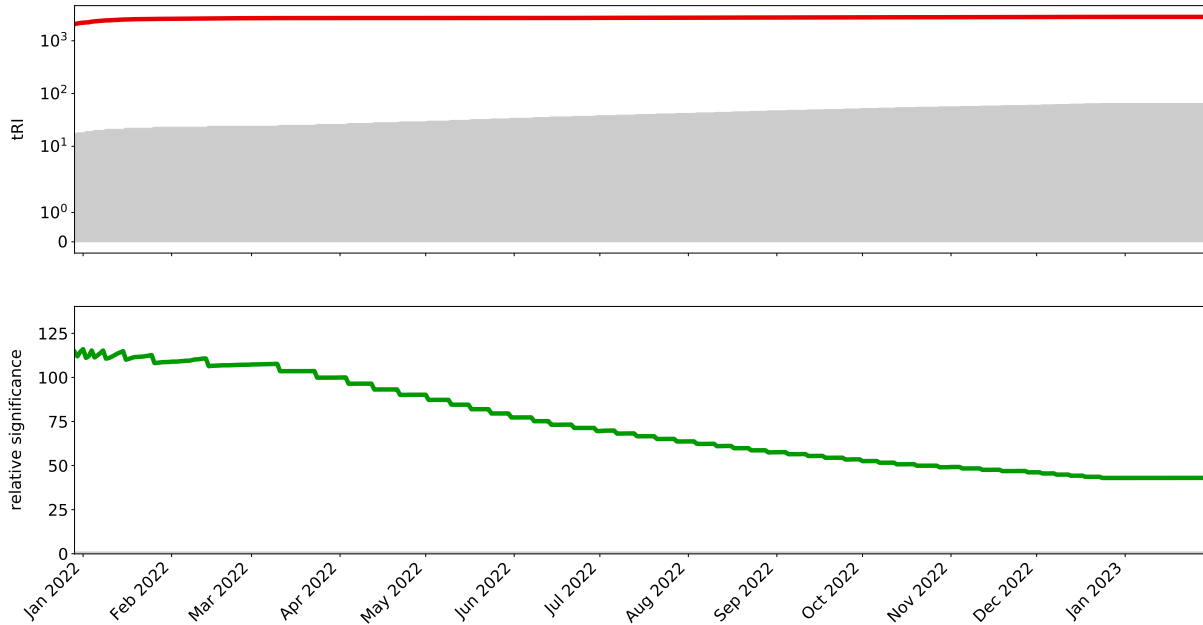
S:LSF | contained in Iota | significant since 2021-12-29



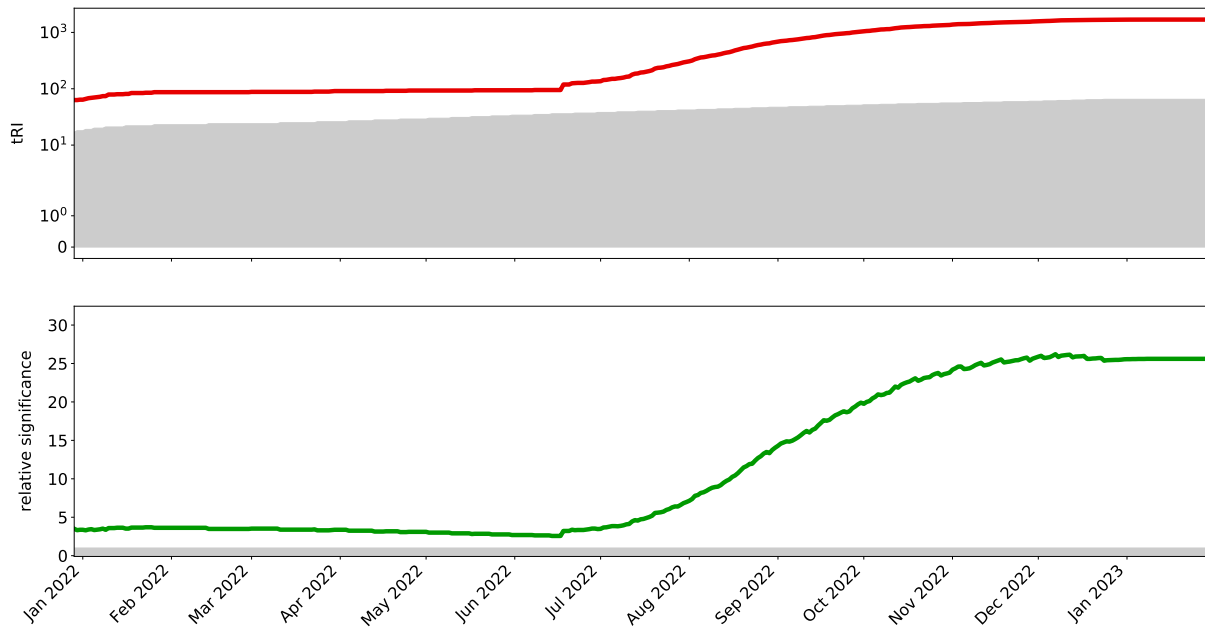
S:R408S | contained in Omicron | significant since 2022-03-02



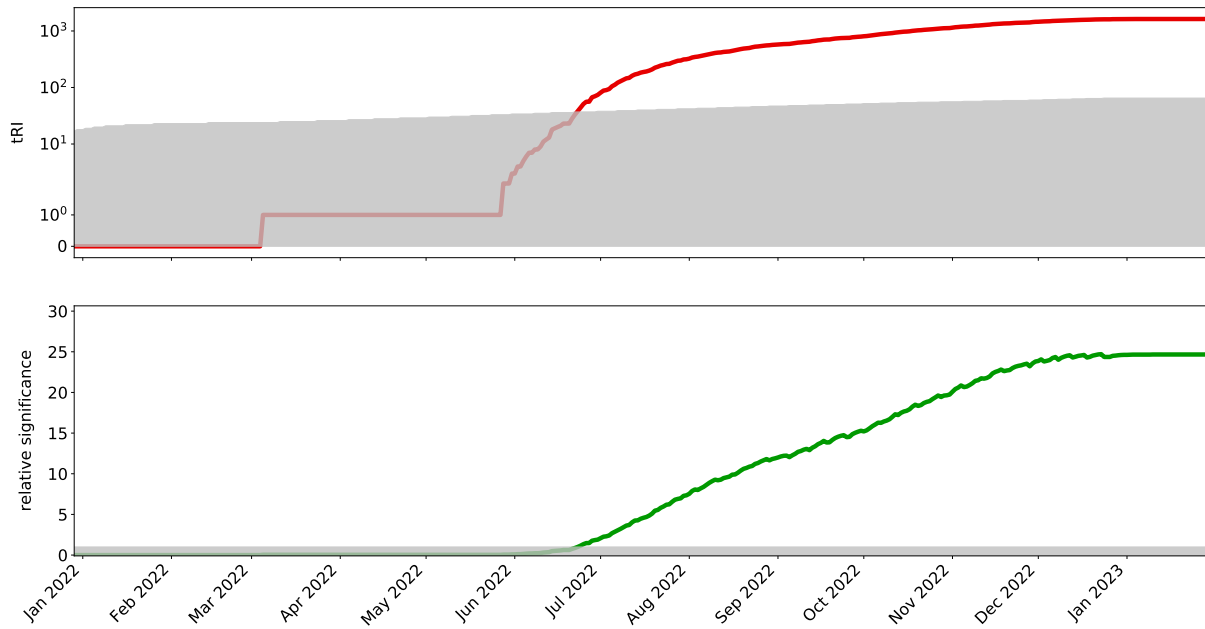
S:T95I | contained in Delta, Omicron, Iota, Kappa, Mu | significant since 2021-12-29



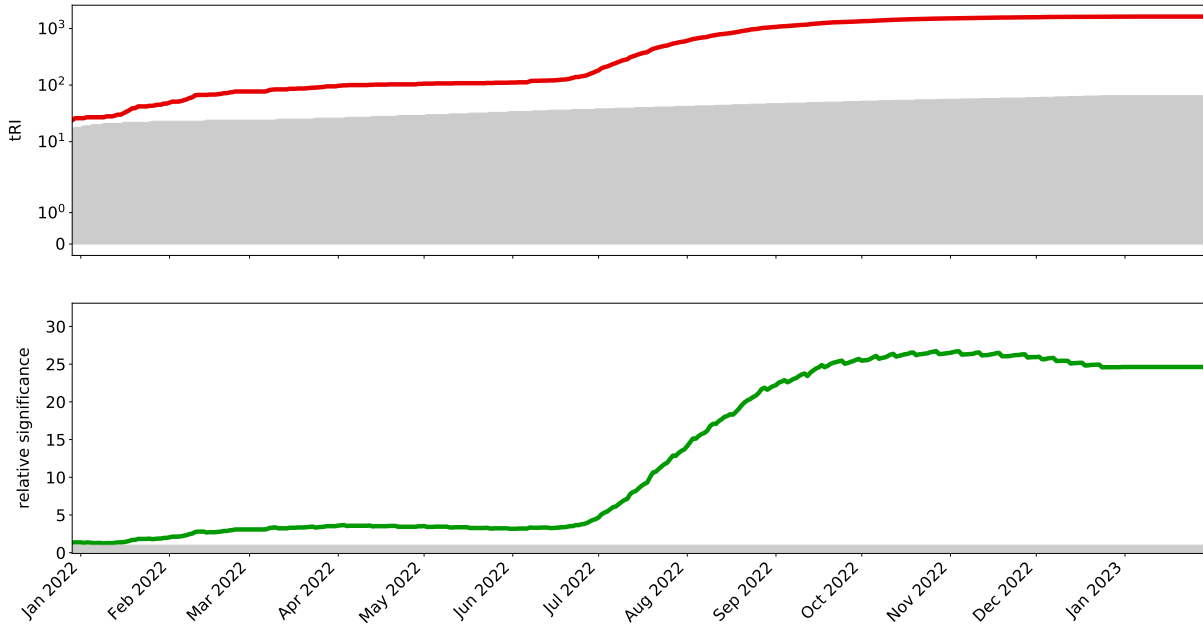
S:A1020S | significant since 2021-12-29



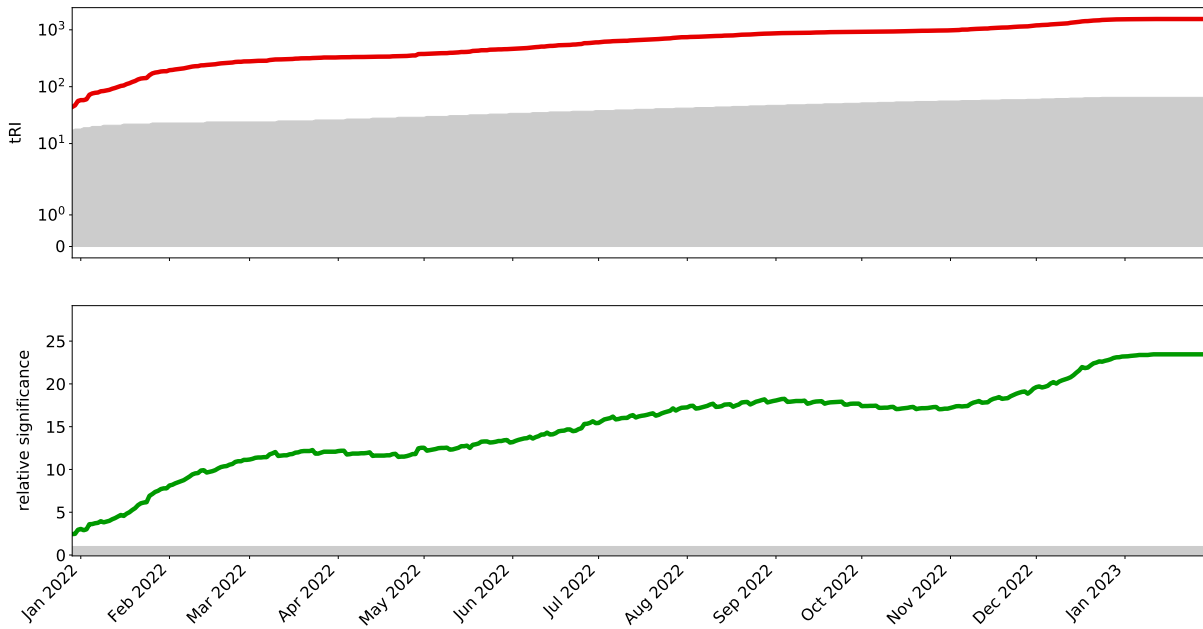
S:N658S | significant since 2022-06-23



S:T76I | contained in Lambda | significant since 2021-12-29



S:K417N | contained in Beta, Omicron, Mu | significant since 2021-12-29



Methods

Data acquisition and data preparation

Our analysis is based on the alignment `msa_0129.fasta` downloaded from the GISAID EpiCoV Database [2, 3] on 31 January 2023. This alignment comprises 13,250,133 SARS-CoV-2 whole genome sequences that have been aligned to the reference sequence Wuhan/WIV04 with GISAID accession number EPI_ISL_402124 using MAFFT [5]. Sequences in this alignment were truncated to the Spike gene (reference site positions 21,563 to 25,384), and subsequently sequences containing any characters other than A, C, T, G or - were removed. This resulted in an alignment comprising 4,520,649 complete SARS-CoV-2 Spike genes of length 7,740nt. A list of accession numbers of all sequences in this alignment, along with an acknowledgement of the contributions of both the submitting and the originating laboratories, is accessible at <https://doi.org/10.55876/gis8.230210cf>.

Topological recurrence analysis

The Spike gene alignment contains 252,412 genetically distinct sequences. We used `Hammingdist` (Version 0.18.0) [6] to compute the genetic distance matrix of this alignment. Subsequently we used `Ripser` [7] to compute the representative cycles for the persistent homology of the Vietoris–Rips filtration associated to the genetic distance matrix. The computation of persistence barcodes was restricted to small genetic distance scales (`Ripser` scale parameter threshold set to 2). Next a complete list of SNV cycles (topological cycles all of whose edges correspond to single nucleotide variations) in the given alignment was generated from the corresponding `Ripser` output. Then we used custom code implemented in Python to compute the *topological recurrence index (tRI)* for each such SNV. Summing over all SNVs determining an SAAV (single amino acid variation), we computed the tRI for each SAAV. Lastly, from the distribution of the tRI measurements over the whole Spike gene we inferred the level of significance for the tRI per SAAV. For each SAAV, its *relative significance* is then defined as the quotient of its tRI by the level of significance. Using Vietoris–Rips transformations in multipersistent homology, we computed tRI time series analysis charts at daily resolution from the natural stratification by time of genomic data. For a more detailed description of the topological recurrence analysis see [1, 4].

Data availability

All SARS-CoV-2 genome data used in this work are available from the GISAID EpiCov Database [2, 3] at <https://www.gisaid.org> and are accessible at <https://doi.org/10.55876/gis8.230210cf>.

Code availability

Code used for the analyses is available at <https://github.com/ssciwr/hammingdist> and <https://github.com/Ripser/ripser/tree/tight-representative-cycles>. All other code is available from the corresponding authors upon request.

Acknowledgements

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Author contributions

M.B., L.H., M.N., A.O. designed the study; A.O. curated data; A.O. performed computational analyses; M.B., L.H., M.N., A.O., S.B., H.O., M.S., R.C. developed and implemented software; M.B., L.H., A.O. acquired computing resources; M.B., L.H., A.O., M.N. drafted the manuscript; all authors contributed to the final version of the report.

Competing interests

The authors declare no competing interests.

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